
# The 2nd EITA-Bio Conference

(The EITA-Bio 2012)

# "Recent Advances in Biomedical Research"

## Conference Proceedings

The Frick Chemistry Laboratory
Princeton University
Princeton, New Jersey, U.S.A.

Saturday-Sunday, October 27-28, 2012

## Table of Content

# Planning Committee

## General Conference Chair

| | | |
|---|---|---|
| Wei-Jen Tang | (湯惟仁) | The University of Chicago |
| Haw Yang | (楊　皓) | Princeton University |

## Conference Organizers

| | | |
|---|---|---|
| Shiou-Chuan (Sheryl) Tsai | (蔡秀娟) | University of California, Irvine |
| Sun-Yuan Kung | (貢三元) | Princeton University |
| Howard Chen | (陳　浩) | IBM T.J. Watson Research Center |
| Li-San Wang | (王立三) | University of Pennsylvania |
| Jung-Chi Liao | (廖仲麒) | Columbia University |
| Jerry K. Chen | (陳寬享) | TECRO in the U.S. |
| James H. Chang | (張和中) | TECRO in the U.S. |
| Kevin K. H. Wei | (魏光勛) | Taiwan Trade Center, New York |
| Chih-Hao Hsia | (夏志豪) | Princeton University |
| Amy Wu | (吳映嫻) | Princeton University |
| Hsin-Jung (Sophia) Li | (李欣融) | Princeton University |
| Ai-Lei Sun | (孫愛蕾) | Princeton University |
| Shuay-Pwu Ho | (何率菩) | Princeton University |

## Project Manager

| | | |
|---|---|---|
| Li-San Wang | (王立三) | University of Pennsylvania |

## Program Steering Committee

| | | |
|---|---|---|
| Ruby B. Lee | (李佩露) | Princeton University |
| Gene-Jack Wang | (王俊傑) | Brookhaven National Laboratory |
| Chyung-Ru Wang | (王瓊如) | Northwestern University |

## Program Committee - Workshop Chairs

### Workshop 1: In Silico Research and Biomedical Informatics

| | | |
|---|---|---|
| Jhih-Wei Chu | (朱智瑋) | University of California at Berkeley |
| Li-San Wang | (王立三) | University of Pennsylvania |

### Workshop 2: Biomedical Science and Engineering

| | | |
|---|---|---|
| Chyung-Ru Wang | (王瓊如) | Northwestern University |
| Tso-Pang Yao | (姚佐邦) | Duke University |

### Workshop 3: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS

| | | |
|---|---|---|
| Jeff Tza-Huei Wang | (王澤輝) | Johns Hopkins University |
| Fan-Gang Tseng | (曾繁根) | National Tsing Hua University |

## Conference Manager

| | | |
|---|---|---|
| Hsin-Jung (Sophia) Li | (李欣融) | Princeton University |

## Publication

### Publication Manager

| | | |
|---|---|---|
| Woei-Jyh (Adam) Lee | (李偉智) | National Institutes of Health |

### Conference Program

| | | |
|---|---|---|
| Woei-Jyh (Adam) Lee | (李偉智) | National Institutes of Health |

### Conference Proceedings

| | | |
|---|---|---|
| Fanny Yuk-Yee Leung | (梁玉儀) | University of Pennsylvania |
| Kaijia Cao | (曹卡佳) | University of Pennsylvania |
| Chiao-Feng Lin | (林嬌鳳) | University of Pennsylvania |

## Conference Treasurer

Chinese Institute of Engineers – USA, Greater New York Chapter (CIE-USA/GNYC)
(美洲中國工程師學會大紐約分會)

## Local Management (Student Volunteers)

| | | |
|---|---|---|
| Yu-Cheng Tsai | (蔡佑錚) | Princeton University |
| Chung-Yang Huang | (黃仲揚) | Princeton University |
| Che-Yu Liu | (劉哲宇) | Princeton University |
| Oliver Huang | (黃　皓) | Princeton University |
| Po-Hsuan Chen | (陳柏亘) | Princeton University |
| Jen-Tang Lu | (呂任棠) | Princeton University |
| YenTing Chiu | (邱雁亭) | Princeton University |
| Ching-Yu Chen | (陳靜妤) | Princeton University |
| | (陳天立) | Princeton University |
| Ben Lee | | Princeton University |
| Kimberly Chen | | Princeton University |

## On-Site Registration

Princeton Association of Taiwanese Students
(普林斯頓大學台灣同學會)

## General Inquiries & Pre-registration

Investment & Trade Office, TECRO in the U.S.
(駐美投資貿易服務處)

## Web Operations

| | | |
|---|---|---|
| Michael Hwa-Han Wang | (王華漢) | EBMedia, L.L.C. |

## Workshop Topics

The EITA-Bio 2012 at Princeton University consists of following 3 parallel workshops:

- **Workshop 1 (W1)**: In Silico Research and Biomedical Informatics
- **Workshop 2 (W2)**: Biomedical Science and Engineering
- **Workshop 3 (W3)**: Bio-Materials, Bio-Nanotech, Bio-NEMS, Bio-MEMS

# Conference Program

## Day 1 (Saturday, October 27, 2012)

**10/27 (Sat) 8:00 am - 6:00 pm: Registration**
Room: The Frick Atrium

**10/27 (Sat) 8:30 am - 9:50 am: Opening Session**

Chair: **Dr. Wei-Jen Tang**, Ben May Department for Cancer Research, The University of Chicago (芝加哥大學生物醫學研究所湯惟仁教授)
Room: The Taylor Auditorium

**Dr. Ruby B. Lee**, Department of Electrical Engineering, Princeton University (普林斯頓大學電機系李佩露教授)

**10/27 (Sat) 9:50 am - 11:10 am: Plenary Session (1)**

Chair: **Dr. Ruby B. Lee**, Department of Electrical Engineering, Princeton University (普林斯頓大學電機系李佩露教授)
Room: The Taylor Auditorium

"Neurodegenerative Disease Genetics; GWAS, Exomes and Beyond"
**Dr. Gerard D. Schellenberg**
Professor, The Department of Pathology and Laboratory Medicine
The Perelman School of Medicine
The University of Pennsylvania

"Biophotonics Imaging Platforms towards Translational Applications"
**Dr. Xingde Li**
Professor, Department of Biomedical Engineering
Johns Hopkins University
(约翰霍普金斯大学生物医学工程系李兴德教授)

**10/27 (Sat) 11:10 am - 11:25 am: Break**
Room: The Frick Atrium

**10/27 (Sat) 11:25 am – 12:45 pm: Plenary Session (2)**

Chair: Dr. Sun-Yuan Kung, Department of Electrical Engineering, Princeton University (普林斯頓大學電機系貢三元教授)
Room: The Taylor Auditorium

"From the Era of Gigabyte Data to the Era of Petabyte Data: Are we ready for the next generation sequencing data?"
**Dr. Yu Shyr**
Director, Vanderbilt Center for Quantitative Sciences
Associate Director for Quantitative Sciences Integration, VICC
Ingram Professor of Cancer Research
Professor, Department of Biostatistics, Biomedical Informatics, Cancer Biology and Preventive Medicine
Vanderbilt University
(范德堡大學癌症中心生物統計主任石瑜教授)

"Combination of Genomic Technologies and Bioinformatics for Exploring New Cancer Biomarkers"
**Dr. Eric Y. Chuang**
Professor and Director, Graduate Institute of Biomedical Electronics and Bioinformatics
Department of Electrical Engineering
National Taiwan University

(臺灣大學生醫電子與資訊學研究所所長莊曜宇教授)

**10/27 (Sat) 12:45 pm - 2:15 pm: Lunch**
Room: The Frick Atrium

**Parallel Sessions:**
**10/27 (Sat) 2:15 pm – 3:35 pm: Technical Session D1-W1-T1: In Silico Research and Biomedical Informatics**
Chair: **Dr. Jhih-Wei Chu**, Department of Chemical and Biomolecular Engineering, University of California, Berkeley (加州大學柏克萊分校化學及分子生物工程系朱智瑋教授)
Room: 124

"How Important is Each Behavior of the AADE7?"
**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**)**

**Dr. Yi-Hsiang (Sean) Hsu**
Assistant Professor, School of Medicine
Harvard University
(哈佛大學醫學院許益祥教授)

**10/27 (Sat) 2:15 pm – 3:35 pm: Technical Session D1-W2-T1: Biomedical Science and Engineering**
Chair: **Dr. Chyung-Ru Wang**, Department of Microbiology and Immunology, Feinberg School of Medicine, Northwestern University (西北大學醫學院王瓊如教授)
Room: 224

"The Addiction-obesity Connection Viewed in the Light of Medical Imaging"
**Dr. Gene-Jack Wang**
Senior Scientist and Chair, Medical Department
Brookhaven National Laboratory
(美國國家布魯克海文實驗室醫學部主任王俊傑醫師)

"Brain Imaging of Cognitive Control"
**Dr. Chiang-shan Ray Li**
Associate Professor, Department of Psychiatry and of Neurobiology
School of Medicine, Yale University
(耶魯大學醫學院精神病學及神經生物學系李江山教授)

"Mechanisms of Epigenetic Regulation"
**Dr. Hua-Ying Fan**
Assistant Professor, Department of Biochemistry and Biophysics
The Perelman School of Medicine, the University of Pennsylvania
(賓州大學醫學院生物化學與生物物理系范華英教授)

**10/27 (Sat) 2:15 pm – 3:35 pm: Technical Session D1-W3-T1: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS**
Chair: **Dr. Gou-Jen Wang**, Department of Mechanical Engineering and Graduate Institute of Biomedical Engineering, National Chung-Hsing University (中興大學機械工程學系王國禎特聘教授)
Room: 324

"Epidermal Electronics"
**Dr. Nanshu Lu**
Assistant Professor, Department of Aerospace Engineering and Engineering Mechanics

Texas Materials Institute, The University of Texas at Austin
(德克萨斯州大学奥斯汀分校航空和工程力学系与德克萨斯州材料研究所鲁南姝教授)

“Label-Free Coloring Biofluids on Nanophotonic Device”
**Dr. Gang Logan Liu**
Assistant Professor, Department of Electrical and Computer Engineering and Bioengineering
University of Illinois at Urbana-Champaign

“Programmable Microcapsules”
**Dr. Daeyeon Lee**
Assistant Professor, Department of Chemical and Biomolecular Engineering
The University of Pennsylvania

**10/27 (Sat) 3:35 pm – 3:50 pm: Break**
Room: The Frick Atrium

**Parallel Sessions:**
**10/27 (Sat) 3:50 pm – 5:10 pm : Technical Session D1-W1-T2: In Silico Research and Biomedical Informatics**
Chair: **Dr. Li-San Wang**, Department of Pathology and Laboratory Medicine, The Perelman School of Medicine, the University of Pennsylvania (賓州大學醫學院王立三教授)
Room: 124

“Biomedical Image Processing and Neuronal Structures Analysis”
**Dr. Yu-Tai Ching**
Director, Institute of Biomedical Engineering
National Chiao Tung University
(交通大學生醫工程研究所所長荊宇泰教授)

“Analysis of Retinal Development using RNA-seq”
**Dr. Li Cai**
Associate Professor, Department of Biomedical Engineering
Rutgers University

**Dr. Jessica C. Mar**
Assistant Professor, Departments of Systems & Computational Biology and
Department of Epidemiology & Population Health
Albert Einstein College of Medicine of Yeshiva University

**10/27 (Sat) 3:50 pm – 5:10 pm: Technical Session D1-W2-T2: Biomedical Science and Engineering**
Chair: **Dr. Tso-Pang Yao**, Department of Pharmacology and Cancer Biology, Duke University Medical Center (杜克大學醫學中心姚佐邦教授)
Room: 224

“Control of Retinal Progenitor Fates by Transcription Factors and Notch Signaling”
**Dr. Mengqing Xiang**
Professor, Center for Advanced Biotechnology and Medicine & Department of Pediatrics
UMDNJ-Robert Wood Johnson Medical School
(新泽西州罗伯屋强森医学院高级生物技术与医学中心与儿科系向孟清教授)

**Dr. Wenqin Luo**
Assistant Professor, Department of Neuroscience
The Perelman School of Medicine, the University of Pennsylvania
(宾夕法尼亚大学医学院神经科学系罗文琴教授)

"The Role of Natural Killer T Cells in Intestinal Inflammation"
**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)

**10/27 (Sat) 3:50 pm – 5:10 pm : Technical Session D1-W3-T2: Bio-Materials. Bio-Nanotechnology/Bio-NEMS/Bio-MEMS**

Chair: **Dr. Fan-Gang Tseng**, Department of Engineering and System Science and Biomedical Technology Research Center, National Tsing-Hua University (清華大學工程與系統科學系主任曾繁根教授)
Room: 324

"Electric Tweezers"
**Dr. Donglei (Emma) Fan**
Assistant Professor, Department of Mechanical Engineering
The University of Texas, Austin

"Single-Cell Bio-MEMS for Systems Oncology"
**Dr. Rong Fan**
Assistant Professor, Department of Biomedical Engineering
Yale University
(耶魯大學生物醫學工程系樊榮教授)

"Photothermal Nanoblade for Single Cell Surgery and Cargo Delivery"
**Dr. Pei-Yu (Eric) Chiou**
Associate Professor, Department of Bioengineering
University of California, Los Angeles
(加州大學洛杉磯分校生物工程系邱培鈺教授)

## Day 2 (Sunday, October 28, 2012)

**10/28 (Sun) 9:00 am - 12:45 pm: Registration**
Room: The Frick Atrium

**Parallel Sessions:**
**10/28 (Sun) 9:50 am – 11:10 am: Technical Session D2-W1-T1: In Silico Research and Biomedical Informatics**
Chair: **Dr. Jhih-Wei Chu**, Department of Chemical and Biomolecular Engineering, University of California, Berkeley (加州大學柏克萊分校化學及分子生物工程系朱智瑋教授)
Room: 124

"Integrative Bioinformatics for Knowledge Discovery of PTM Networks"
**Dr. Cathy H. Wu**
Edward G. Jefferson Chair and Director, Center for Bioinformatics & Computational Biology
University of Delaware
(德拉威爾大學生物資訊及計算系統生物中心主任吳慧華教授)

"Data Mining in RNA Informatics"
**Dr. Jason Tsong-Li Wang**
Professor, Department of Computer Science
Director, Data and Knowledge Engineering Lab and Bioinformatics Center
New Jersey Institute of Technology
(紐澤西理工學院電腦科學系暨數據知識工程實驗室及生物資訊中心主任王中力教授)

"Computational Methods for Studying In Vivo Macromolecular Motion"
**Dr. Edmond Chow**
Associate Professor, School of Computational Science and Engineering
Georgia Institute of Technology

**10/28 (Sun) 9:50 am – 11:10 am: Technical Session D2-W2-T1: Biomedical Science and Engineering**
Chair: **Dr. Chyung-Ru Wang**, Department of Microbiology and Immunology, Feinberg School of Medicine, Northwestern University (西北大學醫學院王瓊如教授)
Room: 224

"Menin, a Contextual Tumor Suppressor and Promoter in Controlling Endocrine Tumor and Leukemia"
**Dr. Xianxin Hua**
Associate Professor, Department of Cancer Biology
University of Pennsylvania Perelman School of Medicine

**Dr. Jianming Hu**
Professor, Department of Microbiology and Immunology
College of Medicine
The Pennsylvania State University

"Mitochondrial Quality Control and its Disease Implication"
**Dr. Tso-Pang Yao**
Professor, Department of Pharmacology and Cancer Biology
Duke University Medical Center
(杜克大學醫學中心姚佐邦教授)

**10/28 (Sun) 9:50 am – 11:10 am: Technical Session D2-W3-T1: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS**
Chair: **Dr. Fan-Gang Tseng**, Department of Engineering and System Science and Biomedical Technology Research Center, National Tsing-Hua University (清華大學工程與系統科學系主任曾繁根教授)

Room: 324

**Dr. Nicholas X. Fang**
Associate Professor, Department of Mechanical Engineering
Massachusetts Institute of Technology
(麻省理工学院机械工程系方绚莱教授)

"Optofluidic Lasers: Principles and Applications"
**Dr. Xudong (Sherman) Fan**
Associate Professor, Department of Biomedical Engineering
University of Michigan, Ann Arbor
(密歇根大学安娜堡分校生物医学工程系范旭东教授)

"Miniature MEMS-scanned Dual-axis Confocal Microscopy for Guiding Tumor Resection"
**Dr. Jonathan T.C. Liu**
Assistant Professor and Director, Molecular Biophotonics Lab
Department of Biomedical Engineering
The State University of New York, Stony Brook

**10/28 (Sun) 11:10 am – 11:25 am: Break**
Room: The Frick Atrium

**Parallel Sessions:**
**10/28 (Sun) 11:25 am – 12:45 pm: Technical Session D2-W1-T2: In Silico Research and Biomedical Informatics**
Chair: **Dr. Li-San Wang**, Department of Pathology and Laboratory Medicine, The Perelman School of Medicine, the University of Pennsylvania (賓州大學醫學院王立三教授)
Room: 124

"Statistical Methods to Infer Drug Target Pathways from High Throughput Data"
**Dr. Hongyu Zhao**
Chair, Biostatistics Division
Professor of Public Health (Biostatistics), of Genetics and of Statistics
School of Public Health
Yale University
(耶魯大學醫學院生物統計組主任趙宏宇教授)

"Flexible Methods for Assessing Interactions in Genetic Association Studies"
**Dr. Michael Chiao-An Wu**
Assistant Professor, Department of Biostatistics
The University of North Carolina at Chapel Hill
(北卡萊羅納大學教堂山分校生物統計系吳肇安教授)

**Dr. Jhih-Wei Chu**
Assistant Professor, Department of Chemical and Biomolecular Engineering
University of California, Berkeley
(加州大學柏克萊分校化學及分子生物工程系朱智瑋教授)

**10/28 (Sun) 11:25 am – 12:45 pm: Technical Session D2-W2-T2: Biomedical Science and Engineering**
Chair: **Dr. Tso-Pang Yao**, Department of Pharmacology and Cancer Biology, Duke University Medical Center (杜克大學醫學中心姚佐邦教授)
Room: 224

**Dr. Fu-Hsiung Chang**
Professor, Department of Biochemistry and Molecular Biology
National Taiwan University
(臺灣大學醫學院生物化學暨生物分子研究所張富雄教授)

"Understanding Biology via Discovering the Activities of "Orphan" Enzymes"
**Dr. Hening Lin**
Assistant Professor, Department of Chemistry and Chemical Biology
Cornell University

"Single Cell Genomics"
**Dr. Honghua Li**
Associate Professor, Department of Pharmacology
University of Medicine and Dentistry of New Jersey Robert Wood Johnson Medical School
(新泽西州罗伯屋强森医学院李洪華教授)

**10/28 (Sun) 11:25 am – 12:45 pm : Technical Session D2-W3-T2: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS**

Chair: **Dr. Yihua Bruce Yu**, Department of Pharmaceutical Sciences, University of Maryland, Baltimore (马里兰大学巴尔的摩分校药学院药物科学系虞一华教授)

Room: 324

"Biomimetic Approaches for the in vitro Engineering of 3D Prostate Cancer Models"
**Dr. Xinqiao Jia**
Associate Professor, Materials Science and Engineering Department, Biomedical Engineering Program
University of Delaware
(德拉维尔大学材料科学与工程系生物醫學工程组贾新桥教授)

"Multifunctional Polymeric Nanoparticles for Targeted Cancer Therapy and Diagnosis"
**Dr. Shaoqin "Sarah" Gong**
Associate Professor, Department of Biomedical Engineering &
Wisconsin Institutes for Discovery
University of Wisconsin, Madison

"Engineering Virus Nanoparticles for Biomedicine"
**Dr. Junghae Suh**
Assistant Professor, Department of Bioengineering
Rice University

**10/28 (Sun) 12:45 pm - 2:15 pm: Lunch**
Room: The Frick Atrium

**Parallel Sessions:**
**10/28 (Sun) 2:15 pm – 3:35 pm: Technical Session D2-W1-T3: In Silico Research and Biomedical Informatics**

Chair: **Dr. Jhih-Wei Chu**, Department of Chemical and Biomolecular Engineering, University of California, Berkeley (加州大學柏克萊分校化學及分子生物工程系朱智瑋教授)

Room: 124

"A Variable-Selection-Based Novel Statistical Approach to Identify Susceptible Rare Variants Associated with Complex Diseases with Deep Sequencing Data"
**Dr. Shuang Wang**
Associate Professor, Department of Biostatics
(哥伦比亚大学公共卫生学院王爽教授)
**Dr. Hokeun Sun**
Associate Research Scientist, Department of Biostatics
The Mailman School of Public Health
Columbia University

"NIA Genetics of Alzheimer's Disease Data Storage Site (NIAGADS)"
**Dr. Li-San Wang**
Assistant Professor, Department of Pathology and Laboratory Medicine

University of Pennsylvania Perelman School of Medicine
Penn Center for Bioinformatics
(賓州大學醫學院王立三教授)

**10/28 (Sun) 2:15 pm – 3:35 pm: Technical Session D2-W2-T3: Biomedical Science and Engineering**
Chair: **Dr. Chyung-Ru Wang**, Department of Microbiology and Immunology, Feinberg School of Medicine, Northwestern University (西北大學醫學院王瓊如教授)
Room: 224

"New Directions for Neural Prostheses to Treat Hearing Loss and Tinnitus"
**Dr. Hubert H. Lim**
Assistant Professor, Departments of Biomedical Engineering and Otolaryngology
University of Minnesota, Twin Cities

"A Multi-step Self-organization of Centimeter-long Epithelial Tubules"
**Dr. Chin-Lin Guo**
Assistant Professor of Bioengineering and Applied Physics
California Institute of Technology
(加州理工學院生物工程系與應用物理系郭青齡教授)

"Advance Bio Sensing by Nanopatterning"
**Dr. Stephen Y. Chou**
Member of National Academy of Engineering
Professor, Department of Electrical Engineering
Princeton University
(美国国家工程院院士普林斯顿大学电机系周郁教授)
**Dr. Liangcheng Zhou**
Postdoctoral Research Associate, Department of Electrical Engineering
Princeton University

**10/28 (Sun) 2:15 pm – 3:35 pm: Technical Session D2-W3-T3: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS**
Chair: **Dr. Yihua Bruce Yu**, Department of Pharmaceutical Sciences, University of Maryland, Baltimore (马里兰大学巴尔的摩分校药学院药物科学系虞一华教授)
Room: 324

"An Electrochemical Impedimetric Biosensor Based on a Nanostructured Polycarbonate (PC) Substrate"
**Dr. Gou-Jen Wang**
Distinguished Professor, Department of Mechanical Engineering and Graduate Institute of Biomedical Engineering
National Chung-Hsing University
(中興大學機械工程學系王國禎特聘教授)

"Biologically Inspired Microsystems Engineering"
**Dr. Mingming Wu**
Associate Professor, Department of Biological and Environmental Engineering
Cornell University
(康奈尔大学生物工程和环境工程系吴珉珉教授)

"BioMEMS for Blood Sample Preparation and Cell Analysis"
**Dr. Siyang Zheng**
Assistant Professor, Department of Bioengineering
The Pennsylvania State University
(宾州州立大学生物工程系郑斯扬教授)

**10/28 (Sun) 3:35 pm – 3:50 pm: Break**

Room: The Frick Atrium

**Parallel Sessions:**

**10/28 (Sun) 3:50 pm – 5:10 pm: Technical Session D2-W1-T4: In Silico Research and Biomedical Informatics**

Chair: **Dr. Li-San Wang**, Department of Pathology and Laboratory Medicine, The Perelman School of Medicine, the University of Pennsylvania (賓州大學醫學院王立三教授)

Room: 124

"Hidden Markov Models with Applications in Cell Adhesion Experiments"
**Dr. Ying Hung**
Assistant Professor, Department of Statistics and Biostatics
Rutgers University

"Cellular Commitment in the Epithelial-Mesenchymal-Transition"
**Dr. Yibin Kang**
Professor, Department of Molecular Biology
(普林斯顿大学分子生物学系康毅滨教授)

**Dr. Caleb Bastian**
PhD Candidate, Applied and Computational Mathematics
Princeton University

**Dr. Woei-Jyh (Adam) Lee**
National Institutes of Health
(美國國家衛生研究院李偉智博士)

**10/28 (Sun) 3:50 pm – 5:10 pm: Technical Session D2-W2-T4: Biomedical Science and Engineering**

Chair: **Dr. Tso-Pang Yao**, Department of Pharmacology and Cancer Biology, Duke University Medical Center (杜克大學醫學中心姚佐邦教授)

Room: 224

"Dendrimer-based Imaging Agents for 19F Magnetic Resonance Imaging"
**Dr. Yihua Bruce Yu**
Associate Professor, Department of Pharmaceutical Sciences
University of Maryland, Baltimore
(马里兰大学巴尔的摩分校药学院药物科学系虞一华教授)

"Superresolution STED Imaging Reveals Distinct States of Intraflagellar Transport in Primary Cilia"
**Dr. Jung-Chi Liao**
Assistant Professor, Department of Mechanical Engineering and Biomedical Engineering
Columbia University
(哥倫比亞大學機械工程系與生物醫學工程系廖仲麒教授)

"Human Insulin Degrading Enzyme"
**Dr. Wei-Jen Tang**
Professor, Ben May Department for Cancer Research
The University of Chicago
(芝加哥大學生物醫學研究所湯惟仁教授)

**10/28 (Sun) 3:50 pm – 5:10 pm: Technical Session D2-W3-T4: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS**

Chair: **Dr. Fan-Gang Tseng**, Department of Engineering and System Science and Biomedical Technology Research Center, National Tsing-Hua University
(清華大學工程與系統科學系主任曾繁根教授)

Room: 324

"Microelectromechanical Systems for Biomolecular Sensing and Manipulation"

**Dr. Qiao Lin**
Associate Professor, Department of Mechanical Engineering
Columbia University

**Dr. Fan-Gang Tseng**
Professor and Chairman, 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主任曾繁根教授)

**Dr. Jeff Tza-Huei Wang**
Associate Professor
Departments of Mechanical Engineering, Biomedical Engineering and Oncology
Johns Hopkins University
(約翰霍普金斯大學機械工程系與生物醫學工程系王澤輝教授)

# Abstracts and Biographies

*Opening Session*

## General Conference Co-Chair

## Wei-Jen Tang

Professor, Ben May Department for Cancer Research
The University of Chicago
E-mail: wtang@uchicago.edu
(芝加哥大學生物醫學研究所湯惟仁教授)

BIOGRAPHY

| NAME | POSITION TITLE |
|---|---|
| Wei-Jen Tang | Professor |

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include*

| INSTITUTION AND LOCATION | DEGREE *(if applicable)* | YEAR(s) | FIELD OF STUDY |
|---|---|---|---|
| National Taiwan University | B.S. | 1978-1982 | Zoology |
| University of Texas, Austin | Ph.D. | 1984-1988 | Biological Science |

**A. Personal Statement:**
My research program involves in elucidating the molecular basis of cellular signal transduction. The research is based on the premise that the better understanding of protein-protein and protein-ligand interaction is key to elucidating the fundamental principles governing cellular signaling network. I apply X-ray crystallography and various biochemical, biophysical, cellular and pharmacological tools to address the protein functions and regulations. I am known for the studies on the catalysis and regulation of mammalian adenylyl cyclase, anthrax and pertussis adenylyl cyclase toxins, and insulin degrading enzyme. I am a very strong believer in collaboration.

**B. Positions and Honors.**

**Positions:**

| | |
|---|---|
| 1988 | Postdoctoral fellow with Dr. William R. Folk, U Texas Austin |
| 1988-1991 | Postdoctoral fellow with Dr. Alfred G. Gilman, U Texas Southwestern Medical School |
| 1991-1993 | Instructor, Dept. of Pharmacology, University of Texas Southwestern Medical School |

| | |
|---|---|
| 1993-1994 | Assistant Professor, Dept. of Pharmacology, UT Southwestern Medical School |
| 1994-1998 | Assistant Professor, Dept. of Pharmacol. & Physiol. Sciences, U of Chicago |
| 1998-2001 | Assistant Professor, Dept. of Neurobiol. Pharmacol. & Physiol., U of Chicago |
| 2001-2007 | Associate Professor, Ben-May Institute for Cancer Research, U of Chicago |
| 2007- | Professor, Ben-May Department for Cancer Research, U of Chicago |

**Honors and Federal Government Public Advisory Committee:**

| | |
|---|---|
| 1987-1988 | University Fellowship, University of Texas, Austin |
| 1999-2002 | American Heart Association Established Investigator |
| 1998-present | Ad Hoc NIH and NSF grant reviewing panels |
| 2007-2011 | Regular member of NIH MSF-C study section |
| 2009-present | The advisory Board, Structure Biology Center, APS, Argonne National Lab. |

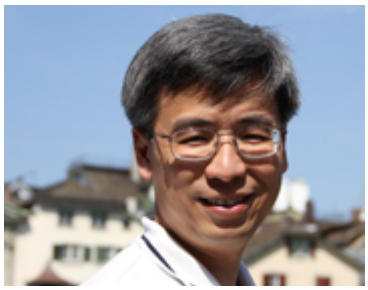
*Opening Session*

**General Conference Co-Chair**


## Haw Yang

Associate Professor, Department of Chemistry
Princeton University
E-mail: hawyang@princeton.edu
(普林斯頓大學化學系楊皓教授)


BIOGRAPHY



*Plenary Session (1)*

**Opening Speech and Session Chair**

## Ruby B. Lee

Professor, Department of Electrical Engineering
Princeton University
E-mail: rblee@ee.princeton.edu
(普林斯頓大學電機系李佩露教授)

BIOGRAPHY

**Ruby B. Lee** is the Forrest G. Hamrick Professor of Engineering and Professor of Electrical Engineering at Princeton University, with an affiliated appointment in the Computer Science department. She is the director of the Princeton Architecture Laboratory for Multimedia and Security (PALMS). Her current research is in designing security and new media support into core computer architecture, embedded systems and global networked systems, and in architectures resistant to Distributed Denial of Service attacks and Internet-scale epidemics. She teaches courses in *Cyber Security* and *Processor Architectures for New Paradigms*. She is a Fellow of the Association for Computing Machinery (ACM) and a Fellow of the Institute of Electrical and Electronic Engineers (IEEE). She is Associate Editor-in-Chief of *IEEE Micro* and Editorial Board member of *IEEE Security and Privacy*.

Prior to joining the Princeton faculty in 1998, Dr. Lee served as chief architect at Hewlett-Packard, responsible at different times for processor architecture, multimedia architecture and security architecture for e-commerce and extended enterprises. She was a key architect in the definition and evolution of the PA-RISC architecture used in HP servers and workstations, and also led the first CMOS PA-RISC single-chip microprocessor design. As chief architect for HP's multimedia architecture team, Dr. Lee led an inter-disciplinary team focused on architecture to facilitate pervasive multimedia information processing using general-purpose computers. This resulted in the first desktop computer family with integrated, software-based, high fidelity, real-time multimedia. Dr. Lee also co-led a multimedia architecture team for IA-64. Concurrent with full-time employment at HP, Dr. Lee also served as Consulting Professor of Electrical Engineering at Stanford University. She has a Ph.D. in Electrical Engineering and a M.S. in Computer Science, both from Stanford University, and an A.B. with distinction from Cornell University, where she was a College Scholar. She is an elected member of Phi Beta Kappa and Alpha Lambda Delta. She has been granted 115 United States and international patents, with several patents pending.

*Plenary Session (1)*

## Plenary Speaker

## Neurodegenerative disease genetics; GWAS, exomes and beyond


**Gerard D. Schellenberg**

Professor, Department of Pathology and Laboratory Medicine
Perelman School of Medicine
University of Pennsylvania
E-mail: gerardsc@mail.med.upenn.edu



ABSTRACT

Genome-wide genetic approaches are now being successfully used to understand the genetic architecture of Alzheimer's disease (AD). Early work identified APOE as a major susceptibility gene for late-onset AD (LOAD). Genetic analysis of the APOE show that the signal from this gene comes entirely from the ε2/ε3/ε4 polymorphism and no other variants in the region. Genome-wide association studies (GWAS) performed by the Alzheimer's disease Genetics Consortium (ADGC) and others have now identified 9 different loci that contribute to AD susceptibility. These are ABCA7, BIN1, CD2AP, CD33, CR1, CLU, EPHA1, MS4A4/MS4A6E, and PICALM. Recently, using combined Caucasian and Japanese cohorts, we show that SORL1, a gene previously implicated by candidate gene studies, is significant at the genome-wide level. We have also extended these findings in to an African America population. To increase power to detect AD loci, we formed the International Alzheimer Genomic Project (IGAP) which is an international collaboration of all major AD genetics groups. We performed a mega-meta analysis using 17,008 AD cases and 45,962 controls. We identified 4 new AD genes. In a replication study, we designed a custom genotyping array of SNPs that had a P < 10-3 and are genotyped an additional 14,000 cases and 14,000 controls. The next phase of analysis is to identify rare variants that contribute to AD risk using using exome chips, whole exome sequencing, and whole genome sequencing. Whole-genome approaches for AD and other neurodegenerative disorders (e.g. progressive supranuclar palsy) will hopefully lead to the identification of new AD therapeutic targets.


BIOGRAPHY

Dr. Schellenberg was born in Reedley, California, USA on September 29, 1951. He received a BS in biochemistry and a minor in chemistry from the University of California Riverside in 1973. Dr. Schellenberg received his Ph.D. in biochemistry with a minor in cell biology from the University of California, Riverside in 1978.

Dr. Schellenberg moved to the University of Washington in 1979 where he was a Post-Doctoral Fellow in genetics and Neurology at the University of Washington. In 1983 he was appointed Research Assistant Professor in Neurology where he rose to the rank of Research Professor in 1995. At this point, his primary appointment was in the Division of Gerontology and Geriatric Medicine, Department of Medicine and he was also an adjunct Research Professor in the Departments of Neurology and Pharmacology. In 1995, he became Associate Director for Research, Geriatrics Research Education and Clinical Center at the Veterans Affairs Puget Sound Health Care System, Seattle Division. Dr. Schellenberg moved to the University of Pennsylvania in 2008 where he is presently a Professor in the Department of Pathology and Laboratory Medicine in the Perelman School of Medicine at the University of Pennsylvania in Philadelphia, Pennsylvania, USA. For the past 22 years, Dr. Schellenberg has worked on the genetics of Alzheimer's disease, starting with ground-breaking research on early-onset familial Alzheimer's disease followed by work on late-onset dementia which is where much of his current effort is focused. He is founder and head of the Alzheimer's Disease Genetics Consortium supported by the National Institute on Aging. Dr. Schellenberg is a co-founder of the International Genomics Alzheimer's Project (IGAP) which is an international consortium that has all the world's Alzheimer's disease genetics groups as members. IGAP has assembled genetic data for over 50,000 subjects to study Alzheimer's disease genetics. He also worked on the genetics of aging and his group identified the gene for Werner's

Syndrome, a premature aging syndrome. He is also working on the molecular genetics on other neurodegenerative disorders related to Alzheimer's disease with a focus on frontotemporal dementia, Guam amyotrophic lateral sclerosis/parkinsonism dementia complex and progressive supranuclear palsy. This work includes using a using both invertebrate and vertebrate model organisms to study tauopathies. Dr. Schellenberg is also working on unraveling the genetics of autism, a complex neurodevelopmental disorder. He participates in the Autism Genome Project consortium. His current efforts focus on deep sequencing of genes suspected of being involved in autism risk.

Dr. Schellenberg has received awards for his research including: the John Douglas French Foundation for Alzheimer's Disease, Investigator Award in 1986, the Potamkin Prize for Alzheimer's Disease Research, Potamkin Foundation and the American Academy of Neurology in 1994, Metropolitan Life Foundation in Awards for Medical Research in 1995, the Alzheimer's Association Medical Honoree, for outstanding commitment to the research of Alzheimer's disease in 1996, and a Merit Award from the National Institute on Health in 2004.

*Plenary Session (1)*

## Plenary Speaker

## Biophotonics Imaging Platforms towards Translational Applications

**Xingde Li**

Professor, Department of Biomedical Engineering
Johns Hopkins University
E-mail: xingde@jhu.edu
(约翰霍普金斯大学生物医学工程系李兴德教授)

ABSTRACT

This talk will focus on our recent developments of ultracompact endomicroscopy technologies, which literally miniaturize a bench-top scanning laser microscope down to a flexible fiber-optic scanning probe of an ~1-2 mm diameter. The ultimate goal is to translate the powerful high-resolution optical imaging technologies, such as multiphoton fluorescence and harmonics generation microscopy as well as optical coherence tomography (OCT), to clinical practice, and enable noninvasive "optical biopsy" of internal organs in situ and in real time with a resolution approaching or at the level of standard histology but without the need for tissue removal. We will discuss some key technological and engineering challenges and solutions related to the development of endomicroscopes, including novel optical fibers, advanced micro-optics, and MEMS technologies. Preliminary results of Barrett's esophagus and breast cancer imaging with the endomicroscopes will be presented. Other potential applications such as preterm birth and liver fibrosis detection will also be discussed. In addition, we will present our fast-track approach to translate optical molecular imaging by developing functional near-infrared fluorescent polymeric nanocapsules, which are formulated by self-assembling of only FDA approved materials.

BIOGRAPHY

Dr. Xingde Li graduated from the University of Science and Technology of China (USTC) with a B.S. degree in Physics in 1990, and from the University of Pennsylvania with a PhD degree in Physics and Astronomy in 1998 under the supervision of Prof. Arjun Yodh and (late) Prof. Britton Chance. He then joined Prof. James Fujimoto's group at MIT and conducted postdoctoral research for about 3 years. He became a tenure-track assistant professor at the Department of Bioengineering University of Washington (Seattle) in 2001 and was promoted to Associate Professor with tenure in 2006-2007. In 2009 he moved his lab to Baltimore and joined the Department of Biomedical Engineering at the Johns Hopkins University. In December 2011, he was promoted to full professor. His research centers on development advanced and biophotonics technologies and functional nanomaterials, including OCT, two-photon endomicroscopy, fluorescence tomography/molecular imaging, structured gold nanoparticles and polymeric nanocapsules, for translational biomedical and clinical applications. Dr. Li received the Teacher/Mentor of the Year Award (UW 2002), the NSF Early Career Award (USA 2004), the International Association of Dental Research Innovation in Oral Care Award (2009), and recently the Individual Biomedical Research Award from the Hartwell Foundation (2011). In addition to chairing many national and international conference sessions and conferences, Dr. Li also served as the Chair of the Emerging Technologies Committee of IEEE – EMBS society between 2006-2010, and he is currently an associate editor or on the editorial board

for *the Journal of Biomedical Optics* (SPIE), *Biomedical Optics Express* (OSA), *the IEEE Transactions on Biomedical Engineering* and three other international journals in the area of biomedical optics and biophotonics. He has participated in 40+ various proposal review panels, has been helping review proposals from other regions and countries outside the USA, and is currently serving as a charter member of an NIH imaging study section. He has published about 75 peer-reviewed journal papers with a total citation more than 6,800 times and an H-index of about 37 (according to Google Scholar), and has delivered more than 90 invited talks at conferences and outside home institutions. He is currently a Fellow of the Optical Society of America (OSA) and the International Society for Optics and Photonics (SPIE).

*Plenary Session (2)*

**Session Chair**

## Sun-Yuan Kung

Professor, Department of Electrical Engineering
Princeton University
E-mail: kung@princeton.edu
**(普林斯頓大學電機系貢三元教授)**

BIOGRAPHY

*Plenary Session (2)*

## Plenary Speaker

# From the Era of Gigabyte Data to the Era of Petabyte Data: Are we ready for the next generation sequencing data?


**Yu Shyr**

Director, Vanderbilt Center for Quantitative Sciences
Ingram Distinguished Professor of Cancer Research
Associate Director for Quantitative Sciences Integration, Vanderbilt-Ingram Cancer Center
Professor and Chief, Division of Cancer Biostatistics
Professor of Biostatistics, Biomedical Informatics, Cancer Biology and Preventive Medicine
Vanderbilt University School of Medicine
E-mail: yu.shyr@vanderbilt.edu
(范德堡大學癌症中心生物統計主任石瑜教授)



ABSTRACT

Traditional biomedical research focuses on one or two biological features at a time, by contrast, cutting-edge "-Omics" approaches (proteomics, genomics, lipidomics, metabolomics, etc.) generate data for thousands of biological features with each experiment. This talk will span from principles for design of high-dimensional biomedical research through its data analysis. Couple examples of statistical bioinformatics features for designing and analyzing the next generation sequencing data will be given in this talk. The statistical bioinformatics challenges such as data storing, sharing, preprocessing, analyzing, and interpreting will be highlighted.


BIOGRAPHY

Yu Shyr received his PhD in biostatistics from University of Michigan (Ann Arbor) in 1994 and subsequently joined the faculty at Vanderbilt University School of Medicine. 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 methodologies for clinical trial design, high-dimensional data preprocessing, estimating relative potency in a parallel line bioassay, and other statistical approaches, published in journals such as Statistics in Medicine, Bioinformatics, Clinical Trials, Computational Statistics and Data Analysis, BMC Bioinformatics, and Journal of Bioinformatics and Computational Biology in the last three years.

Dr. Shyr is a Fellow of the American Statistical Association and US FDA advisory committee voting member. He has delivered more than 185 abstracts at professional meetings and published more than 275 peer-reviewed papers in a variety of journals. Dr. Shyr has served as a member of the 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, since 2004, has been a member of the invited faculty at the AACR/ASCO Methods in Clinical Cancer Research Vail Workshop. He currently serves on the external advisory board for Northwestern University's Robert H. Lurie Comprehensive Cancer Center, University of Kentucky Markey Cancer Center, University of Colorado SPORE in Lung Cancer, Moffitt Cancer Center SPORE in Lung Cancer, and Arizona University SPORE in GI cancer; is a member of the editorial board for the Journal of Clinical Oncology and Cancer Prevention Research Journal as well as ASCO's Cancer

Research Committee; and directs the biostatistics and bioinformatics cores for the NCI-funded Vanderbilt University Breast Cancer SPORE, GI Cancer SPORE, Lung Cancer SPORE, and other program projects. In addition, Dr Shyr is the Principle Investigator of the NCI UO1 grant of Barrett's esophagus translational research network coordinating center (BETRNetCC). Dr. Shyr's current research interests lie in developing and analyzing predictive models of the statistical relationships between multiple-variable protein and next generation sequencing data and clinical endpoints using both supervised and unsupervised classification and pattern recognition approaches, which focus on analyses of gene expression array and protein expression profile data to identify the molecular "fingerprint" of different types of cancers.

*Plenary Session (2)*

## Plenary Speaker

# Combination of Genomic Technologies and Bioinformatics for Exploring New Cancer Biomarkers


**Eric Y. Chuang**

Director, Graduate Institute of Biomedical Electronics and Bioinformatics
Professor, Department of Electrical Engineering
National Taiwan University
E-mail: chuangey@cc.ee.ntu.edu.tw
(臺灣大學生醫電子與資訊學研究所所長莊曜宇教授)



ABSTRACT

With the expansion of available genome-wide screening technologies such as microarray and next generation sequencing, knowing how to use appropriate software tools running on powerful computers is a necessity for biologists to identify new genes or targets. The development of user-friendly analytical tools/systems by bioinformaticians, researchers can efficiently analyze massive genomic data and select genes with modulated expression patterns and altered characters. Based on the modulated genes identified from various genomic analyses, researchers can further analyze and investigate possible regulatory mechanisms of human genes and diseases, and then discover potential therapeutic targets. In my talk, I will present few bioinformatics tools developed in my lab for analyzing genomic data. Furthermore, I will provide a few studies how we utilized different analytical tools to identify new molecular signatures or biomarkers for diagnosis, prognosis, and treatment response of various cancers.


BIOGRAPHY

Prof. Chuang was born in 1964, Taipei, Taiwan, who earned cancer biology Sc.D. degree in 1997 from Harvard University located at Boston, MA. USA. Before entering Harvard University, he majored Biology and obtained Master degree in Illinois Institute of Technology, which established well subject foundation and enriched research experience for him to aspire further related specialized knowledge.

After earning Sc.D. degree, he worked as Postdoctoral Research Fellow at cancer cell biology department at HU for a year then served as CRTA Fellow in Radiation Biology Branch and the Head of Microarray Laboratory, Radiation Oncology Sciences Program in National Cancer Institute. Studying and working in U.S for 23 years, he came back to Taiwan by 2004 and started to teach as Associate Professor in Department of Electrical Engineering; Associate Professor in Department of Life Science and Associate Professor in Graduate Institute of Epidemiology in National Taiwan University. Now he primarily works as Professor in Graduate Institute of Biomedical Electronics and Bioinformatics, National Taiwan University in Taipei, Taiwan. In this period, he had published a number of articles such as Use of Germline Polymorphisms in Predicting Concurrent Chemoradiotherapy Response in Esophageal Cancer. Int J Radiat Oncol Biol Phys. 2011; Identification of a Novel Biomarker, SEMA5A, for Non–Small Cell Lung Carcinoma in Nonsmoking Women. Cancer Epidemiology, Biomarkers & Prevention 2010; Verifying expressed transcript variants by detecting and assembling stretches of consecutive exons. Nucleic Acids Res 2010; and two books. His primary research goals are to elucidate the radiation-induced responses and mechanisms related to cell proliferation and survival. Multiple microarray platforms, including single nucleotide polymorphism, gene expression, methylation, and microRNA arrays are performed to dissect how genomic variations and transcriptional modulations regulate cellular functions after radiation exposure. Secondary emphasis of his research program is to develop systems biology approaches to study cancer

biology. Different mathematical models and statistical methods are utilized to integrate data from multiple platforms to provide a comprehensive analysis on cancer cells.

Prof. Chuang is the member of American Association for Cancer Research and Radiation Research Society, which provide a platform for scholars and professionals exchange their research results and latest information. In addition to his extensive research and work experience, he also performance well in many competitions and once awarded On-the-Spot Award, US Department of Health and Human Services, Public Health Service, 2001; Travel Award (top 5-ranked winner), 11th International Congress of Radiation Research, Dublin, Ireland, 1999, etc.

## Workshop and Session Chairs

**Jhih-Wei Chu**

Assistant Professor, Department of Chemical and Biomolecular Engineering
University of California, Berkeley
E-mail: jwchu@berkeley.edu
(加州大學柏克萊分校化學及分子生物工程系朱智瑋教授)

BIOGRAPHY

# How important is each behavior of the AADE7

**Feipei Lai**

Professor, Department of Electrical Engineering
National Taiwan University
Email: flai@ntu.edu.tw
**(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)**

ABSTRACT

The patients with DM need to be cared for a long period of time. Therefore, patient self-management is necessary for care and management of this chronic disease. It can help patients to have a better understanding of their own lifestyle and health behavior and thus improve the disease condition and health status. Our approaches to the care of patients with DM follow the principle of AADE7 that involves seven evaluation items, namely; 1) healthy eating, 2) being active, 3) continuously monitoring, 4) taking medication, 5) problem solving capability, 6) reducing risks and 7) healthy mind which are proposed by American Association of Diabetes Educators (AADE), in designing our telehealthcare platform. This study aimed at quantifying the importance of each evaluation item in AADE7. Using these results, we can refine our platform to improve the clinical decision support system (CDSS). The outcomes reveal that the decreased HbA1C of patients for intervention group (76.1%) is much better than control group (34.5%) after monitoring for three months. The platform not only assists patients in being actively involved in their own health management, but also improves their health status as well. The Fisher scores of the 394 features from data mining are mapped to the corresponding AADE7 evaluation items and summed up as follows: 1) continuously monitoring: 0.216, 2) problem solving capability: 0.182, 3) Healthy eating: 0.168, 4) taking medication: 0.145, 5) reducing Risks: 0.121, 6) being active: 0.105, 7) healthy mind: 0.066.

BIOGRAPHY

Feipei Lai received a B.S. degree in Electrical Engineering from National Taiwan University in 1980, and M.S. and Ph.D. degrees in computer science from the University of Illinois at Urbana-Champaign in 1984 and 1987, respectively.

He is a professor in the Graduate Institute of Biomedical Electronics and Bioinformatics, the Department of Computer Science & Information Engineering and the Department of Electrical Engineering at National Taiwan University. He was a vice superintendent of National Taiwan University Hospital. He was the chairman of Taiwan Network Information Center. He was a visiting professor in the Department of Computer Science and Engineering at the University of Minnesota, Minneapolis, USA. He was also a guest Professor at University of Dortmund, Germany and a visiting senior computer system engineer in the Center for Supercomputing Research and Development at the University of Illinois at Urbana-Champaign. Dr. Lai holds 10 Taiwan patents and 4 USA patents currently. His current research interest is Medical Informatics.

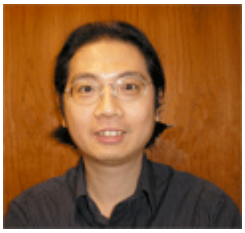
Prof. Lai is one of the founders of the Institute of Information & Computing Machinery and serve as the President during 2009/7-2013/7. He is also a member of Phi Kappa Phi, Phi Tau Phi, Chinese Institute of Engineers, Chinese Institute of Electrical Engineers. Prof. Lai was the chairman of Taiwan Internet Content Rating Foundation. He received the Taiwan Fuji Xerox Research award in 1991, K-T Li Breakthrough award in 2008, IBM faculty Award, NTU Distinguished Service Award in 2009 and Taiwan 2010 IT Distinguished Professionals.

*Technical Session D1-W1-T1: In Silico Research and Biomedical Informatics*


## Yi-Hsiang (Sean) Hsu

Assistant Professor, School of Medicine
Harvard University
E-mail: yhh5402@gmail.com
(哈佛大學醫學院許益祥教授)


BIOGRAPHY



Dr. Yi-Hsiang Hsu is an Assistant Professor in Medicine, Harvard Medical School, Beth Israel Deaconess Medical Center and Hebrew SeniorLife Institute for Aging Research. He also directs the High Performance Computing System Lab at Institute for Aging Research. Dr. Hsu is a statistical geneticist who has extensive experience with the genetic fields using genome-wide association approach (GWAS), linkage and candidate gene association methods to find genes associated with musculoskeletal disorders, osteoporosis, cancers, type 2 diabetes and drug response of blood pressure to hypertensive medications. Dr. Hsu also involved in the statistical method development for GWAS, such as multivariate GWAS methods and to study the pleiotropic effects on skeletal and energy metabolisms. Dr. Hsu has experience using systems biology approaches to integrate GWAS, genomics, trascriptomics, proteomics and metabolomics resources for better understanding relationships between the biological components that work together to drive a complex pathophysiological process of common diseases across signal pathways, organisms and even species on a global scale.

*Technical Session D1-W2-T1: Biomedical Science and Engineering*

## Workshop and Session Chairs


## Chyung-Ru Wang

Professor, Department of Microbiology-Immunology
Feinberg School of Medicine
Northwestern University
Email: chyung-ru-wang@northwestern.edu
(西北大學醫學院王瓊如教授)


BIOGRAPHY

**EDUCATION:**

| | | |
|---|---|---|
| 1979-1982 | National Taiwan University, Taiwan, R.O.C. | B.S. (Zoology) |
| 1982-1987 | University of Texas, Austin, TX | Ph.D. (Biology) |

PROFESSIONAL APPOINTMENTS:

| | |
|---|---|
| 1987-1991 | Postdoctoral Associate (Sponsor: Dr. Kirsten Fischer Lindahl)<br>Howard Hughes Medical Institute, University of Texas Southwestern Medical School |
| 1991-1993 | Postdoctoral Associate (Sponsor: Dr. Johann Deisenhofer)<br>Department of Biochemistry, University of Texas Southwestern Medical School |
| 1993-1994 | Instructor (Sponsor: Dr. Johann Deisenhofer)<br>Department of Biochemistry, University of Texas Southwestern Medical School |
| 1994-2001 | Assistant Professor<br>Department of Pathology, Committee on Immunology, University of Chicago |
| 2001-2007 | Associate Professor<br>Department of Pathology, Committees on Immunology and Microbiology, University of Chicago |
| 2007-2008 | Professor<br>Department of Pathology, Committees on Immunology and Microbiology, University of Chicago |
| 2008-present | Professor<br>Department of Microbiology and Immunology, Northwestern University |

**HONORS AND AWARDS:**

| | |
|---|---|
| 1979-1982 | Book Coupon Awards (National Taiwan University, top 5 % of the Class) |
| 1980-1982 | Natural Science Fellowship |

| | |
|---|---|
| 1982 | Member of Phi Tau Phi Scholastic Honor Society |
| 1995 | Cancer Research Foundation Young Investigator Awards |
| 1996-1999 | Searle Scholars Award |
| 2006 | Future Faculty Mentorship Award (University of Chicago) |

**MEMBERSHIP IN PROFESSIONAL SOCIETIES:**

| | |
|---|---|
| 1994-present | American Society of Immunology |

# The addiction-obesity connection viewed in the light of medical imaging

**Gene-Jack Wang**

Senior Scientist and Chair, Medical Department
Brookhaven National Laboratory
Email: gjwang@bnl.gov
(美國國家布魯克海文實驗室醫學部主任王俊傑醫師)

ABSTRACT

Both drug addiction and obesity can be defined as disorders in which the saliency value of one type of reward (drugs and food, respectively) becomes abnormally enhanced relative to, and at the expense of others. Both drugs and food have powerful reinforcing effects-partly mediated by dopamine increases in the limbic system-that, under certain circumstances or in vulnerable individuals, could overwhelm the brain's homeostatic control mechanisms. Such parallels have generated significant interest in understanding the shared vulnerabilities and trajectories between addiction and obesity. Recent brain imaging studies have started to uncover common features between these two conditions and to delineate some of the overlapping brain circuits whose dysfunctions may explain stereotypic and related behavioral deficits in human subjects. These results suggest that both obese and drug-addicted individuals suffer from impairments in dopaminergic pathways that regulate neuronal systems associated not only with reward sensitivity and incentive motivation, but also with conditioning, impulse control, stress reactivity, and interoceptive awareness. Our imaging findings shed light on the role of brain dopamine in drug addiction and in obesity.

BIOGRAPHY

Dr. Gene-Jack Wang was born in Tainan, Taiwan in 1954. He received a medical doctor degree from the Kaohsiung Medical University in Taiwan, in 1980, and a master's degree in radiation health sciences from the Johns Hopkins University in 1984. After finishing medical training at the Stony Brook University, he began working at the Brookhaven National Laboratory (BNL) medical department in 1990. He is a board certified nuclear medicine physician and a senior medical scientist of the department. In addition to performing his own research, he is the chairman of the BNL medical department and holds a joint appointment as a professor of psychiatry at the Mount Sinai School of Medicine and an adjunct professor of psychiatry and radiology at the Stony Brook University.

His research focuses on the application of positron emission tomography (PET) and magnetic resonance imaging (MRI) to the study of various brain disorders. He is interested in using PET to study the neuro-psychiatric mechanisms and manifestations of alcoholism, drug addiction, obesity and eating disorder in humans and in animal models. Using PET, he reported similarity of brain circuits' disruption in drug addiction and in obesity. His ongoing research includes using PET to study the relationship between peripheral metabolic signals and brain neurotransmitters and functional MRI to study effect of diet control drug on brain satiety circuit and cognitive function in obese subjects.

Dr. Wang is a member of the Society of Nuclear Medicine, the American College of Neuropsychopharmacology and the Obesity Society. He received Science and Technology award from the BNL and Distinguished Asian American professional award from Suffolk County, New York. He has published over 240 peer-reviewed original papers and 50 review articles/book charters on his imaging research. The National Institute of Health and pharmaceutical companies fund his ongoing research.

*Technical Session D1-W2-T1: Biomedical Science and Engineering*

# Brain imaging of cognitive control


## Chiang-shan Ray Li

Associate Professor, Departments of Psychiatry/Neurobiology
Yale University
E-mail: chiang-shan.li@yale.edu
(耶魯大學醫學院精神病學及神經生物學系李江山教授)



ABSTRACT

Cognitive control is a brain function that allows us to inhibit habitual acts, detect errors, and adjust behavior following errors. Studies of cognitive control are of importance to both basic and clinical neuroscience, because deficits in cognitive control are implicated in a number of neurological and psychiatric conditions.

There is growing evidence from systems and imaging neuroscience that each of these component processes engages distinct brain regions. Here, I will discuss brain imaging studies from my laboratory, highlighting how the neural processes of cognitive control are compromised in cocaine addicts and how methylphenidate may remediate these cognitive deficits.


BIOGRAPHY

Dr. Li was born in 1962 in Taipei, Taiwan. He graduated MBBS from College of Medicine, National Taiwan University in 1989 and PhD in Computation and Neural Systems from the California Institute of Technology, Pasadena, CA, USA in 1996.

He served in the Taiwan Navy from 1989 to 1991 and completed psychiatry residency training and board licensing examination in Taiwan after postdoctoral work at the Massachusetts Institute of Technology. He has been a faculty at Yale University since 2003. His research has focused on combining brain imaging, psychophysics, and computational modeling to understand the functional organization of the human brain in health and disease.

Dr. Li is currently an Associate Professor of Psychiatry and Neurobiology at the School of Medicine, Yale University. He has published over 70 original research articles in peer-reviewed journals and been an ad-hoc grant reviewer for NIDA since 2008.

*Technical Session D1-W2-T1: Biomedical Science and Engineering*

# MECHANISMS OF EPIGENETIC REGULATION

**Hua-Ying Fan**

Assistant Professor, Department of Biochemistry and Biophysics
Perelman School of Medicine, University of Pennsylvania
E-mail: hfan@mail.med.upenn.edu
(賓州大學醫學院生物化學與生物物理系范華英教授)

ABSTRACT

The ATP-dependent chromatin remodeler CSB is essential for transcription-coupled DNA repair, and mutations in CSB lead to Cockayne syndrome. We examined the recruitment of CSB to chromatin after ultraviolet (UV) irradiation and uncovered a regulatory mechanism that ensures the specific association of this remodeler with chromatin. We demonstrate that ATP hydrolysis by CSB is essential for stable CSB-chromatin association after UV irradiation and that defects in this association underlie some forms of Cockayne syndrome. We also show that the N-terminal region of CSB negatively regulates chromatin association during normal cell growth. Interestingly, in the absence of the negative regulatory region, ATP hydrolysis becomes dispensable for chromatin association, indicating that CSB uses energy from ATP hydrolysis to overcome the inhibitory effect imposed by its N-terminal region. Together, our results suggest that the recruitment of CSB to lesion-stalled transcription is an ATP-dependent process and involves a gross conformational change of CSB.

BIOGRAPHY

After graduating from New York University Medical School, Hua-Ying did Postdoctoral researches at several places and is now an assistant professor in the department of Biochemistry and Biophysics at University of Pennsylvania Perelman School of Medicine, Philadelphia, PA, USA.

Hua-Ying's doctoral research focused on the dissecting of mechanisms of genome stability maintenance using genetic and molecular biological approaches. She extent her training with biochemical approaches during her postdoctoral researches. Currently, Dr. Fan's laboratory is interested in understanding the mechanisms of epigenetic regulation and how defects in epigenetic regulation lead to human diseases.

Dr. Fan is a member of several professional societies and received several awards.

*Technical Session D1-W3-T1: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*

## Session Chair

## Gou-Jen Wang

Professor, Department of Mechanical Engineering
Graduate Institute of Biomedical Engineering
National Chung-Hsing University
E-mail: gjwang@dragon.nchu.edu.tw
(中興大學機械工程學系王國禎特聘教授)

BIOGRAPHY

**Dr. Gou-Jen Wang** received the B.S. degree on 1981 from National Taiwan University and the M.S. and Ph.D. degrees on 1986 and 1991 from the University of California, Los Angeles, all in Mechanical Engineering. Following graduation, he joined the Dowty Aerospace Los Angeles as a system engineer from 1991 to 1992. Dr. Wang joined the Mechanical Engineering Department at the National Chung-Hsing University, Taiwan on 1992 as an Associate Professor and has become a Professor on 1999. From 2003-2006, he served as the Division Director of Curriculum of the Center of Nanoscience and Nanotechnology. From 2007-2010, he was the adjunct Professor and Chairman of the Graduate Institute of Biomedical Engineering, National Chung-Hsing University, Taiwan. On 2008, he served as the Conference Chair of the Microfabrication, Integration and Packaging Conference (April/2008, Nice, France). From 2009, he is a Committee member of the Micro- and Nanosystem Division of the American Society of Mechanical Engineers (ASME) and serves as the organizer of the BIO MEMS/NEMS Symposium of the International Conference on Micro and Nanosystems (MNS). His research interests include tissue engineering, biomedical micro/nano devices, nano fabrication, and dye-sensitized solar cells.

*Technical Session D1-W3-T1: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*

# Epidermal Electronics


## Nanshu Lu

Assistant Professor
Department of Aerospace Engineering and Engineering Mechanics, Texas Materials Institute
University of Texas at Austin
E-mail: nanshulu@mail.utexas.edu
(德克萨斯州大学奥斯汀分校航空和工程力学系与德克萨斯州材料研究所鲁南姝教授)



ABSTRACT

Hybrid combinations of brittle inorganic semiconductors (e.g. silicon) and soft polymers (e.g. silicone) can yield electronic systems with excellent performance characteristics and mechanical properties matched to human tissue. We describe integrated circuits and sensors with thicknesses, effective moduli and areal mass loadings matched to the epidermis. These devices can be mounted on the surface of the skin in way that is mechanically invisible to the user, to provide various functions, including measurement of electrophysiological signals associated with activity in the heart, brain and skeletal muscles.


BIOGRAPHY

Dr. Lu was born in Chengdu, China, on March 11, 1983. She received her Bachelor of Engineering degree in solid mechanics Tsinghua University, Beijing, China, in 2005. She obtained her Ph.D. in mechanics of materials from Harvard University, Cambridge, MA, in 2009.

She then became a postdoctoral researcher at the University of Illinois at Urbana-Champaign. After two years postdoc training she joined the Department of Aerospace Engineering and Engineering Mechanics at The University of Texas at Austin as an Assistant Professor in August 2011. Her research focuses on all aspects of mechanics of flexible/stretchable electronics from materials properties to configurational design, from micro-fabrication to bio-integration. Her representative work includes highly stretchable metal thin films supported by polymer substrates, instrumented multifunctional balloon catheters for minimally invasive surgeries, and tattoo-like epidermal electronics. Her research has been highlighted by news media such as “Nature News”, “Science News”, “CNN News”, “BBC News”, and others.

Dr. Lu is a member of Materials Research Society (MRS) and American Society of Mechanical Engineering (ASME) since 2007. She is the symposium organizer of the 2012 Fall MRS and the 2012 ASME IMECE. She has received Winston Chen Graduate Fellowship from Harvard University and the Beckman Postdoctoral Fellowship from the University of Illinois at Urbana-Champaign. Her publications are listed below.

# Label-Free Coloring Biofluids on Nanophotonic Device

**Gang Logan Liu**

Assistant Professor, Department of Electrical and Computer Engineering & Bioengineering
University of Illinois at Urbana-Champaign
E-mail: loganliu@illinois.edu

ABSTRACT

Most biomolecules, either in free solution or immobilized on surface, are colorless. The interactions of the colorless biomolecules on surface or in free solution are not visible to naked eyes or a regular bright field imaging system, e.g. color camera. Often fluorescent or chromatic labels have to be added to render colorfully visible biomolecules. For the first time, I will demonstrate, without any labeling, the colorless biomolecule solutions become colorful on top of a unique nanophotonic biochip device, distinctively visible to naked eyes and color cameras. The huge optical transmission and reflection wavelength shifts or the "color changes" upon binding of molecules or merely the application of biomolecule solutions on our nanophotonic device are up to 200 nm, giving the sensitivity of 46,000 nm per refractive-index unit (RIU) and figure of merit (FOM) of 1,022, which is much greater than the any other existing optical resonator sensors, hence completely eliminating the need for precision spectrometer or fluorescence labeling. I will show ultrasensitive label free colorimetric imaging of different refractive indices solutions, oligonucleotide hybridizations and protein interactions on device surface, in free solutions and in microfluidics on our nanophotonic device.

BIOGRAPHY

Dr. Gang "Logan" Liu was born in Wuhan, China. He obtained his B.S. degree in biomedical engineering from Huazhong University of Science and Technology at Wuhan, China in 2000. He then obtained his Ph.D. degree in bioengineering from University of California-Berkeley and UC-San Francisco in 2006. From 2006 to 2008, he finished his postdoctoral training in the Helen Diller comprehensive cancer center at San Francisco as well as Lawrence Livermore national lab in Livermore, CA where he was a Department of Energy Lawrence fellow.

In 2008 he joined University of Illinois at Urbana-Champaign as an assistant professor in Department of Electrical and Computer Engineering and Department of Bioengineering. He is also a faculty fellow of National Center for Supercomputing Applications (NCSA). He has published over 60 journal and conference papers as well as several book chapters. His research focuses on designing and developing integrative bionano and microfluidic technologies and devices for the applications of advanced nanomanufacturing, bioimaging, cancer diagnostics and therapy, environmental sensing and mobile health.

Prof. Liu has been awarded and nominated for several major awards in the past including outstanding publication award from UC-Berkeley in 2006, finalist for ALA innovator award in 2006, Lawrence fellowship in 2007, finalist for innovation award from Damon Runyon-Rachleff cancer research foundation in 2010, and notably Presidential Early-Career Award for Scientists and Engineers (PECASE) from U.S. White House in 2011.

# Programmable Microcapsules

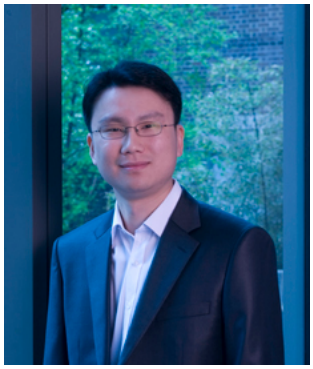
**Daeyeon Lee**

Assistant Professor
Department of Chemical and Biomolecular Engineering, University of Pennsylvania
220 S. 33rd St. 311A Towne, Philadelphia, PA 19104
Tel: +1-215-573-4521
Email: daeyeon@seas.upenn.edu

ABSTRACT

We present the generation of near-infrared (NIR)-sensitive microcapsules and demonstrate that the release properties of these microcapsules can be tailored by controlling their morphology. Hollow microcapsules containing an aqueous core covered by a thin shell are useful for encapsulating, protecting and delivering active ingredients. In this study, we present the generation of near-infrared-responsive PLGA microcapsules with release properties that can be programmed by controlling the morphology of the microcapsules. A biocompatible polymer, poly(DL-lactic-co-glycolic)acid (PLGA), is used to form hollow microcapsules from monodisperse water-in-oil-in-water (W/O/W) double emulsions[1]. Both the composition of PLGA and the oil phase of W/O/W double emulsions significantly influence the morphology of the subsequently formed microcapsules. PLGA microcapsules with vastly different morphologies, from spherical to "snowman-like" capsules, are obtained due to changes in the solvent quality of the oil phase during solvent removal. The adhesiveness of the PLGA-laden interface plays a critical role in the formation of snowman-like microcapsules. NIR-sensitive PLGA microcapsules are designed to have responsive properties by incorporating gold nanorods into the microcapsule shell, which enables the triggered release of encapsulated materials. The effect of capsule morphology on the NIR responsiveness and release properties of PLGA microcapsules is demonstrated.

BIOGRAPHY



Daeyeon Lee (born in Seoul, Korea) received his B.S. in Chemical Engineering from Seoul National University in 2001 and received his Ph.D. in Chemical Engineering/Program in Polymer Science and Technology at MIT in 2007 co-supervised by Robert E. Cohen and Michael F. Rubner. After his Ph.D., Daeyeon was a postdoctoral fellow in the School of Engineering and Applied Sciences at Harvard University where he worked with David A. Weitz. Daeyeon joined the Department of Chemical and Biomolecular Engineering at the University of Pennsylvania in 2009 as an assistant professor. Daeyeon has won numerous awards and recognitions including the 2010 Victor K. LaMer Award from ACS Colloid and Surface Chemistry Division, the NSF CAREER Award (2011), the 2011 Korean-American Scientists and Engineers Association Young Investigator Award and the 2012 KIChE President Young Investigator Award.

*Technical Session D1-W1-T2: In Silico Research and Biomedical Informatics*

## Workshop and Session Chairs


## Li-San Wang

Assistant Professor
Department of Pathology and Laboratory Medicine
University of Pennsylvania Perelman School of Medicine
E-mail: lswang@mail.med.upenn.edu
(賓州大學醫學院王立三教授)


BIOGRAPHY

Li-San Wang received his B.S. (1994) and M.S. (1996) in Electrical Engineering from the National Taiwan University. He received his M.S. (2000) and Ph.D. (2003) from the University of Texas at Austin, both in Computer Sciences, and was a postdoctoral fellow at the University of Pennsylvania between 2003 and 2006. Currently he is an Assistant Professor of Pathology and Laboratory Medicine, a faculty member of Penn Center for Bioinfomatics, and a fellow of Institute on Aging and Penn Genome Frontiers Institute, University of Pennsylvania. Dr. Wang's research integrates bioinformatics, genomics, and genetics to study neurodegeneration and psychiatric disorders. He has authored sixty peer-reviewed book chapters and journals on these topics and served on the program and organizing committees of various international workshops and conferences. He is the Principal Investigator of the National Institute on Aging Genetics of Alzheimer's Disease Data Storage Site (NIAGADS) and a Co-PI of the Alzheimer's Disease Genetics Consortium (ADGC).

# Biomedical Image Processing and Neuronal Structures Analysis

**Yu-Tai Ching**

Director, Institute of Biomedical Engineering
National Chiao Tung University
E-mail: ytc@cs.nctu.edu.tw
(交通大學生醫工程研究所所長荊宇泰教授)

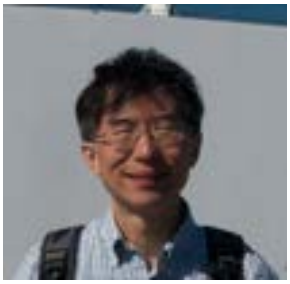
ABSTRACT

Two problems studied, one is to construct the structure of a neuron from a stack of volume image of Drosophila brain acquired using confocal microscopy. The other is to compute the changes of a neuron in two time-points. To the second problem, the images were acquired by multi-photon microscope.

Single neuron can be labeled by GFP in the fly brain. We present a high-throughput method to constructed the neuronal structure from a stack of volume data acquired by confocal microscope. We proposed to compute the 2D skeleton of the neuron in each slice. The 3D neuronal structure is then constructed from the 2D skeleton employing the shortest path algorithm. The method has been applied to more than 15000 neurons. Further analysis can be performed by using the traced neurons. We show an example of finding tracts in the fly brain.

GFP-expression DNA constructs were electroporated into the tectum Xenopus laevis tadpoles. Images of the neuron at different time-points were acquired using multi-photon microscope. We present a semi-automatic method to compute the alteration of the neuron. For a branch at time-point 1, the method produces a suggestion list of the matched branches of the neuron in time-point 2. With the help of the method, we are able to classify the neuronbranches into the categories of remaining, retracted, or newly grown.

BIOGRAPHY



Yu-Tai Ching was born in Taipei, 1957. He received his BS degree in Industrial Engineering from National Tsing Hua University, Hsin Chu, Taiwan, in 1980, and MS and PhD in Computer Science from Northwestern University, Evanston, Illinois, USA, in 1983 and 1987 respectively.

He joined the Institute of Information Science, Academia Sinica, in 1987; he then transfer to the Department of Information Science, National Chiao Tung University in 1991. In 1995, he visited the Department of Radiology, The University of Chicago as a visiting scholar. He is currently a Professor in the Department of Computer Science, National Chiao Tung University, Hsin Chu, Taiwan. Starting from August 2011, he serves as the Director of the Institute of Biomedical Engineering. His research interests are design and analysis of algorithms, computer graphics, biomedical images analysis, and Computational Biology.

# Analysis of retinal development using RNA-seq

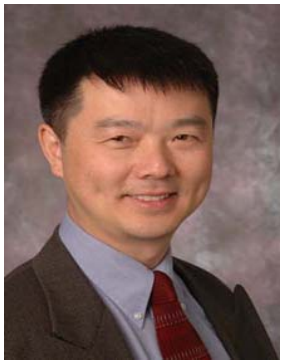
**Li Cai**

Associate Professor, Department of Biomedical Engineering
Rutgers University
E-mail: lcai@rutgers.edu

ABSTRACT

RNA-seq method provides a new strategy for both categorizing and quantifying transcriptome of particular cells under specific conditions with much more complex information on expression levels, differential splicing, allele-specific expression, RNA editing and fusion transcripts when reaches sufficient sequence coverage. With RNA-seq analysis, a complete genome-wide transcriptional architecture of genes can be characterized, which is central for the understanding of development, physiology and diseases. This study focuses on the role of topoisomerase II beta (Top2b) in retinal development with RNA-seq analysis. Top2b is a member of the DNA topoisomerase family. Top2b assists DNA structure re-organization during replication, transcription, recombination, and chromatin remodeling. Top2b is ubiquitously expressed in terminally differentiated cells. Emerging evidence have demonstrated the role of Top2b in neurite growth and guidance, neuronal migration, cerebral stratification, and neuronal survival. To determine the molecular mechanism underlying the Top2b functions during retinal development, retina-specific knockout mice were generated. RNA-seq was performed on retina samples from Top2b wild-type and knockout mice. Differential gene and transcript expression analysis of RNA-seq experiments was followed with TopHat and Cufflinks. Differentially expressed genes (DEGs) in Top2b wild-type and knockout retina samples were identified. Consistent with many studies on Top2b functions, DEGs were found to be associate with 1) neural cell death/apoptosis (e.g., Igf1, Grin1, Vegfa, etc); 2) neurite outgrowth (e.g., Reln, Pdia3, Creb1, etc). Together, this study demonstrates that RNA-seq is a powerful method for the studies of developmental systems. The data provide interesting findings on genes and gene networks that are important for neuronal survival/death and neurite growth.

BIOGRAPHY



Dr. Cai has a broad background in developmental biology, neuroscience, stem cell research, and genomics/bioinformatics. As a postdoctoral fellow at Harvard Medical School, he carried out research on the role(s) of transcription factors, e.g., basic helix-loop-helix (bHLH) genes, in the developing mammalian retina and cerebral cortex. At Dana-Farber Cancer Institute/Harvard Medical School, his research focused on statistical analysis of genome-wide transcription profiling data on breast cancer and neural development, and developed novel mathematical/statistical methods for such data analysis. At Rutgers, he successfully administered research projects focusing on breast cancer stem cells, neural stem cells, spinal cord development and regeneration, collaborated with other researchers, and produced peer-reviewed publications from each project.

*Technical Session D1-W1-T2: In Silico Research and Biomedical Informatics*


## Jessica C. Mar

Assistant Professor, Departments of Systems & Computational Biology and
Department of Epidemiology & Population Health
Albert Einstein College of Medicine of Yeshiva University
E-mail: Jessica.Mar@einstein.yu.edu



ABSTRACT

Characterizing cellular phenotypes based on distinct gene expression profiles has become a standard part of understanding biological function. Typically, we identify subsets of genes with differential expression levels that on average distinguish one phenotypic group from another. While studying genes on the basis of absolute expression is important to understanding regulation, we are only just beginning to recognize that variability in gene expression is an insightful regulatory parameter too. Work from our lab, as well as others, has shown that variability gives us an additional window into regulatory control of the transcriptome. In this talk, we outline some of the research directions the Mar lab is taking to understand how variability in gene expression contributes to controlling pluripotency in human stem cells, and its impact on other biological systems.


BIOGRAPHY

Jessica Mar received her Bachelor of Science degree in mathematics at the University of Queensland in Brisbane, Australia and First Class Honors in statistics in 2002. She received her PhD in biostatistics from Harvard University in 2008.

She currently runs a computational biology lab as an Assistant Professor at the Albert Einstein College of Medicine in the Department of Systems and Computational Biology in the Bronx, New York. Previously she was a postdoctoral research fellow at the Dana-Farber Cancer Institute in Boston, and a visiting scientist at the European Bioinformatics Institute in the United Kingdom. The focus of the Mar lab is to understand how variability of biological signals is involved in cellular regulation and its role in human disease.

Prof. Mar is a member of the International Society of Computational Biology, the Australian Society for Biochemistry and Molecular Biology and the Australasian Microarray and Associated Technologies Association. She is a recipient of a University of Queensland medal and an American-Australian Fulbright award. She is currently an Associate Editor of *Genomics*.

*Technical Session D1-W2-T2: Biomedical Science and Engineering*

# Control of Retinal Progenitor Fates by Transcription Factors and Notch Signaling

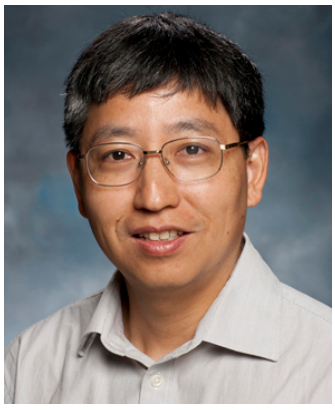
**Mengqing Xiang**

Professor, Center for Advanced Biotechnology and Medicine
& Department of Pediatrics
UMDNJ-Robert Wood Johnson Medical School
E-mail: xiang@cabm.rutgers.edu
(新泽西州罗伯屋强森医学院高级生物技术与医学中心与儿科系向孟清教授)

## ABSTRACT

The generation of diverse neuronal types and subtypes from multipotent progenitors during development is crucial for assembling functional neural circuits in the adult central nervous system. During mouse retinogenesis, early retinal progenitors give rise to several cell types including ganglion, amacrine, horizontal, cone, and rod cells. It is unknown at present how each of these cell fates is selected from the multiple neuronal fates available to the early progenitor. Using a combination of bioinformatic, genetic and biochemical approaches, we investigated the mechanism by which the Foxn4 winged-helix/forkhead transcription factor selects the amacrine and horizontal cell fates from multipotential retinal progenitors. These studies indicate that Foxn4 has an intrinsic activity to suppress the alternative photoreceptor cell fates of early retinal progenitors by selectively activating Dll4-Notch signaling. Gene expression and conditional ablation analyses reveal that Dll4 is directly activated by Foxn4 via phylogenetically conserved enhancers and that Dll4 can partly mediate the Foxn4 function by serving as a major Notch ligand to expand the progenitor pool and limit photoreceptor production. Our data together define a Foxn4-mediated molecular and signaling pathway that underlies the suppression of alternative cell fates of early retinal progenitors.

## BIOGRAPHY



Dr. Xiang received his BS degree in plant genetics in 1985 from Sun Yat-sen University, Guangzhou, China, and earned his Ph.D. degree in molecular biology and biochemistry from the University of Texas M.D. Anderson Cancer Center, Houston, in 1991.

He is currently a Professor at the Center for Advanced Biotechnology and Medicine and Department of Pediatrics, UMDNJ-Robert Wood Johnson Medical School in Piscataway NJ, USA. Before joining Robert Wood Johnson Medical School as an Assistant Professor in 1996, he conducted his postdoctoral studies at the Johns Hopkins University School of Medicine. He has authored/coauthored about 60 refereed articles in the areas of neurodevelopment and diseases. His research interests center on understanding the molecular mechanisms and regulatory gene networks that govern the determination, differentiation and survival of sensory neurons and cells. His lab employs a variety of molecular, genetic and bioinformatic approaches to identify and study transcription factors and signaling molecules that are required for programming development of the retina, inner ear, spinal cord, and other CNS areas.

Prof. Xiang is a member of the Society for Neuroscience and the Association for Research in Vision and Ophthalmology, and serves as a Review Editor for the journal Frontiers in Neurogenomics. He has received a number of honors including the CUSBEA (China-United States Biochemistry Examination and Application) Graduate Study Fellowship, Howard Hughes Medical Institute Postdoctoral Fellowship, Basil O'Connor Starter Scholar Research Award, Sinsheimer Scholar Award, and the Wolf, Block, Schorr and Solis-Cohen, LLP Award in Auditory Science.

*Technical Session D1-W2-T2: Biomedical Science and Engineering*


## Wenqin Luo

Assistant Professor, Department of Neuroscience
The Perelman School of Medicine, the University of Pennsylvania
E-mail: luow@mail.med.upenn.edu
(宾夕法尼亚大学医学院神经科学系罗文琴教授)



ABSTRACT

The spinal cord contains many descending and ascending axonal bundles, which are essential for the communication between peripheral nervous system and brain. The spinal cord injury usually disrupts some of these axonal bundles and causes severe sensory and motor deficits. Thus, it is of fundamental importance to thoroughly understand the functional organization, developmental establishment, and regeneration of these axonal bundles.

The spinal cord dorsal column is one of the major ascending axonal tracks, which mediates the discriminative touch and proprioceptive information to brain. It is mainly composed of ascending axons of discriminative-touch-sensing mechanoreceptors and body-position-sensing proprioceptors, which terminate in the dorsal column nuclei of medulla. Since the dorsal column is a main focus for spinal cord injury and regeneration and stimulating the dorsal column is used to treat patients with chronic pain and brain injuries, elucidating the functional organization of dorsal column will provide an important anatomical reference for related researches and clinical practices.

The textbook dogma about the dorsal column is that ascending somatosensory axons are organized by the location of their receptive fields, but independent of their respective subtypes ("somatotopic map"). Unexpectedly, with the modality specific genetic tracing, we discovered that RA mechanoreceptor axons are highly enriched in the (medial) gracile fasciculus, while proprioceptor axons are mainly located in the (lateral) cuneate fasciculus. These novel results suggest that dorsal column axons are sorted according to their subtypes ("modality segregation"), which directly challenges the classic "somatotopic map" dogma. Using a combination of anatomical and mouse genetic approaches, we have determined the key morphological differences between ascending axons of mechanoreceptors and proprioceptors, which explains the formation of "modality segregation". In addition, we found that this "modality segregation" is conserved in multiple mammalian species, including human. In summary, our research establishes a new model for the functional organization of mammalian spinal cord dorsal column, which will modify the current textbook "dogma".


BIOGRAPHY

| NAME | POSITION TITLE |
|---|---|
| Wenqin Luo | Assistant Professor of Neuroscience |

EDUCATION/TRAINING

| INSTITUTION AND LOCATION | DEGREE *(if applicable)* | YEAR(s) | FIELD OF STUDY |
|---|---|---|---|
| Hunan Medical University, ChangSha, China | MD | 1991-1996 | Medicine |
| Peking Union Medical College, Beijing, China | MS | 1996-1999 | Molecular Biology |
| Johns Hopkins University | Ph.D. | 1999-2005 | Neuroscience |
| Duke University | | 2005-2006 | Neuroscience |
| Johns Hopkins University | | 2006-2010 | Neuroscience |

**A. Positions and Honors.**

**Positions and Employment**

| | |
|---|---|
| 02/2005- 02/2006 | Postdoctoral fellow, Dr. Lawrence Katz's lab, Howard Hughes Medical Institute, Department of Neurobiology, Duke University, Durham, NC |
| 02/2006- 02/2010 | Postdoctoral fellow, Dr. David Ginty's lab, Howard Hughes Medical Institute, Department of Neuroscience, Johns Hopkins University School of Medicine, Baltimore, MD |
| 03/2010- 02/2011 | Postdoctoral fellow, Dr. David Ginty's lab, Department of Neuroscience, Johns Hopkins University School of Medicine, Baltimore, MD |
| 03/2011- | Tenure-track assistant professor, Department of Neuroscience, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA |

**Professional Memberships**

| | |
|---|---|
| 2004- Present | Member, Society of Neuroscience |
| 2012- | Member, American Pain Society |

**Honors**

| | |
|---|---|
| 2004 | Best Poster Award, John Hopkins School of Medicine, Baltimore, MD |
| 2008 | Best Poster Award, Gordon Conference of Molecular and Cellular Neuroscience, Hong Kong, China |
| 03/2010 | K99/R00 Pathway to Independence Award from NINDS |
| 04/2010 | The A. McGehee Harvey Research Award, Johns Hopkins School of Medicine, Baltimore, MD |
| 07/2011 | McCabe Pilot Award, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA |
| 02/2012 | Basil O'Connor Starter Scholar Research Award, March of Dime, White Plains, NY |

*Technical Session D1-W2-T2: Biomedical Science and Engineering*

# The Role of Natural Killer T Cells in Intestinal Inflammation


**Chyung-Ru Wang**

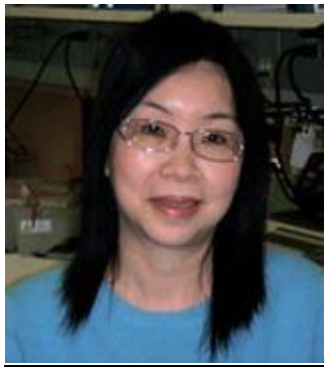
Professor, Department of Microbiology and Immunology
Feinberg School of Medicine
Northwestern University
E-mail: chyung-ru-wang@northwestern.edu
(西北大學醫學院王瓊如教授)



ABSTRACT

Natural killer T (NKT) cells are a subset of T cells that are notable for their rapid cytokine secretion in response to lipid antigens bound to the CD1d protein. Cytokines produced by NKT cells during the early phase of the immune response can subsequently activate other immune cells and elicit their respective immune functions. Patients with ulcerative colitis, one common type of inflammatory bowel disease (IBD), have a higher numbers of CD1d-restricted NKT cells in the affected area. To understand how these immune cells are regulated and how they contribute to the pathogenesis of IBD, my lab created genetically engineered mice that have increased numbers of NKT cells as well as high levels of the CD1d protein. These mice spontaneously develop an IBD-like disease. We have used this newly developed animal model to study how dysregulated NKT cell responses lead to intestinal inflammation and how such responses can be suppressed.


BIOGRAPHY



**EDUCATION:**

| | | |
|---|---|---|
| 1979-1982 | National Taiwan University, Taiwan, R.O.C. | B.S. (Zoology) |
| 1982-1987 | University of Texas, Austin, TX | Ph.D. (Biology) |

PROFESSIONAL APPOINTMENTS:

| | |
|---|---|
| 1987-1991 | Postdoctoral Associate (Sponsor: Dr. Kirsten Fischer Lindahl)<br>Howard Hughes Medical Institute, University of Texas Southwestern Medical School |
| 1991-1993 | Postdoctoral Associate (Sponsor: Dr. Johann Deisenhofer)<br>Department of Biochemistry, University of Texas Southwestern Medical School |
| 1993-1994 | Instructor (Sponsor: Dr. Johann Deisenhofer)<br>Department of Biochemistry, University of Texas Southwestern Medical School |
| 1994-2001 | Assistant Professor<br>Department of Pathology, Committee on Immunology, University of Chicago |
| 2001-2007 | Associate Professor<br>Department of Pathology, Committees on Immunology and Microbiology, University of Chicago |
| 2007-2008 | Professor<br>Department of Pathology, Committees on Immunology and Microbiology, |

| | |
|---|---|
| | University of Chicago |
| 2008-present | Professor |
| | Department of Microbiology and Immunology, Northwestern University |

**HONORS AND AWARDS:**

| | |
|---|---|
| 1979-1982 | Book Coupon Awards (National Taiwan University, top 5 % of the Class) |
| 1980-1982 | Natural Science Fellowship |
| 1982 | Member of Phi Tau Phi Scholastic Honor Society |
| 1995 | Cancer Research Foundation Young Investigator Awards |
| 1996-1999 | Searle Scholars Award |
| 2006 | Future Faculty Mentorship Award (University of Chicago) |

**MEMBERSHIP IN PROFESSIONAL SOCIETIES:**

| | |
|---|---|
| 1994-present | American Society of Immunology |

*Technical Session D1-W3-T2: Bio-Materials. Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*

## Workshop and Session Chairs


## Fan-Gang Tseng

Professor and Chairman, Department of Engineering and System Science
Deputy Director, Biomedical Technology Research Center
National Tsing-Hua University
E-mail: fangang@ess.nthu.edu.tw
(清華大學工程與系統科學系主任曾繁根教授)


BIOGRAPHY

# Electric Tweezers

**Donglei (Emma) Fan**

Assistant Professor, Department of Mechanical Engineering
The University of Texas, Austin
E-mail: dfan@austin.utexas.edu

ABSTRACT

Electric tweezers utilize DC and AC electric fields through voltages applied on patterned electrodes to manipulate nanoentities suspended in a liquid. Nanowires with a large aspect ratio are particularly suitable for use in electric tweezers for patterning, assembling, and manipulation. Despite operating in the regime of extremely small particle Reynolds number [of order 10−5], electric tweezers can manipulate nanowires with high precision to follow any prescribed trajectory, to rotate nanowires with controlled chirality, angular velocity and rotation angle, and to assemble nanowires to fabricate nanoelectromechanical system (NEMS) devices such as nanomotors and nano-oscillators. Electric tweezers have also been used to transport in a highly controlled manner drug-carrying functionalized nanowires for cell-specific drug delivery.

BIOGRAPHY

***Education***

- **May 2007, Ph. D.** in Materials Science and Engineering, *Johns Hopkins University*
- **May 2005, Master** in Electrical and Computer Engineering, *Johns Hopkins University*
- **May 2003, Master** in Materials Science and Engineering, *Johns Hopkins University*
- **July 1999, Bachelor** in Chemistry, Department of Intensive Instruction, honor program for gifted youth, *Nanjing University, China*

***Professional Experience***

- 2010~ present, Assistant professor @ University of Texas at Austin
- 2006~ 2009, Postdoctoral Fellow @ Johns Hopkins University

***Honors and Awards***

- National Science Foundation CAREER Award (2012)
- Nominated for 2010 MIT Technology Review's prestigious TR35 awards, which recognizes the world's top young innovators (2010)
- NSF Fellowship for Summer Program at California Institute of Technology (2007)
- Postdoctoral Merit Fellowship, Johns Hopkins University (2006- 2009)

- Profiled Graduate Student by the Whiting School of Engineering at Johns Hopkins University (200 5)
- Graduate Merit Award, Johns Hopkins University (2000)
- Scholarship for Academic Excellency, Nanjing University, China (every year 1996-1999)
- Early Admission to Nanjing University waived of National College Entrance Examination and provided with scholarship (1995)
- Prize Winner in Multiple National High-School Competitions in the Fields of Physics, Chemical, and Biology, China (1992- 1994)

***Professional Affiliation***

Member: American Physical Society (APS), Materials Research Society (MRS)

# Single-Cell Bio-MEMS for Systems Oncology

**Rong Fan**

Assistant Professor, Department of Biomedical Engineering
Yale University
Email: rong.fan@yale.edu
(耶魯大學生物醫學工程系樊榮教授)

ABSTRACT

The singular term "cancer" is never one kind of disease, but deceivingly encompasses a large number of heterogeneous disease states, which makes it impossible to completely treat cancer using a generic approach. Rather systems approaches are urgently required to assess cancer heterogeneity, stratify patients and enable the most effective, individualized treatment. The heterogeneity of tumors at the single-cell level is reflected by the hierarchical complexity of tumor microenvironment. To identify all the cellular components, including both tumor and infiltrating immune cells, and to delineate the associated cell-to-cell signaling network that dictates tumor initiation, progression and metastasis, we developed a single-cell bio-MEMS chip that can analyze a panel of proteins that are potentially associated inter-cellular signaling network in tumor microenvironment from hundreds of single cells in parallel. This platform integrates two advanced technologies – microfluidic single cell handling and ultra-high density protein array. This device was first tested for highly multiplexed profiling of secreted proteins including tumor-immune signaling molecules from monocytic leukemia cells. We observed profound cellular heterogeneity with all functional phenotypes quantitatively identified. Correlation analysis further indicated the existence of an inter-cellular cytokine network, in which TNFα-induced secondary signaling cascades further increased functional cellular diversity. It was also exploited to evaluate polyfunctionality of tumor antigen-specific T cells from melanoma patients being treated with adoptive T cell transfer immunotherapy. This platform was further extended to the analysis of both solid tumor cells (e.g. human lung carcinoma cells) and infiltrating immune cells (e.g. macrophages) in order to enable systems analysis of the complex tumor microenvironment from small amounts of clinical specimens, e.g. skinny needle biopsies. Thus, it could potentially become a clinical tool for patient stratification based upon the inter-cellular signaling network and designing new anti-cancer therapy by targeting microenvironmental components.

BIOGRAPHY

Dr. Rong Fan was born in Chongqing, China and earned his B.S. and M.S. in chemistry from University of Science and Technology of China in 1999 and 2001, respectively. Afterwards, he went to University of California at Berkeley to pursue a graduate study with Professor Peidong Yang in Department of Chemistry, where his PhD work involves the study of nanowires for thermoelectric energy conversion and nanotube nanofluidic transistors for molecular and ion transport control.

After graduation, he went on to join the NanoSystems Biology Cancer Center at CalTech, working in the laboratory of Professor Jim Heath, where he developed an ultra-high density barcode chip that can measure an array of protein biomarkers from minute amounts of whole blood samples or even single immune cells from cancer patients. Currently, he is Assistant Professor in Department of Biomedical Engineering at Yale University (New Haven, CT, U.S.A.). His research focuses on the development of micro-/nano-technologies for single-cell proteomic and functional genomic analysis and the application of these technologies in conduction with systems biology principles to investigate tumor heterogeneity, tumor microenvironment and cellular immunity.

Dr. Fan is a member of Biomedical Engineering Society, Materials Research Society, American Physical Society, and American Chemical Society. He is the recipient of numerous awards including the MRS Graduate Student Award (Gold Medal), The NCI Howard Temin Pathway-to-Independence Award (K99/R00), the Bill & Melinda Gates Foundation GCE Award and the Alzheimer's Association New Investigator Research Award.

# Photothermal Nanoblade for Single Cell Surgery and Cargo Delivery

**Pei-Yu (Eric) Chiou**

Associate Professor, Department of Bioengineering
University of California, Los Angeles
E-mail: pychiou@seas.ucla.edu
(加州大學洛杉磯分校生物工程系邱培鈺教授)

ABSTRACT

I present a novel photothermal nanoblade system that utilizes metallic nanostructures to harvest short laser pulse energy and convert it into highly localized and shaped explosive cavitation bubbles, which rapidly puncture a lightly contacting cell membrane via high-speed fluidic flows and induced transient shear stress. Photothermal nanoblade can generate micrometer-sized membrane access ports for delivering highly concentrated, large-size cargo with high efficiency and cell viability into mammalian cells. Biologic and inanimate cargo over 3-orders of magnitude in size including DNA, RNA, quantum dots, 200 nm polystyrene beads, to 2 μm bacteria have also been delivered into multiple mammalian cell types including neuron cells and human embryonic stem cells.

BIOGRAPHY

Prof. Eric P. Y. Chiou received his Ph.D. degree in Electrical Engineering and Computer Sciences Department from the University of California at Berkeley in 2005. He received his M.S. degree in Electrical Engineering Department in the University of California at Los Angeles and B.S. degree in Mechanical Engineering Department from National Taiwan University in Taiwan. He joined the University of California at Los Angeles in 2006. He is now an associate professor in Mechanical and Aerospace Engineering Department and Bioengineering Department. His research interests are in optofluidics, laser surgery, biophotonics, nanophotonics, and Lab-on-Chip systems. He received the NSF CAREER award in 2008.

# Integrative Bioinformatics for Knowledge Discovery of PTM Networks

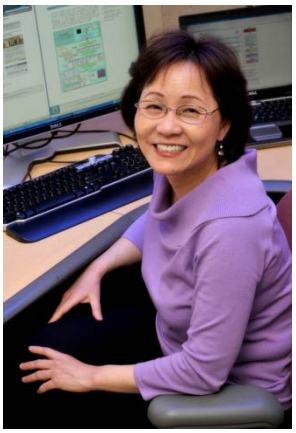
**Cathy H. Wu**

Edward G. Jefferson Chair and Director
Center for Bioinformatics & Computational Biology
University of Delaware
E-mail: wuc@udel.edu
(德拉威爾大學生物資訊及計算系统生物中心主任吳慧華教授)

ABSTRACT

Facilitated by proteomic and other high-throughput studies, the number of protein phosphorylation related resources has been growing along with pertinent literature. However, our understanding of phosphorylation events in signaling networks is still fragmented. The iPTMnet (http://proteininformationresource.org/iPTMnet) is a new bioinformatics resource being developed for integrative understanding of protein post-translational modifications (PTMs) in systems biology context, with the initial focus on phosphorylation. The iPTMnet bioinformatics framework consists of: (i) the PIR iProClass database for molecular and omics data integration, including many phosphorylation, pathway, and interaction databases, (ii) the RLIMS-P/eFIP text mining system for knowledge extraction from scientific literature, (iii) the Protein Ontology (PRO) for knowledge representation of specific protein PTM forms, and (iv) a web portal linking data and analysis tools with Cytoscape network visualization for scientific queries and exploration. The text mining system allows researchers to provide PubMed IDs or proteins of interest as input, and returns a ranked list of abstracts with evidence tagging for phosphsorylation information (kinase, substrate, site) and functional impact, particularly interaction partners of phosphorylated proteins. The interface supports community annotation to validate text mining results and capture knowledge about PTM forms in PRO. A PTM database is under development to combine text mining results and data extracted from related databases to capture relevant kinase-substrate information and their functional impact and biological context. Scientific use cases have been developed to demonstrate the integrative bioinformatics approach for exploring and discovering PTM networks.

BIOGRAPHY



Cathy H. Wu was born in Taipei, Taiwan, ROC. She received her BS in Plant Pathology from National Taiwan University (Taipei, Taiwan) in 1978, MS and PhD in Plant Pathology from Purdue University (West Lafayette, IN) in 1984, and a second MS in Computer Science from University of Texas at Tyler (Tyler, TX) in 1989.

She is the Edward G. Jefferson Chair and Director of the Center for Bioinformatics & Computational Biology, Professor of Computer & Information Sciences and Biological Sciences, and Director of Bioinformatics Master's and PhD Programs at the University of Delaware (Newark, DE). She is also Director of the Protein Information Resource (PIR) and Adjunct Professor at Georgetown University (Washington, DC). Previously she was Professor of Biochemistry and Molecular Biology at Georgetown University (2001-2008), and Assistant to Full Professor of Biomathematics at University of Texas at Tyler (1990-1999). She has conducted bioinformatics research for over 20 years, encompassing protein structure-function, biological text mining and ontology, proteomic informatics, systems biology, and translational bioinformatics. She has published about 180 peer-reviewed papers and eight books and conference proceedings, including the book "Bioinformatics for Comparative Proteomics" (Methods in Molecular Biology, Vol. 694, Humana Press, 2011).

Prof. Wu is the PI/Co-PI on several consortium projects, including the UniProt, Protein Ontology and BioCreative. She serves on several advisory boards, including the NIH NIGMS Protein Structure Initiative Advisory Committee,

HUPO (Human Proteome Organization) Council, USHUPO Board of Directors, the PDB (Protein Data Bank) Advisory Board, and the ACM (Association for Computing Machinery) SIGBioinformatics Board of Directors. She has served on over 50 conference organizing committees, and given about 140 invited talks.

# Data Mining in RNA Informatics

**Jason Tsong-Li Wang**

Professor, Department of Computer Science
Director, Data and Knowledge Engineering Lab and Bioinformatics Center
New Jersey Institute of Technology
E-mail: wangj@njit.edu
(紐澤西理工學院電腦科學系暨數據知識工程實驗室及生物資訊中心主任王中力教授)

ABSTRACT

I will present some new techniques for data mining in RNA informatics. In particular, I will describe an algorithm for predicting coaxial helical stacking in RNA junctions, and show how this algorithm can be extended to identify coaxial helical stacking motifs in genomic sequences. Traditional methods for non-coding RNA (ncRNA) discovery are capable of identifying sequence patterns or motifs with simple secondary structures in genomes. This work extends the traditional methods for genome-wide ncRNA discovery by exploring more complicated RNA tertiary structures through feature collection and supervised learning techniques.

BIOGRAPHY

Jason T. L. Wang received the B.S. degree in mathematics from National Taiwan University, Taipei, Taiwan, in 1980, and the Ph.D. degree in computer science from the Courant Institute of Mathematical Sciences at New York University in 1991.

He is a full professor in the Computer Science Department at the New Jersey Institute of Technology, and Director of the University's Data and Knowledge Engineering Laboratory. He has published 120 refereed papers and six books including *Pattern Discovery in Biomolecular Data: Tools, Techniques and Applications* (New York, NY: Oxford University Press, 1999), *Data Mining in Bioinformatics* (London, UK: Springer, 2005) and *Computational Intelligence and Pattern Analysis in Biological Informatics* (Hoboken, NJ: Wiley, 2010). His research interests center on data mining in bioinformatics, particularly genome-wide ncRNA discovery, gene network prediction, and biomedical text ranking through semi-supervised learning.

Dr. Wang is the executive editor of the World Scientific Book Series on Science, Engineering and Biology Informatics, and has been a program committee member of over 100 national and international conferences. He is a Founding Chair of the ACM SIGKDD Workshop on Data Mining in Bioinformatics, a Workshop Co-Chair of the 2010 ACM International Conference on Bioinformatics and Computational Biology, a Co-Chair of the 2006 IEEE ICDM Workshop on Data Mining in Bioinformatics, and the 2012 IEEE ICDM Workshop on Biological Data Mining and its Applications in Healthcare.

# Computational Methods for Studying *In Vivo* Macromolecular Motion

**Edmond Chow**

Associate Professor, School of Computational Science and Engineering
Georgia Institute of Technology
E-mail: echow@cc.gatech.edu

ABSTRACT

Cells contain billions of proteins and other biologically important macromolecules. The simulation of large parts of the cell, or even the complete cell, can lead to invaluable insights on the complex, interrelated processes responsible for life and disease. In this talk, we focus on the Brownian Dynamics method, and the related Stokesian Dynamics method, for simulating the motions of molecules interacting in a fluid medium. The computationally expensive parts of these methods include computing the long-ranged force on each molecule due to the motion of all other molecules. We discuss new numerical methods for reducing the cost and algorithmic complexity of these computations, as well as how these methods may be adapted to run efficiently on high-performance computer architectures.

BIOGRAPHY

Edmond Chow was born in Taipei in 1969. He earned an Hons. B.A.Sc. Degree in systems design engineering from the University of Waterloo (Waterloo, Ontario, Canada) in 1993 and a Ph.D. degree in computer science from the University of Minnesota (Minneapolis, MN, USA) in 1998.

He is currently an Associate Professor in the School of Computational Science and Engineering in the College of Computing at Georgia Institute of Technology (Atlanta, GA, USA). He has held positions at Columbia University, D. E. Shaw Research, and Lawrence Livermore National Laboratory. His research interests are in developing and applying numerical and discrete algorithms for solving large-scale scientific computing problems.

Prof. Chow is an Associate Editor of SIAM Journal on Scientific Computing and has served on the program committee of many conferences, including as Algorithms Chair for the 2012 ACM/IEEE International Conference for High Performance Computing, Networking, Storage and Analysis. His awards include a Presidential Early Career Award for Scientists and Engineers and an ACM Gordon Bell Prize.

# Menin, a contextual tumor suppressor and promoter in controlling endocrine tumor and leukemia

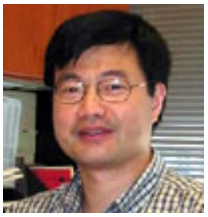
**Xianxin Hua**

Associate Professor, Department of Cancer Biology
University of Pennsylvania Perelman School of Medicine
E-mail: huax@mail.med.upenn.edu

ABSTRACT

Multiple endocrine neoplasia type 1 (MEN1), an inherited tumor syndrome, is characterized by development of tumors in multiple endocrine organs. The MEN1 gene encodes a nuclear protein menin, a bona fide tumor suppressor for many endocrine organs. We have shown that acute Men1 excision in mice leads to enhanced proliferation of beta cells. However, it is not well understood how menin represses proliferation of endocrine cells including beta cells. On the other hand, we have demonstrated that menin acts as an oncogenic protein in mixed lineage leukemia (MLL). MLL protein encodes a large protein containing a conserved SET domain that catalyzes histone H3 lysine 4 (H3K4) methylation. In a subset of acute leukemia cells, the MLL gene undergoes chromosomal translocations, resulting in formation of various MLL fusion proteins (MLL-FP), and we have found that menin, by interacting with MLL, promotes proliferation of the leukemia cells. However, it has been challenging to understand how menin suppresses proliferation of endocrine cells, yet promotes leukemogenesis in hematopoietic cells. We have recently made significant progress in understanding the underlying mechanisms. We have demonstrated that Men1 ablation enhances Hedgehog (Hh) signaling, a pro-proliferative and oncogenic pathway, via a protein arginine methyltransferase (PRMT)-related epigenetic pathway. On the other hand, we have recently discovered that acute depletion of the Trx protein MLL, or menin, a close partner of MLL that is critical for recruitment of MLL or MLL-AF9 oncogenic fusion protein to target genes, triggers MLL-AF9 leukemia cell differentiation. Menin/MLL deletion-induced differentiation is mediated, at least partly, via upregulating polycomb gene Ezh2, which normally antagonizes the function of Trx proteins. Therefore, in contrast to its classical role in antagonizing Trx function, polycomb EZH2 collaborates with Trx-associated menin to block MLL-AF9 leukemia cell differentiation, a novel mechanism suppressing leukemia cell differentiation. These findings provide novel insights into the opposite function of the menin pathway in a tissue-specific manner.

BIOGRAPHY



Xianxin Hua, MD, Hubei Medical College, China, 1983; PhD in molecular genetics, University of Texas Southwestern Medical Center in Dallas, 1995. Postdoctoral research at Whitehead Institute, Massachusetts Institute of Technology, on cancer biology and TGF-beta signaling.

He is an associate professor of cancer biology, Abramson Cancer Research Institute, Department of Cancer Biology, University of Pennsylvania Perelman School of Medicine, Philadelphia, USA. Part of his research team focuses on elucidating the molecular mechanisms as to how neuroendocrine tumors are molecularly regulated. In particular, his team has been trying to understand how an inherited tumor syndrome, multiple endocrine neoplasia type 1 (MEN1), develops and how the mechanistic insights can lead to improving therapy against this type of endocrine tumors. Moreover, his group has also discovered that the MEN1 gene promotes the development of a group of aggressive leukemia as well as development of diabetes. His team has found that the menin-related epigenetic pathway may be exploited to improve therapy of the neuroendocrine tumors, mixed lineage leukemia, and diabetes.

Dr. Hua is a member of American Association of Cancer Research, AAAS, American Society of Molecular Biology and Biochemistry, Faculty 1000. He has served in editorial boards for several cancer research-related journals and NIH study section. Dr. Hua has received multiple prestigious awards for his accomplishment in biomedical research, including Howard Temin Award, Burroughs Wellcome Career Development Award, Scholar of American Cancer Society, and Rita Allen Award.

*Technical Session D2-W2-T1: Biomedical Science and Engineering*


## Jianming Hu

Professor, Department of Microbiology and Immunology
The Pennsylvania State University College of Medicine
E-mail: juh13@psu.edu



ABSTRACT

Hepatitis B virus (HBV) is a significant global human pathogen, with over 350 million people chronically infected worldwide. Chronic HBV infection is the number one cause of hepatocellular carcinoma, a highly malignant cancer with few treatment options, and other end-stage liver diseases. HBV replicates a peculiar circular DNA genome via a reverse transcription pathway that is similar to, yet distinct from, that of retroviruses. We have focused our studies on the virus-host interactions, at the molecular and cellular level, which are critical to HBV replication and persistence. Cellular factors that positively or negatively regulate viral replication and assembly are sought using cell-free as well as cell culture systems that have been established or are being developed. We have discovered that cellular chaperones and other yet-to-be identified host factors are required for protein-primed initiation of HBV reverse transcription. We have also discovered that progression of viral reverse transcription is regulated by dynamic phosphorylation and dephosphorylation of the viral nucleocapsids, which are controlled by host kinases and phosphatases that we are trying to identify. Moreover, we have begun to identify specific intracellular factors involved in controlling HBV persistence. Based on our in vitro and in vivo studies of HBV secretion, we have recently proposed a novel model, "single strand blocking," to explain the selective HBV morphorgenesis. In contrast to the classical maturation signal model, our new model can account for the secretion of HBV virions containing double-stranded DNA or no nucleic at all (empty virions) but not those containing single-stranded DNA or RNA, a defining feature of HBV as a pararetrovirus. A long-range goal of our studies is to identify novel viral as well as host targets for developing effective anti-HBV therapies to clear chronic HBV infections.


BIOGRAPHY

**Academic Background**

| | |
|---|---|
| 1978 - 1983 | Bachelor of Medicine (M.D.)<br>Wuhan University School of Medicine, Wuhan, Hubei, China |
| 1983 - 1986 | Master of Medicine (M.S.)<br>Institute of Medical Virology, Wuhan University School of Medicine, Wuhan, Hubei, China |
| 1988 - 1993 | Doctor of Philosophy (Ph.D.)<br>Department of Microbiology and Immunology, The Pennsylvania State University College of Medicine, Hershey, Pennsylvania |

**Professional Background**

| | |
|---|---|
| 2010 - | Director, Office of Postdoctoral Affairs, The Pennsylvania State University College of Medicine, Hershey, PA |
| 2009 - | Professor, Department of Microbiology and Immunology, The Pennsylvania State University College of Medicine, Hershey, PA |
| 2007 - | Director, Graduate Program in Microbiology and Immunology, The Pennsylvania State University College of Medicine, Hershey, PA |
| 2004 - 2009 | Associate Professor, Department of Microbiology and Immunology, The Pennsylvania State University College of Medicine, Hershey, PA |
| 1997 - 2004 | Assistant Professor, Department of Microbiology, Boston University School of Medicine, Boston, MA |
| 1993 - 1997 | Postdoctoral Fellow, Institute for Cancer Research, Fox Chase Cancer Center, Philadelphia, Pennsylvania |
| 1987 - 1988 | Postdoctoral Associate, Virology Reference Laboratory, Department of Laboratory Medicine, Yale University School of Medicine, New Haven, Connecticut |
| 1987 - 1988 | Assistant Professor, Institute of Medical Virology, Wuhan University School of Medicine, Wuhan, Hubei, China |
| 1986 - 1987 | Research Associate, Institute of Medical Virology, Wuhan University School of Medicine, Wuhan, Hubei, China |

## Honors/Awards

Pasteur Prize for Scholarly Achievement in the Study of Microbiology and Immunology, The Pennsylvania State University College of Medicine, Hershey, Pennsylvania, 1991

Summer Research Award, Graduate School of The Pennsylvania State University, Hershey, Pennsylvania, 1992

John F. Enders Award for Excellence in Microbiology and Immunology, The Pennsylvania State University College of Medicine, Hershey, Pennsylvania, 1994

NRSA Postdoctoral Training Grant Award, Fox Chase Cancer Center, Philadelphia, Pennsylvania, 1994-1997

Herman Lopata Memorial Liver Scholar Award, American Liver Foundation, 1998 - 2001

Young Investigator Award, The Medical Foundation, 1999 - 2001

Invited Speaker, Gordan Research Conference - "Viruses and Cells," 2001; EMBO Symposium - "Hsp90 Chaperone Machine," 2002; International Symposium on Viral Hepatitis and Liver Diseases, 2012

Postdoctoral Mentorship Award, 2006 - 2007, Penn State College of Medicine

## Services

**Editorial Boards:** Journal of Virology, Virus Research, Virologica Sinica, Chinese Journal of Viral Diseases, Emerging Microbes and Infections,

**Ad Hoc Journal Reviewer:** Antimicrobial Agents and Chemotherapy, American Journal of Pathology, Bioorganic & Medicinal Chemistry Letters, Emerging Infectious Diseases, Gastroenterology, Hepatology, Journal of Biological Chemistry, Journal of Clinical Microbiology, Journal of Hepatology, Journal of Infectious Diseases, Journal of Molecular Biology, Journal of Virological Methods, Nature Protocols, PLoS One, PLoS Pathogens, Proceedings of the National Academy of Sciences USA, Vaccine, Virology

**Grants Reviewer: Standing Member** - NIH VirB Study Section; **Ad Hoc Reviewer** for numerous NIH panels, National Science Foundation of China, Philip Morris External Research Program, American Cancer Society, Medical Research Council of UK

**Conference Organizer/Organizing Committee,** International Meeting of the Molecular Biology of Hepatitis B Viruses, Woods Hole; International Symposium on Viral Hepatitis and Liver Diseases, Shanghai

# Mitochondrial quality control and its disease implication

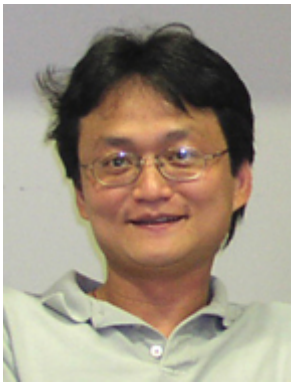
**Tso-Pang Yao**

Professor, Department of Pharmacology and Cancer Biology
Duke University Medical Center
E-mail: yao00001@mc.duke.edu
(杜克大學醫學中心姚佐邦教授)

ABSTRACT

As symbiotic organelles, mitochondria play a delicate role in host cells, where they provide energetic, metabolic and signaling function but also pose risks associated with oxidative stress. Impaired mitochondria, indeed, are prevalent in many age-associated disorders. Whether mitochondria can be pharmacologically rejuvenated is an intriguing question, whose answer would require better understanding of machinery that recognizes and manages damaged mitochondria. Recent research on Parkinson¹s disease has uncovered a potential quality control mechanism where impaired mitochondria are recognized and eliminated by a form of autophagy, termed mitophagy. Mitophagy, however, represents only one element of an elaborate mitochondrial QC network. I will discuss our effort to characterize additional components of this network and explore pharmacological means to strengthen mitochondrial quality control.

BIOGRAPHY



**Research Interests**

My laboratory studies the regulatory functions of protein acetylation in cell signaling and human disease. We focus on a class of protein deacetylases, HDACs, which we have discovered versatile functions beyond gene transcription. We wish to use knowledge of HDAC biology to develop smart and rational clinical strategies for HDAC inhibitors, a growing class of compounds that show potent anti-tumor and other clinically relevant activities. Currently, there are two major research areas in the laboratory: aging/age-related disease, and mitochondrial biology/cancer metabolism.

(1) HDAC, quality control (QC) autophagy, and neurodegenerative disease. The accumulation of damaged proteins and organelles is prominently linked to aging and age-associated disease, including neurodegeneration and metabolic disorders. Autophagy has emerged as specialized degradation machinery for the disposal of damaged protein aggregates and mitochondria, two common denominators in neurodegenerative diseases. We have discovered that this form of quality control (QC) autophagy is controlled by a ubiquitin-binding deacetylase, HDAC6. Using both mouse and cell models, we are investigating how HDAC6 controls QC autophagy, and its importance in the development of neurodegenerative disease and metabolic disorders. The potential of HDAC6 as a therapeutic target is being actively pursued.

(2) HDAC, mitochondria, and cancer metabolism. Acetyl-CoA is the donor of acetyl group for protein acetylation and numerous metabolic reactions. Remarkably, many mitochondrial enzymes and proteins are subject to acetylation. We have identified HDACs that regulate mitochondrial function and metabolic enzyme acetylation. We wish to uncover the role of HDAC in mitochondrial adaptation to different metabolic demands, including those associated with tumor-specific metabolism. We are also pursuing HDAC-dependent cancer metabolism as a novel therapeutic target in cancer treatment.

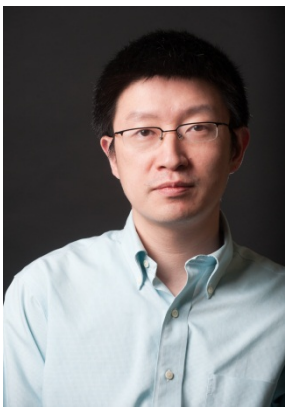
(3) HDAC, skeletal muscle remodeling, and neuromuscular disease. Skeletal muscle undergoes active remodeling in response to change in neural inputs. Loss in neural input causes dramatic muscle dysfunction and disease, such as ALS. We have discovered that neural activity controls muscle phenotype by a specific HDAC, whose activity becomes deregulated in ALS patients. We are characterizing this novel HDAC-dependent signaling pathway and developing modulators of this pathway for potential clinical utility in motor neuron disease.

*Technical Session D2-W3-T1: BioMaterials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*


**Nicholas X. Fang**

Associate Professor, Department of Mechanical Engineering
Massachusetts Institute of Technology
E-mail: nicfang@mit.edu
(麻省理工学院机械工程系方绚莱教授)


BIOGRAPHY



*Technical Session D2-W3-T1: BioMaterials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*

# Optofluidic lasers: principles and applications

**Xudong (Sherman) Fan**

Associate Professor, Department of Biomedical Engineering
University of Michigan, Ann Arbor
E-mail: xsfan@umich.edu
(密歇根大学安娜堡分校生物医学工程系范旭东教授)

ABSTRACT

I will review various optofluidic lasers and compare their performance. Direct and indirect excitation schemes will be discussed followed by possible biosensing applications and future research directions.

BIOGRAPHY

Dr. Fan obtained B.S. and M.S. from Peking University in 1991 and 1994, respectively, and Ph.D. in physics and optics from Oregon Center for Optics at the University of Oregon in 2001. Between 2000 and 2004, he was a project leader at 3M Company on fiber optics and photonic sensing devices for biomedical applications. In August of 2004, he joined the Department of Biological Engineering at the University of Missouri as an assistant professor. In January of 2010, he joined the Biomedical Engineering Department at the University of Michigan as an associate professor.

Dr. Fan's research includes photonic bio/chemical sensors, micro/nano-fluidics, and nano-photonics for disease diagnostics and bio/chemical molecule analysis. He has over 80 peer-reviewed publications and over 12 issued/pending patents. Presently, Dr. Fan serves as Associate Editor for Optics Express, responsible for optical biological and chemical sensors and optofluidics, and as a chair and organizer of numerous conferences for OSA, SPIE, and MRS. He is a recipient of 3M Non-Tenured Faculty Award (2004, 2005, and 2006), American Chemical Society Young Faculty Award, the Wallace H. Coulter Early Career Award (Phase I and Phase II), and the National Science Foundation CAREER Award. His research is supported by the National Science Foundation, National Institute of Health, private foundations, and industrial companies.

*Technical Session D2-W3-T1: BioMaterials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*

# Miniature MEMS-scanned dual-axis confocal microscopy for guiding tumor resection

**Jonathan T.C. Liu, PhD**

Assistant Professor and Director, Molecular Biophotonics Lab
Department of Biomedical Engineering
The State University of New York, Stony Brook
E-mail: jonathan.liu@stonybrook.edu

## ABSTRACT

There is a need for a real-time alternative to frozen-section pathology for accurate delineation of tumor margins, allowing for complete tumor resection in the brain without the debilitating effects of over-aggressive resection. We have developed a surgical microscope utilizing a novel dual-axis confocal architecture for deep optical sectioning within tissues. The dual-axis configuration has been shown – through diffraction-theory modeling, Monte-Carlo scattering simulations, tissue phantom studies, and tissue-imaging experiments – to efficiently reject out-of-focus and multiply scattered light for high-contrast optical sectioning within tissues. Our surgical prototype incorporates a custom-designed biaxial-scanning MEMS mirror for high-speed imaging over a large field of view. Ex vivo and in vivo imaging studies have been performed on tissues stained with targeted fluorescent contrast agents. A ratiometric microscopy technique has been developed to quantify the specific vs. nonspecific binding of biomarker-targeted contrast agents.

## BIOGRAPHY

Jonathan Liu was born in Albany, New York and was raised in Honolulu, Hawaii, where he attended the Iolani School. Jonathan received degrees in mechanical engineering at Princeton University (B.S.E., 1999) and at Stanford University (M.S., 2000 & Ph.D., 2005). Jonathan was a postdoctoral fellow in the Ginzton Labs and the Molecular Imaging Program at Stanford (2005-2009), and was later appointed as an instructor within the Stanford University School of Medicine (2009-2010).

Jonathan is currently an assistant professor in the biomedical engineering department at the State University of New York (SUNY) at Stony Brook. His research interests are in biomedical optics, where he is funded by the NIH to develop miniature optical-sectioning microscopes and molecularly targeted contrast agents for cancer diagnostics and therapy. He is also developing endoscopic spectral imaging devices and Raman-coded nanoparticles for multiplexed molecular imaging of tumor biomarkers.

Dr. Liu is an active member of the Optical Society of America (OSA), the Society of Photo-Optical Instrumentation Engineers (SPIE), and the World Molecular Imaging Society (WMIS). He received an award as the top graduate in mechanical engineering at Princeton in 1999, an NSF graduate research fellowship, a Canary Foundation / American Cancer Society postdoctoral fellowship, and a K99/R00 career-development award from the NIH. Lab website: http://bme.sunysb.edu/people/faculty/j_liu.html

*Technical Session D2-W1-T2: In Silico Research and Biomedical Informatics*

# Statistical Methods to Infer Drug Target Pathways from High Throughput Data

**Hongyu Zhao**

Chair, Biostatistics Division
Professor of Public Health (Biostatistics), of Genetics and of Statistics
School of Public Health
Yale University
E-mail: hongyu.zhao@yale.edu
(耶魯大學醫學院生物統計組主任趙宏宇教授)

ABSTRACT

Pathway-based drug discovery considers the therapeutic effects of compounds in the global physiological environment. This approach has been gaining popularity in recent years because the target pathways and mechanism of action for many compounds are still unknown, and there are also some unexpected off-target effects. Therefore, the inference of drug-pathway associations is a crucial step to fully realize the potential of system-based pharmacological research. Transcriptome data offer valuable information on drug pathway targets because the pathway activities may be reflected through gene expression levels. Hence, it is of great interest to jointly analyze drug sensitivity and gene expression data from the same set of samples to investigate the gene-pathway-drug associations. In this presentation, we discuss statistical methods that can be used to jointly analyze the paired gene expression and drug sensitivity datasets as well as paired pre- and post-treatment expression data to infer pathways targeted by specific drugs. Our model can incorporate prior knowledge regarding gene-pathway and/or drug-pathway associations to aid the discovery of new association relationships. The usefulness of our modeling approach will be demonstrated through both synthetic and real data sets.

BIOGRAPHY

Dr. Hongyu Zhao is the Chair of the Biostatistics Department and the Ira V. Hiscock Professor of Biostatistics and Professor of Statistics and Genetics at Yale University. He received his B.S. in Probability and Statistics from Peking University in 1990 and Ph.D. in Statistics from the University of California at Berkeley in 1995.

His research interests are the applications of statistical methods in molecular biology, genetics, drug developments, and personalized medicine. He has published over 250 articles in statistics, human genetics, bioinformatics, and proteomics, and edited two books on human genetics analysis and statistical genomics. Dr. Zhao is a Co-Editor of Statistics in Biosciences, and serves on the editorial boards of several leading statistical and genetics journals. He

was the recipient of the Mortimer Spiegelman Award for a top statistician in health statistics under the age of 40 awarded by the American Public Health Association.

His research has also been recognized by the Evelyn Fix Memorial Medal and Citation by UC Berkeley, a Basil O'Connor Starter Scholar Award by the March of Dimes Foundation, election to the fellowship of the American Association for the Advancement of Science, the American Statistical Association, and the Institute of Mathematical Statistics.

*Technical Session D2-W1-T2: In Silico Research and Biomedical Informatics*

# Flexible Methods for Assessing Interactions in Genetic Association Studies

**Michael Chiao-An Wu**

Assistant Professor, Department of Biostatistics
The University of North Carolina at Chapel Hill
E-mail: mwu@bios.unc.edu
(北卡萊羅納大學教堂山分校生物統計系吳肇安教授)

ABSTRACT

Advances in high-throughput genotyping and next generation sequencing have culminated in the development of large scale genetic association studies for identifying both common and rare gene variants that are related to complex traits. Importantly, genetic variants have the potential to strongly interact with each other and with external environmental exposures/risk factors in order to influence complex phenotypes and diseases. Studies of interactions can potentially address many questions that have confounded biological, medical, and public health researchers for decades. However, the ability of gene variants and environmental exposures/risk factors to influence the outcome in a complex and interactive manner poses a grand challenge for statisticians. To overcome such difficulties, we develop a new, adaptable statistical framework to flexibly model complicated genetic effects and/or environmental effects under a single regression framework. We further develop a powerful strategy for testing the interaction between one or more genetic markers and one or more environmental exposures (or another group of genetic markers) that readily accommodates complex, high-order interactions and simultaneously allows for highly non-linear effects. Simulations and applications to real data are used to justify our strategy.

BIOGRAPHY

Originally from Columbia, Maryland, Dr. Michael Chiao-An Wu received his B.S. in mathematical and computational science from Stanford University, Stanford CA, in 2000. He earned his A.M. and Ph.D. degrees in biostatistics from Harvard University, Cambridge MA, in 2006 and 2009, respectively. His Ph.D. research was conducted under the supervision of Drs. Xihong Lin and Tianxi Cai.

In fall 2009, he joined the Department of Biostatistics at The University of North Carolina at Chapel Hill, Chapel Hill NC, as an assistant professor. His group's current research focuses on the development of statistical methods for high-dimensional genomic data with an emphasis on variable selection and kernel machine based statistical learning approaches. Particular interested lies in development of tools for finding genes that modify response to environmental exposures and methods for analysis of high-throughput sequencing data.

Dr. Wu's is a member of the American Statistical Association (ASA), Eastern North American Region (ENAR) of the International Biometrics Society, International Society for Computational Biology, Institute of Mathematical Statistics, International Chinese Statistical Association (ICSA), Mu Sigma Rho National Statistics Honorary Society, American Society for Human Genetics, and International Genetic Epidemiology Society. His research has received awards from the ASA Section on Statistical Computing and ASA Section on Graphical Statistics, ENAR, and the ICSA.

*Technical Session D2-W1-T2 In Silico Research and Biomedical Informatics*


**Jhih-Wei Chu**

Assistant Professor, Department of Chemical and Biomolecular Engineering
University of California, Berkeley
E-mail: jwchu@berkeley.edu
(加州大學柏克萊分校化學及分子生物工程系朱智瑋教授)


BIOGRAPHY

*Technical Session D2-W2-T2: Biomedical Science and Engineering*


## Fu-Hsiung Chang

Professor, Department of Biochemistry and Molecular Biology
National Taiwan University
E-mail: fhchang@ntu.edu.tw
(臺灣大學醫學院生物化學暨生物分子研究所張富雄教授)


BIOGRAPHY

# Understanding biology via discovering the activities of "orphan" enzymes

**Hening Lin**

Assistant Professor, Department of Chemistry and Chemical Biology
Cornell University
E-mail: hl379@cornell.edu

ABSTRACT

Genomics and bioinformatics provide many putative enzymes with no robust enzymatic activities. In analogy to orphan receptors without identified ligands, I refer to such enzymes as orphan enzymes. Here I wish to illustrate that by finding out the true enzymatic activities of orphan enzymes, new chemical logics of biology can be discovered. Several mammalian sirtuins are examples of orphan enzymes. Sirtuins have been implicated in the regulation of transcription, apoptosis, genome stability, metabolism, and lifespan. Sirtuins were known as nicotinamide adenine dinucleotide (NAD)-dependent protein lysine deacetylases. However, among the seven sirtuins in humans, four of them do not have or have very weak deacetylase activity. We are interested in understanding why some sirtuins do not have deacetylase activity. We found that several of them can catalyze the hydrolysis of other acyl lysine modifications. The finding led to the discovery of new protein posttranslational modifications and new ways cells use to regulate protein function.

BIOGRAPHY

Dr. Hening Lin obtained his BS degree in chemistry from Tsinghua University in Beijing, China in 1998, and his PhD degree in bio-organic chemistry from Columbia University in New York City in 2003. After his postdoctoral studies at Harvard Medical School, he became a faculty member of Department of Chemistry and Chemical Biology of Cornell University in Ithaca, New York. His laboratory studies the chemistry, biology, and application enzymes, in particular $NAD^+$-dependent enzymes, such as sirtuins and PARPs. His work has been published in *Science*, *Nature*, *Journal of the American Chemical Society*, and other chemistry journals. Dr. Lin was Jane Coffin Childs Fellow while at Harvard Medical School. His awards include the Camille and Henry Dreyfus New Faculty Award and CAPA Distinguished Junior Faculty Award.

# Single Cell Genomics

**Honghua Li**

Associate Professor, Department of Pharmacology
University of Medicine and Dentistry of New Jersey Robert Wood Johnson Medical School
E-mail: holi@umdnj.edu
(新泽西州罗伯屋强森医学院李洪華教授)

ABSTRACT

Understanding the human genome is not only complicated by genetic variation but also by different parental origins of genetic materials within each cell and extensive repetitive sequences. To understanding the human genome in a great depth that cannot be reached by analyzing bulk cells or diploid cells, a highly sensitive and efficient experimental system has been developed for genome-scale analyses of genetic composition in haploid cells. The system allows separate study of genetic materials from different parents. It was used to determine the genetic composition of the highly variable human immunoglobulin heavy chain gene complex on single chromosomes, for high resolution study of meiotic recombination, and for detailed genetic structure of chromosomal regions containing copy number variants. By study of gene expression profiling of single cells, it is also possible to study the impact of genetic variation on gene activity. Determination of complete sequence of the entire genome in single sperm cells may change the landscape of many ongoing genome-scale studies including those based on high-throughput sequencing.

BIOGRAPHY

Dr. Honghua Li was born in Shandong, China. He earned his bachelor's degree in agronomy from the Shandong University of Agriculture, China, Ph.D. degree in Human Genetics and Molecular Biology from the University of Southern California, Los Angeles, California, USA, and received his postdoctoral training in Human Genetic and Genomics at the California Institute of Technology, Pasadena, California, USA.

He worked as a TEACHING ASSISTANT and then RESEARCH ASSISTANT during his graduate study and POSTDOCTORAL ASSOCIATE after graduate study. He accepted an ASSISTANT PROFESSOR position at the Coriell Institute for Medical Research after postdoctoral training. Currently he is an ASSOCIATE PROFESSOR at the University of Medicine and Dentistry of New Jersey Robert Wood Johnson Medical School, Piscataway, New Jersey, USA. His research interest is in understanding genetic impact on biological processes in a comprehensive way.

Dr. Li is a member of the American Society of Human Genetics and American Association for the Advancement of Science. He has served on a number of scientific review committees for the National Institutes of Health, as an editor for two scientific journals, and a reviewer for many scientific journals. He is a member of Cancer Institute of New Jersey.

*Technical Session D2-W3-T2: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*

## Session Chair


## Yihua Bruce Yu

Associate Professor, Department of Pharmaceutical Sciences
University of Maryland, Baltimore
E-mail: byu@rx.umaryland.edu
(马里兰大学巴尔的摩分校药学院药物科学系虞一华教授)


BIOGRAPHY

Yihua Bruce Yu was born in Beijing, China. He obtained his B.S. from Peking University and Ph.D. from the Johns Hopkins University.

He conducted postdoctoral research at the University of Alberta. He joined the University of Utah as assistant professor in 2000 in the Department of Pharmaceutics and Pharmaceutical Chemistry. He joined the University of Maryland as associate professor in 2007 in the Department of Pharmaceutical Sciences.

Dr. Yu received the 2004 Kimmel Scholar Award and the 2005 Presidential Early Career Awards for Scientists and Engineers. He works on image-guided drug delivery and biomaterials engineering.

*Technical Session D2-W3-T2: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*

# Biomimetic Approaches for the in vitro Engineering of 3D Prostate Cancer Models

**Xinqiao Jia**

Associate Professor, Materials Science and Engineering Department
Biomedical Engineering Program
University of Delaware
E-mail: xjia@udel.edu
(德拉维尔大学材料科学与工程系生物醫學工程组贾新桥教授)

## ABSTRACT

We have developed a biologically relevant hydrogel culture system that recaptures the essential feature of prostate cancer (PCa) and its associated stroma. Cell-laden hydrogels were prepared by mixing hyaluronic acid (HA) derivatives carrying complementary reactive groups. The resultant viscoelastic hydrogels are biodegradable and can interact with prostate cancer cells through its receptors, activating specific signaling pathways. Prostate cancer cells entrapped in HA matrices formed distinct multicellular aggregates which grew and merged, reminiscent of real tumors, whereas cells cultured on 2D monolayer adopted atypical spread-out morphology. The engineered tumor model was used successfully to test the efficacy of anti-cancer drugs including camptothecin, docetaxel, and rapamycin, alone and in combination, including specificity, dose and time responses. Responses of cells to anti-neoplastics differed between the 3D HA hydrogel and 2D monolayer systems. To simulate the tumor-stroma cross-talk, a bilayer construct was developed and characterized. The top hydrogel layer contains heparin (HP)-decorated, HA-based hydrogel particles (HGPs) presenting heparin-binding epidermal growth factor-like growth factor (HB-EGF) in a sustained manner. LNCaP cells were embedded within the bottom hydrogel layer and receive growth stimuli from the top. We demonstrate that tumoroids grown in bilayer HA hydrogels reflect features reminiscent of native carcinoma, and exhibit promising angiogenic potential through the upregulation of pro-angiogenic factors, both at the gene and the protein levels. These structured 3D units provide a novel means to study cancer and stroma invasiveness, cell-cell interactions and drug responses.

## BIOGRAPHY

Xinqiao Jia is an Associate Professor in the Department of Materials Science and Engineering at the University of Delaware. She received her B.S. in Applied Chemistry from Fudan University in China in 1995 and her Ph.D. in

Polymer Science and Engineering from the University of Massachusetts Amherst in 2002 under the guidance of Professor Thomas McCarthy. She conducted her postdoctoral training with Professor Robert Langer at MIT prior to joining the University of Delaware in 2005. She is an affiliated faculty with several programs, centers and institutes at the University of Delaware including the Biomedical Engineering Program, the Center for Translation Cancer Research and Delaware Biotechnology Institute. Dr. Jia's current research is focused on the design, synthesis and characterization of biomimetic materials with controlled architectures and functionalities for biomedical applications. Her research activities are currently supported by National Science Foundation and National Institutes of Health. She received a National Science Foundation CAREER Award in 2006 to develop mechano-responsive biomaterials. Dr. Jia has been recognized as an Outstanding Junior Faculty of Engineering and DuPont Young Professor in 2010. She received the Delware BioScience Association's Academic Award in 2011. Work from the Jia group has been featured at the Excellence in Graduate Polymer Research Symposium at the American Chemical Society (ACS) National Meetings. She has authored and coauthored 42 peer reviewed scientific papers since she started her MS thesis work in 1998.

# Multifunctional Polymeric Nanoparticles for Targeted Cancer Therapy and Diagnosis

**Shaoqin (Sarah) Gong**

Associate Professor, Department of Biomedical Engineering &
Wisconsin Institutes for Discovery
University of Wisconsin, Madison
E-mail: sgong@engr.wisc.edu

ABSTRACT

The emerging field of nanomedicine has shown great potential for targeted cancer therapy and diagnosis. During this presentation, several types of unique multifunctional drug/agent nanocarriers—including unimolecular micelles, polymer vesicles, and functionalized inorganic nanoparticles capable of tumor-targeting, pH-controlled drug release, and enhancement of imaging contrast—will be discussed.

BIOGRAPHY

Prof. Gong received dual bachelor's degrees from Tsinghua University in Beijing, China, in 1991, in both materials science and engineering, and economics and management. She also earned a master's degree from Tsinghua University in materials science and engineering in 1994, and a PhD degree from the University of Michigan–Ann Arbor in materials science and engineering in 1999.

She is currently an Associate Professor in the Department of Biomedical Engineering and Wisconsin Institutes for Discovery at the University of Wisconsin–Madison in Madison, Wisconsin. Previously, she was an Associate Professor at the University of Wisconsin–Milwaukee, an Assistant Scientist at the University of Wisconsin-Madison, and a Senior Materials Scientist at Henkel Corporation. She is the author of nearly 150 technical papers and four book chapters. Her current research focuses on the development of multifunctional nanomaterials such as nanomedicines and polymer nanocomposites.

Prof. Gong is a member of the editorial board *for Biofabrication; Theranostics; Journal of Biobased Materials and Bioenergy*. She has won a number of awards including the National Science Foundation CAREER award, the University of Wisconsin–Milwaukee Outstanding Research Award , and the Society for Information Display Award.

# Engineering virus nanoparticles for biomedicine

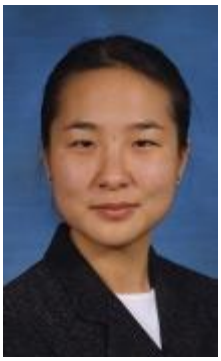
**Junghae Suh, PhD**

Assistant Professor, Department of Bioengineering
Rice University
E-mail: jsuh@rice.edu

ABSTRACT

Delivering nucleic acid-based therapeutics into target cells specifically is a considerable challenge. Using concepts and tools from virology, protein engineering, and molecular biology, we are interested in developing virus-based gene delivery vectors to tackle this challenge in an innovative way. In the first application, we are building a toolkit of innovative virus nanoparticles that can deliver nucleic acids specifically into cancer cells. In particular, we are using advances in protein engineering to develop viruses that are activated by tumor-specific biomolecular inputs. In the second application, we are focused on creating virus nanoparticles that can be used for imaging and therapy simultaneously. Unfortunately, incomplete knowledge of capsid biology makes it difficult to design brightly fluorescent and fully infectious viruses. To overcome this problem, we have generated a novel platform gene library that can be harnessed to make large libraries of virus mutants and then to select for variants with desired infectivity and fluorescent properties. Collectively, our work aims to engineer virus nanoparticles for enhanced targeted gene delivery for a variety of biomedical applications.

BIOGRAPHY



Dr. Suh received her B.S. in Chemical Engineering at MIT and Ph.D. in Biomedical Engineering at Johns Hopkins School of Medicine. Before joining the Rice University department of Bioengineering in 2007, she completed a two-year postdoctoral fellowship in the Laboratory of Genetics at the Salk Institute for Biological Studies. Her graduate research focused on understanding the interaction of nanoscale systems, either nature-derived or human-engineered, with complex biological environments in an effort to discover ruling paradigms that govern the performance of nanoparticles designed for various diagnostic and/or therapeutic applications. Her postdoctoral research focused on studying how natural viruses interface with cellular machinery, particularly those that maintain homeostasis in the cell nucleus. Such studies should uncover new insights into how synthetic nanoparticle systems can be designed to yield the performance efficiencies rivaling that of viruses. Currently, Dr. Suh works at the interface of chemistry, virology, biophysics, molecular biology, and protein engineering to investigate and create novel virus-based materials for various biomedical applications. She was awarded the NSF CAREER Award, MDACC Ovarian Cancer SPORE Career Development Program Award, and the Department of Defense Breast Cancer Concept Award for her innovative work on reprogramming viruses as therapeutic platforms. Additionally, Dr. Suh is part of the multi-institutional team of investigators that was awarded an NIH Grand Opportunities grant aimed at investigating the intracellular transport of a variety of engineered nanomaterials used for biomedical applications.

# A Variable-Selection-Based Novel Statistical Approach to Identify Susceptible Rare Variants Associated with Complex Diseases with Deep Sequencing Data

ABSTRACT

Existing association methods on sequencing data have been focused on aggregating variants across a gene or a genetic region in the past two years due to the fact that analyzing individual rare variants is underpowered. However, to identify which rare variants in a gene or a genetic region out of all variants are associated with the outcomes (either quantitative or qualitative) is a natural next step. Here we proposed a variable-selection-based novel approach that is able to identify the locations of the susceptible rare variants that are associated with the outcomes with sequencing data. More specifically, with all P rare variants in a gene or a genetic region, we generated the power set of the P rare variants except the empty set, that is, subsets S = 2P -1 of the P rare variants. We then treated the S subsets of the P rare variants as the S "new variables" and applied the penalized likelihood estimation using L1-norm regularization in a regression framework where outcomes were regressed on the S subsets. The proposed method only requires the regularization procedure to select the highest impact subset out of the S subsets on the outcome without worrying the selection of an optimal regularization parameter. After a subset of P rare variants is selected as the most associated subset with the outcome, we applied a permutation procedure specifically designed to assess the statistical significance of the selected subset. The selection performance and power of the proposed method were evaluated through intensive simulation studies where different effect sizes, sample sizes and directions of the effects of the individual rare variants were considered. The results demonstrated that the proposed method is able to select subsets with most of the outcome related rare variants in all simulation scenarios considered. The type I error and power of the subsequent permutation procedure demonstrated the validity and advantage of our selection method. The proposed method was also applied to sequence data on the ANGPTL family of genes from the Dallas Heart Study (DHS). Our proposed method was implemented in an R package RVsel which will be freely downloaded at http://www.columbia.edu/~sw2206.

BIOGRAPHY

**Shuang Wang**

Associate Professor, Department of Biostatistics, Mailman School of Public Health
Columbia University
E-mail: sw2206@columbia.edu
(哥伦比亚大学公共卫生学院王爽教授)

BIOGRAPHY

# Hokeun Sun

Associate Research Scientist, Department of Biostatics
The Mailman School of Public Health
E-mail: hs2674@columbia.edu
Columbia University

Dr. Hokeun Sun is currently an associate research scientist in the department of Biostatistics at Columbia University. He earned his Ph.D in statistics at the University of Michigan, where his research focused mainly on statistical genetics problems. Before he joined Columbia University, he was a postdoctoral researcher at the University of Pennsylvania Medical School. His main research is to develop statistical and computational methods useful for analyzing high-dimensional genomic/genetic data.

# NIA Genetics of Alzheimer's Disease Data Storage Site (NIAGADS)

**Li-San Wang**

Assistant Professor, Department of Pathology and Laboratory Medicine
University of Pennsylvania Perelman School of Medicine
Penn Center for Bioinformatics
E-mail: lswang@mail.med.upenn.edu
(賓州大學醫學院王立三教授)

ABSTRACT

Alzheimer's disease (AD) is the most common type of dementia. AD is characterized by gradual but extensive brain atrophy. Patients gradually lose cognitive functions over years and become incapacitated and completely dependent upon caregivers. AD affects 3-5 million people in the United States and costs $24.6 billion/year for health care and an additional $36.5 billion/year for lost productivity.

For the more common late-onset AD (LOAD, age at onset > 65y), the Apolipoprotein E (APOE) gene was discovered in early 1990s to be a susceptibility locus, and is recently shown to be involved in the metabolism of beta amyloid, the main constituent of the senile plaque that is a molecular hallmark found in the brains of Alzheimer's patients. Little is known about other genes until genome-wide association (GWA) studies become available since 2005. The number of susceptibility loci for LOAD has increased to nine when a series of high profile, large-scale GWA studies were published between 2009 and 2011.

This talk is an overview of the National Institute on Aging Genetics of Alzheimer's Disease Data Storage Site (NIAGADS). Established by NIA and currently managed by the University of Pennsylvania, NIAGADS is a data repository to facilitate access by qualified investigators to genotypic data in order to promote the study of the genetics of LOAD. The mission of NIAGADS is to serve as a one-stop access portal for research in AD genetics and genomics and support the research community to address challenges in sharing data and integrating knowledge. The NIAGADS website is at www.niagads.org.

BIOGRAPHY

Li-San Wang received his B.S. (1994) and M.S. (1996) in Electrical Engineering from the National Taiwan University. He received his M.S. (2000) and Ph.D. (2003) from the University of Texas at Austin, both in Computer Sciences, and was a postdoctoral fellow at the University of Pennsylvania between 2003 and 2006. Currently he is an Assistant Professor of Pathology and Laboratory Medicine, a faculty member of Penn Center for Bioinfomatics, and a fellow of Institute on Aging and Penn Genome Frontiers Institute, University of Pennsylvania. Dr. Wang's research integrates bioinformatics, genomics, and genetics to study neurodegeneration and psychiatric disorders. He has authored sixty peer-reviewed book chapters and journals on these topics and served on the program and organizing committees of various international workshops and conferences. He is the Principal Investigator of the National Institute on Aging Genetics of Alzheimer's Disease Data Storage Site (NIAGADS) and a Co-PI of the Alzheimer's Disease Genetics Consortium (ADGC).

# New Directions for Neural Prostheses to Treat Hearing Loss and Tinnitus

**Hubert H. Lim**

Assistant Professor, Departments of Biomedical Engineering and Otolaryngology
University of Minnesota, Twin Cities
E-mail: hlim@umn.edu

ABSTRACT

The cochlear implant (CI) is considered one of the most successful neural prostheses to date and has been implanted in over 200,000 individuals to restore hearing. The CI consists of an electrode array that is implanted into the cochlea and designed to electrically stimulate the remaining auditory nerve fibers in close proximity to the cochlea. However, individuals without a functional auditory nerve or implantable cochlea cannot benefit from a CI. My collaborators and I have developed a new central auditory prosthesis that bypasses the damaged areas and can restore hearing in deaf patients. Through this translational process, we have had a unique opportunity to develop new deep brain stimulation (DBS) technologies with enhanced processing and stimulation capabilities and an electrode array with a greater number of closely spaced sites compared to current DBS devices. These technologies are initially being used for various hearing applications, including hearing restoration and tinnitus suppression. Additionally, my lab is developing new non-invasive electrical stimulation methods across the body and head to induce localized brain activation to treat tinnitus. This “non-invasive DBS” method may provide a new approach for locally activating deep brain structures to treat tinnitus yet without requiring invasive surgery to implant the devices. Our invasive and non-invasive DBS methods and technologies have potential to treat other neurological disorders.

BIOGRAPHY

Dr. Lim was born in California in 1978. He attended the University of California-San Diego and obtained a B.S. in bioengineering in 2000. He then obtained a M.S.E. in biomedical engineering in 2002, M.S.E. in electrical engineering & computer science in 2004, and a Ph.D. in biomedical engineering in 2006 at the University of Michigan-Ann Arbor. His thesis research focused on neural prosthetics and auditory neuroscience, and he was advised by Dr. David J. Anderson, one of the co-inventors of the silicon-substrate electrode array technology known as the “Michigan Probe”.

After his Ph.D., he performed postdoctoral research at Hannover Medical University in Germany with Dr. Thomas Lenarz from 2006 to 2009. He worked with Dr. Lenarz, the Director of the largest auditory implant center in the world, to develop a new central auditory prosthesis for hearing that was initially implanted into five deaf patients. Currently, he is an Assistant Professor in the Department of Biomedical Engineering at the University of Minnesota-Twin Cities. He also has an adjunct faculty position in the Department of Otolaryngology. His current research

focuses on auditory neurophysiology and behavior in animals and humans to guide development of improved neural prosthetics for hearing restoration and tinnitus suppression.

Dr. Lim is a member of the Association for Research in Otolaryngology, Society for Neuroscience, Biomedical Engineering Society, and IEEE. He is the recipient of the prestigious Peter and Patricia Gruber International Research Award in Neuroscience awarded annually at the Society for Neuroscience Meeting as well as the first Institute for Translational Neuroscience Scholar at the University of Minnesota. He is also a Barry M. Goldwater Scholar and a NIH NRSA Predoctoral Fellow. He continues to serve as a reviewer for multiple journals and funding agencies, including the Journal of Neuroscience, Journal of Neurophysiology, Annals of Biomedical Engineering, JARO, IEEE, and NSF; and has co-organized several local neural engineering conferences and sessions.

*Technical Session D2-W2-T3: Biomedical Science and Engineering*

# A multi-step self-organization of centimeter-long epithelial tubules

**Chin-Lin Guo**

Assistant Professor of Bioengineering and Applied Physics
California Institute of Technology
E-mail: guochin@caltech.edu
(加州理工學院生物工程系與應用物理系郭青齡教授)

## ABSTRACT

Enabling long-range transport, tubules are important tissues in our bodies. Current theory is that cells follow extracellular biochemical cues to form long tubules. Whether tubules of lengths longer than centimeters can spontaneously emerge without spatial guidance of biochemical cues or preexisting scaffolds is unclear. Here, we show that without preexisting geometrical cues, epithelial cells and type I collagen molecules can self-organize into single, centimeter-long, hundred-micrometer-wide, and unbranched tubules. The geometrical cue of these tubules is created through sequential events including cell-aided assembly of collagen fibers, collagen-guided correlated cell motions, and long-range (~ 600 micrometers) mechanical interactions between cells. A simple two-state model is proposed to explain the spontaneous formation of long tubules. Our findings suggest that cells can use mechanical forces to create large-scale organization and demonstrate the feasibility to engineer tissues under scaffold-free conditions.

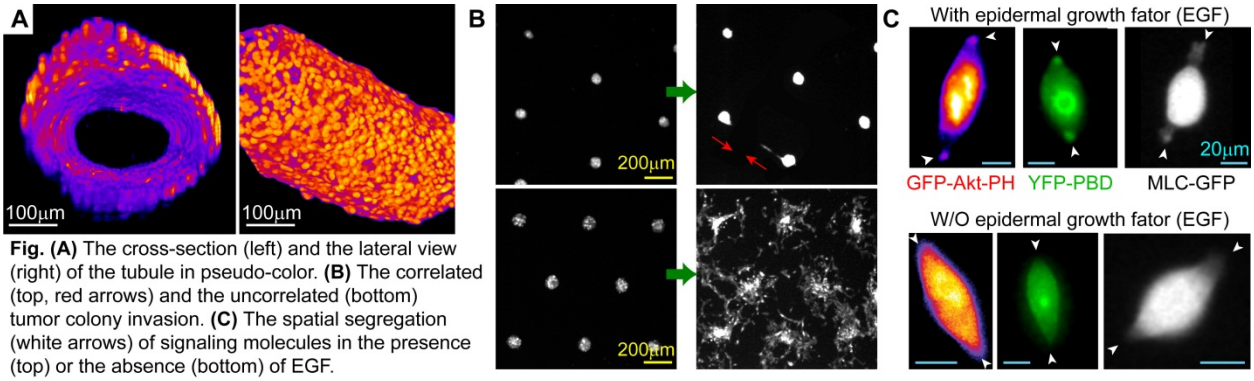



**Fig. (A)** The cross-section (left) and the lateral view (right) of the tubule in pseudo-color. **(B)** The correlated (top, red arrows) and the uncorrelated (bottom) tumor colony invasion. **(C)** The spatial segregation (white arrows) of signaling molecules in the presence (top) or the absence (bottom) of EGF.

## BIOGRAPHY

# Advance Bio Sensing by Nanopatterning

BIOGRAPHY


## Stephen Y. Chou

Member of National Academy of Engineering
Professor, Department of Electrical Engineering
Princeton University
E-mail: chou@Princeton.EDU
(美国国家工程院院士普林斯顿大学电机系周郁教授)


BIOGRAPHY


## Liangcheng Zhou

Postdoctoral Research Associate, Department of Electrical Engineering
Princeton University
E-mail: liangche@princeton.edu


*Technical Session D2-W3-T3: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*

## Session Chair


## Yihua Bruce Yu

Associate Professor, Department of Pharmaceutical Sciences
University of Maryland, Baltimore
E-mail: byu@rx.umaryland.edu
(马里兰大学巴尔的摩分校药学院药物科学系虞一华教授)


BIOGRAPHY

Yihua Bruce Yu was born in Beijing, China. He obtained his B.S. from Peking University and Ph.D. from the Johns Hopkins University.

He conducted postdoctoral research at the University of Alberta. He joined the University of Utah as assistant professor in 2000 in the Department of Pharmaceutics and Pharmaceutical Chemistry. He joined the University of Maryland as associate professor in 2007 in the Department of Pharmaceutical Sciences.

Dr. Yu received the 2004 Kimmel Scholar Award and the 2005 Presidential Early Career Awards for Scientists and Engineers. He works on image-guided drug delivery and biomaterials engineering.

*D2-W3-T3: Bio-Materials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*

# An electrochemical impedimetric biosensor based on a nanostructured polycarbonate (PC) substrate

**Gou-Jen Wang**

Professor, Department of Mechanical Engineering, Graduate Institute of Biomedical Engineering
National Chung-Hsing University
E-mail: gjwang@dragon.nchu.edu.tw

ABSTRACT

This study integrates the techniques of nano electroforming, hot embossing, and electrochemical deposition to develop a disposable, low cost, and high sensitivity nanostructure biosensor. A modified anodic aluminum oxide (AAO) barrier-layer surface is used as the template for nickel thin film deposition. After etching the AAO template off, a 3D mold of the concave nano structure array is created. The fabricated 3D nickel mold is further used for replica molding of a nano-structure polycarbonate (PC) substrate by hot embossing. An Au thin film is then sputtered on the PC substrate to form the electrode followed by the deposition of an orderly and uniform gold nanoparticles (GNPs) layer on the 3D Au electrode using electrochemical deposition. Finally, silver nanoparticles (SNPs) are deposited on the uniformly deposited GNPs to enhance the conductivity of the sensor. Electrochemical impedance spectroscopy (EIS) analysis is then used to detect the concentration of the target element. The sensitivity of the proposed scheme on the detection of the dust mite antigen Der p2 can reach 0.1pg/ml.

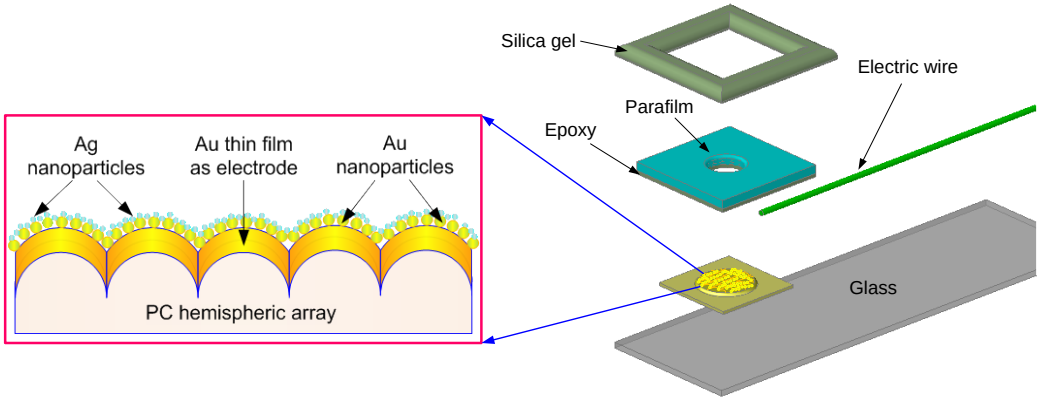



Figure 1. Schematic illustration of the proposed PC-based biosensor

BIOGRAPHY

**Dr. Gou-Jen Wang** received the B.S. degree on 1981 from National Taiwan University and the M.S. and Ph.D. degrees on 1986 and 1991 from the University of California, Los Angeles, all in Mechanical Engineering. Following graduation, he joined the Dowty Aerospace Los Angeles as a system engineer from 1991 to 1992. Dr. Wang joined the Mechanical Engineering Department at the National Chung-Hsing University, Taiwan on 1992 as an Associate Professor and has become a Professor on 1999. From 2003-2006, he served as the Division Director of Curriculum of the Center of Nanoscience and Nanotechnology. From 2007-2010, he was the adjunct Professor and Chairman of the Graduate Institute of Biomedical Engineering, National Chung-Hsing University, Taiwan. On 2008, he served as the Conference Chair of the Microfabrication, Integration and Packaging Conference (April/2008, Nice, France). From 2009, he is a Committee member of the Micro- and Nanosystem Division of the American Society of Mechanical Engineers (ASME) and serves as the organizer of the BIO MEMS/NEMS Symposium of the International Conference on Micro and

Nanosystems (MNS). His research interests include tissue engineering, biomedical micro/nano devices, nano fabrication, and dye-sensitized solar cells.

*Technical Session D2-W3-T3: Biomaterials, Bio-nanotechnology/Bio-Nems/Bio-Mems*

# Biologically Inspired Microsystems Engineering

**Mingming Wu**

Associate Professor, Department of Biological and Environmental Engineering
Cornell University
E-mail: mw272@cornell.edu
(康奈尔大学生物工程和环境工程系吴珉珉教授)

ABSTRACT

Through billions of years of evolution, cells or organisms have acquired incredible feats. E.coli bacterium, for example, is about 1 micrometer in length, and can swim 20 times of its body length in one second. Furthermore, it can sense a few molecules in its surrounding environment (an ultra sensitive micro-meter scale biosensor ) and moves towards where life is better. In this talk, I will present efforts in my lab in understanding fundamental biophysical mechanisms that govern cellular migration both in fluid and in biomatrix using microfluidic models and advanced imaging technique. Two applications will be discussed, one is on the transport of bacteria in environment; and the other is on the roles of cellular microenvironment in cancer metastasis.

BIOGRAPHY

Mingming Wu was born in Wuxi, China. She received the Bachelor of Science degree in physics at Nanjing University, China, in 1984; and the Doctor of Philosophy degree in physics at the Ohio State University, USA, in 1992. She held a postdoctoral research position at Ecole Polytechnique in France, in 1992, and in physics department at University of California at Santa Barbara, USA, in 1993-5.

Prof. Wu has been a member of American Physical Society since 1990, American microbiology society since 2006, and American Biomedical Engineering Society since 2009.

*Technical Session D2-W3-T3: Biomaterials, Bio-nanotechnology/Bio-Nems/Bio-Mems*

# BioMEMS for blood sample preparation and cell analysis


**Siyang Zheng**

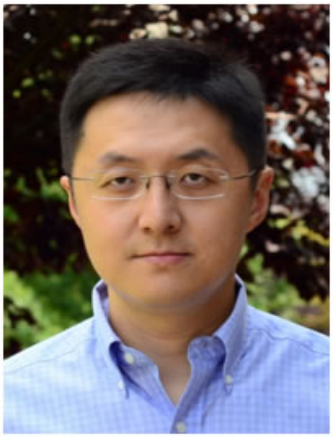
Dorothy Quiggle Assistant Professor of Bioengineering, Member of Penn State Material Research Institute(MRI), Penn State Hershey Cancer Institute (PSHCI) and The Huck Institutes of The Life Sciences
The Pennsylvania State University
E-mail: siyang@psu.edu
(宾州州立大学生物工程系郑斯扬教授)



ABSTRACT

Blood is the most abundant and complicated body fluid. The whole volume of blood circulates the body every a couple of minutes, potentially making blood analysis reflecting the physiological and pathological conditions of the body in nearly real time. In my presentation, I will provide an overview of our efforts in developing microfabricated devices for blood cell separation, circulating tumor cell enrichment from blood, blood count and blood cell differentiation.


BIOGRAPHY



Siyang Zheng, Ph.D., is currently the Dorothy Quiggle Assistant Professor of Bioengineering at The Pennsylvania State University. He obtained his B.S. in Biological Sciences and Biotechnology from Tsinghua University (China) and Ph.D. in Electrical Engineering from California Institute of Technology. Dr. Zheng is interested in developing micro/nano technologies for biomedical applications. Currently he is focusing on developing high-throughput microfluidics, implantable devices, nanomaterial integrated devices, applications in cancer metastasis, blood analysis and volatile organic compounds analysis.

# Hidden Markov Models with Applications in Cell Adhesion Experiments

**Ying Hung**

Assistant Professor, Department of Statistics and Biostatics
Rutgers University
E-mail: yhung@stat.rutgers.edu

ABSTRACT

Estimation of the number of hidden states is challenging in hidden Markov models. Motivated by the analysis of a specific type of cell adhesion experiments, a new frame- work based on hidden Markov model and double penalized order selection is proposed. The order selection procedure is shown to be consistent in estimating the number of states. A modified Expectation-Maximization algorithm is introduced to efficiently estimate parameters in the model. Simulations show that the proposed framework outperforms existing methods. Applications of the proposed methodology to real da- ta demonstrate the accuracy of estimating receptor-ligand bond lifetimes and waiting times which are essential in kinetic parameter estimation.

BIOGRAPHY

**EDUCATION**

2004 – 2008 Ph.D. School of Industrial and Systems Engineering, Georgia Institute of Technology
2001 – 2003 M.S. Statistics, National Tsing Hua University, Taiwan
1997 – 2001 B.S. Mathematics, National Taiwan University, Taiwan

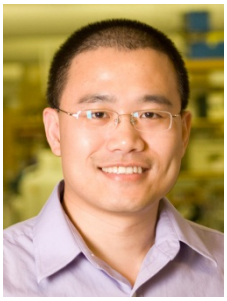
# Cellular Commitment in the Epithelial-Mesenchymal-Transition

ABSTRACT

The epithelial-mesenchymal-transition (EMT) is a key process for invasion in cancer metastasis. In this talk, we illustrate a conjunctive computational-experimental effort that predicts and elucidates key dynamical phenomena in the EMT transcriptional circuit. After careful construction of a biological model, we show EMT theoretically admits bistability and hysteresis and confirm these predictions in vitro. Our armamentarium is composed of computational tools, including differential equations, stochastic analysis, information theory, and Bayesian methods, and modern molecular biology experimental modalities, including qRT-PCR, flow cytometry, immunofluorescence, etc.

BIOGRAPHY

## Yibin Kang



Professor, Department of Molecular Biology
Princeton University
E-mail: ykang@princeton.edu
(普林斯顿大学分子生物学系康毅滨教授)

BIOGRAPHY

## Caleb Bastian

Graduate Student (Applied Mathematics), Princeton University
Princeton, NJ, USA
E-mail: cbastian@math.princeton.edu

Caleb Bastian received B.S. and M.S. in nuclear engineering from the University of Tennessee (2006), M.S. in oral biology (2008; School of Dentistry), M.S. in anatomical sciences and neurobiology (2010; School of Medicine), M.B.A. (2010; Business School), and D.M.D. (2010; School of Dentistry) from the University of Louisville.

He is currently a Ph.D. candidate in the third year of study in the Program in Applied and Computational Mathematics at Princeton University and is supported by a NIH K08 grant. His research interests include stochastic analysis, signal processing, Bayesian methodologies, mathematical biology, and mathematical analysis of datasets.

Dr. Bastian is a member of the American Dental Association and the American and International Associations for Dental Research.

# Modeling carcinogenesis - How similar are ductal carcinoma in situ (DCIS) and invasive ductal carcinoma (IDC) from the same patient?

**Woei-Jyh (Adam) Lee**

Scientist, National Institutes of Health
E-mail: adamlee@mail.nih.gov
(美國國家衛生院李偉智博士)

ABSTRACT

In 2011, an estimated 230,000 new cases of invasive breast cancer were diagnosed in women in the United States (US), along with approximately 58,000 new cases of non-invasive ductal carcinoma in situ (DCIS). DCIS often progresses to breast cancer, if left untreated, but not always. There were more than 2.6 million breast cancer survivors in the US in 2011. However, about 40,000 women in the US died in 2011 from breast cancer. If early diagnostics on breast cancer can be improved, for example by recognizing the mechanisms by which DCIS progresses to cancer, then the survival rate might be improved. Furthermore, it would be useful if DCIS cases that are unlikely to progress to cancer could be recognized and treated less aggressively.
We set up to study the genetic similarities and differences between paired DCIS and invasive ductal carcinoma (IDC) lesions from the same patients. In this study, the technique to make genetic measurements was multi-color fluorescence in situ hybridization (FISH) on eight genes implicated in breast cancer. By measuring copy numbers of multiple genes in different single cells, we may be able to infer a partial order of copy number changes in each sample.

Phylogenetic algorithms, which infer evolutionary histories from profiles of discrete species, have previously proven a powerful tool for interpreting patterns of tumor evolution from profiles of tumors or tumor cells. Phylogenetic inference was performed to find most plausible ancestral trees for each patient from cell-by-cell FISH probe counts, corresponding to predicted progression pathways in those patients. We select sets of genes to model if the carcinogenesis progressions between DCIS and IDC are similar to each other or differed by some particular genes. We applied two phylogenetic inference methods. Our first tree inference method is based on that of Pennington et al. (2007), originally designed for inference from simpler two-probe FISH data in which each cell was assayed on a single gene and the centromere count of the chromosome containing that gene. The original theory and software modeled the copy numbers of a single chromosome and a gene on that chromosome. In the second method, we rely only on gene-specific probe counts, ignoring overall ploidy of each cell.

For each pair of results on the same set of selected genes of DCIS and IDC in the same patient, we can calculate a consensus network to include states occur in either carcinogenesis tree for DCIS or IDC. Our goal is to find to what extent there exist common pathways between DCIS and IDC for each patient. We identify two categories of relationship between DCIS and IDC lesions: 1) DCIS and IDC did progress differently on different sets of genes; 2) DCIS and IDC shared the same set of genes but progressed along different paths in their gene copy number changes.

BIOGRAPHY

Woei-Jyh (Adam) Lee received his BS degree from the Department of Computer Science and Information Engineering at the National Taiwan University in 1993, and his MS degree from the Department of Computer Science at the New York University in 1998. He received his PhD degree from the Department of Computer Science at the University of Maryland at College Park in 2008.

He worked on distributed objects and fault tolerance at AT&T Labs - Research in 1997. He focused on network software and management at Bell Laboratories Research, Lucent Technologies, from 1998 till 2000. He visited Integrated Media Systems Center at the University of Southern California specializing in continuous media streaming and multimedia networking from 2002 to 2003. He also contributed in protein domain parsing and boundary prediction at the National Cancer Institute from 2004 to 2005. He was a fellow at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health from 2009 to 2012. He is currently a scientist at the National Cancer Institute. He is also a teaching fellow at the Robert H. Smith School of Business, University of Maryland since 2012.

Dr. Lee's research interests include bioinformatics, computational biology, cancer biology, genomics and genetics, information integration, data management and mining, and literature-based discovery. He has two US Patents and is a member of the ISENG.

*Technical Session D2-W2-T4: Biomedical Science and Engineering*

# Dendrimer-based Imaging Agents for $^{19}$F Magnetic Resonance Imaging


## Yihua Bruce Yu

Associate Professor, Department of Pharmaceutical Sciences
University of Maryland, Baltimore
E-mail: byu@rx.umaryland.edu
(马里兰大学巴尔的摩分校药学院药物科学系虞一华教授)



ABSTRACT

The development of $^{19}$F imaging agents for in vivo tracking of drugs and cells by magnetic resonance imaging (MRI) will be presented. The imaging agents are denoted as $^{19}$FITs to stand for $^{19}$F Imaging Tracers. Two classes of $^{19}$FITs have been developed, mono-chromic $^{19}$FITs for generating black-and-white images, and multi-chromic $^{19}$FITs for generating color images. The presentation covers the design, synthesis and evaluation of these imaging agents.


BIOGRAPHY

Yihua Bruce Yu was born in Beijing, China. He obtained his B.S. from Peking University and Ph.D. from the Johns Hopkins University.

He conducted postdoctoral research at the University of Alberta. He joined the University of Utah as assistant professor in 2000 in the Department of Pharmaceutics and Pharmaceutical Chemistry. He joined the University of Maryland as associate professor in 2007 in the Department of Pharmaceutical Sciences.

Dr. Yu received the 2004 Kimmel Scholar Award and the 2005 Presidential Early Career Awards for Scientists and Engineers. He works on image-guided drug delivery and biomaterials engineering.

*Technical Session D2-W2-T4: Biomedical Science and Engineering*

# Superresolution STED Imaging Reveals Distinct States of Intraflagellar Transport in Primary Cilia

**Jung-Chi Liao**

Assistant Professor, Department of Mechanical Engineering and Biomedical Engineering
Columbia University
E-mail: jcliao@columbia.edu
(哥倫比亞大學機械工程系與生物醫學工程系廖仲麒教授)

ABSTRACT

A primary cilium is a solitary protrusion from the plasma membrane, with this protruded microdomain acting as a sensory hub of cells, capable of photosensation, mechanosensation, osmosensation, thermosensation, olfactory sensation, and hormone sensation. They also mediate critical cell signaling events for hedgehog, Wnt, cAMP, and several other signaling pathways. Composition of molecules in the primary cilia differs from those in the plasma membrane, with proteins in the transition zone regulating molecules entering the ciliary compartment. The transition zone bridges the basal body and the ciliary compartment of a primary cilium, serving to anchor the axoneme to the plasma membrane and to regulate intraflagellar transport (IFT) complexes entering/exiting the ciliary compartment.

All key molecules in the transition zone are packed within a small volume with relative distances in the range of 50-100 nm, challenging the imaging capability of conventional optical microscopy (resolution ~200 nm) in localizing individual complexes under physiological conditions. Recent advances in superresolution techniques have enabled scientific discoveries in multiple disciplines, providing a novel way in primary cilium studies. Stimulated emission depletion (STED) fluorescent microscopy is one of the most promising superresolution techniques, achieving 4-5-fold resolution improvement over confocal microscopy by transiently de-exciting fluorophores located at the outer rim of a focal spot through stimulated emission. We have built a continuous-wave STED superresolution microscope that achieves 50 nm in resolution in live cell imaging.

Using superresolution STED microscopy, we have identified two distinct distribution patterns of IFT88, an important element of intraflagellar transport complexes, close to the basal end of primary cilia. We found that IFT88 formed either a triangle of a three-puncta pattern across the transition zone, or a Y-shaped pattern with two branches pointing toward the basal end. We examined the populations of these two patterns and their correlation with environmental effects. These two patterns possibly reflect distinct functional states of the transition zone to regulate intraflagellar transport in primary cilia.

BIOGRAPHY

Jung-Chi Liao was born in Taipei, Taiwan in 1971. He received his bachelor's degree in mechanical engineering from National Taiwan University, Taipei, Taiwan in 1993, and his master's and PhD degrees in mechanical engineering from MIT, Cambridge, Massachusetts in 1998 and 2002. He conducted postdoctoral research with Dr. George Oster in molecular and cell biology at University of California, Berkeley from 2002 to 2005.

He served as an Ordnance Second Lieutenant at Taiwan Army Logistics School from 1993 to 1995. After his postdoctoral research, he joined Stanford University as a Research Associate from 2005 to 2008. He then started his current position in 2008 as an Assistant Professor at Columbia University with an appointment from Department of Mechanical Engineering and an affiliated appointment from Department of

Biomedical Engineering. His current research focuses on structural dynamics and intraflagellar transport of molecular motors.

Dr. Liao is a member of Biophysical Society and Biomedical Engineering Society. He has been elected to serve as organizers or session chairs in multiple international conferences, including Biomedical Engineering Society Meeting, United States Association for Computational Mechanics Thematic Conference, Biophysical Society Meeting, and Pacific Symposium of Biocomputing.

*Technical Session D2-W2-T4: Biomedical Science and Engineering*

# Human Insulin Degrading Enzyme

**Wei-Jen Tang**

Professor, Ben May Department for Cancer Research
The University of Chicago
E-mail: wtang@uchicago.edu
(芝加哥大學生物醫學研究所湯惟仁教授)

ABSTRACT

Insulin degrading enzyme (IDE) is a zinc metalloprotease vital for the clearance of insulin and amyloid β, peptides important for the progression of diabetes and Alzheimer's disease, respectively. We have solved structures of human IDE in its closed state in complex with various peptide substrates to decipher how IDE uses unique size, charge, and location of reaction center of its catalytic chamber to preferentially degrade the amyloidogenic peptides. Using the synthetic antibody, we have determined a structure of IDE in its open state to reveal how IDE may undergo the conformational switch between the closed and open states. Working with Haw Yang at Princeton University, we also use single molecule fluorescence resonance energy transfer technique to address the dynamics of IDE in solution. Together, a novel mechanism in how IDE undergoes the conformational switch to capture its substrates emerge.

BIOGRAPHY

| NAME | POSITION TITLE |
|---|---|
| Wei-Jen Tang | Professor |

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, and include*

| INSTITUTION AND LOCATION | DEGREE *(if applicable)* | YEAR(s) | FIELD OF STUDY |
|---|---|---|---|
| National Taiwan University | B.S. | 1978-1982 | Zoology |
| University of Texas, Austin | Ph.D. | 1984-1988 | Biological Science |

**A. Personal Statement:**

My research program involves in elucidating the molecular basis of cellular signal transduction. The research is based on the premise that the better understanding of protein-protein and protein-ligand interaction is key to elucidating the fundamental principles governing cellular signaling network. I apply X-ray crystallography and various biochemical, biophysical, cellular and pharmacological tools to address the protein functions and regulations. I am known for the studies on the catalysis and regulation of mammalian adenylyl cyclase, anthrax and pertussis adenylyl cyclase toxins, and insulin degrading enzyme. I am a very strong believer in collaboration.

**B. Positions and Honors.**

**Positions:**

| | |
|---|---|
| 1988 | Postdoctoral fellow with Dr. William R. Folk, U Texas Austin |
| 1988-1991 | Postdoctoral fellow with Dr. Alfred G. Gilman, U Texas Southwestern Medical School |
| 1991-1993 | Instructor, Dept. of Pharmacology, University of Texas Southwestern Medical School |
| 1993-1994 | Assistant Professor, Dept. of Pharmacology, UT Southwestern Medical School |
| 1994-1998 | Assistant Professor, Dept. of Pharmacol. & Physiol. Sciences, U of Chicago |
| 1998-2001 | Assistant Professor, Dept. of Neurobiol. Pharmacol. & Physiol., U of Chicago |
| 2001-2007 | Associate Professor, Ben-May Institute for Cancer Research, U of Chicago |
| 2007- | Professor, Ben-May Department for Cancer Research, U of Chicago |

**Honors and Federal Government Public Advisory Committee:**

| | |
|---|---|
| 1987-1988 | University Fellowship, University of Texas, Austin |
| 1999-2002 | American Heart Association Established Investigator |
| 1998-present | Ad Hoc NIH and NSF grant reviewing panels |
| 2007-2011 | Regular member of NIH MSF-C study section |
| 2009-present | The advisory Board, Structure Biology Center, APS, Argonne National Lab. |

*Technical Session D2-W3-T4: Biomaterials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*

# Microelectromechanical Systems for Biomolecular Sensing and Manipulation


## Qiao Lin

Associate Professor, Department of Mechanical Engineering
Columbia University
E-mail: qlin@columbia.edu



ABSTRACT

Microelectromechanical systems (MEMS) technology holds the potential to vitally impact biology and medicine. In particular, MEMS can be exploited as innovative tools for biological sensing and manipulation. Such miniaturized systems allow biomolecules to be interrogated in controlled micro/nanoscale environments with orders-of-magnitude reduction in the consumption of biological material. Functional and structural integration enables multi-faceted analysis of complex biomolecular processes with improved sensitivity, reliability and automation. Arrays of devices integrated in a single system afford parallelized, high-throughput processing of biological samples. Ultimately, such systems will enable novel biomolecular investigations that are unattainable with conventional technologies.

This presentation will provide a highlight of our research in applying MEMS to enable and facilitate biological sensing and manipulation. One of our efforts involves manipulation of biomolecules using micro/nanoscale functional materials. For instance, we have been exploiting aptamers, or synthetically developed nucleic acids that bind to target analytes via affinity interactions, as a specific and stimulus-responsive functional material to manipulate and detect biomolecules and cells. In another effort, we integrate sensitive MEMS transducers with microfluidic systems to enable biosensing, creating devices such as miniaturized calorimeters for thermodynamic characterization of biomolecules, and subcutaneously implantable affinity sensors for continuous glucose monitoring. These examples will be presented to demonstrate the potential impact of MEMS on biomedical applications.


BIOGRAPHY

Qiao Lin is an Associate Professor in the Mechanical Engineering Department at Columbia University. He received the Ph.D. degree in Mechanical Engineering from Caltech in 1998, where he pursued thesis research on optimal planning of robotic manipulation. He was a postdoctoral scholar in Electrical Engineering at Caltech from 1998 to 2000, where he conducted microelectromechanical systems (MEMS) research, focusing on silicon-micromachined fluidic and thermal devices. From 2000 to 2005, he was an Assistant Professor of Mechanical Engineering at Carnegie Mellon University. At Columbia since 2005, Dr. Lin pursues research in the design, analysis and fabrication of MEMS and micro/nanofluidic systems for manipulation, detection and characterization of biological systems.

*Technical Session D2-W3-T4: Biomaterials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*


## Fan-Gang Tseng

Professor and Chairman, Department of Engineering and System Science
Deputy Director, Biomedical Technology Research Center
National Tsing-Hua University
E-mail: fangang@ess.nthu.edu.tw
(清華大學工程與系統科學系主任曾繁根教授)


BIOGRAPHY

*Technical Session D2-W3-T4: Biomaterials, Bio-Nanotechnology/Bio-NEMS/Bio-MEMS*


## Jeff Tza-Huei Wang

Associate Professor
Departments of Mechanical Engineering, Biomedical Engineering and Oncology
Johns Hopkins University
E-mail: thwang@jhu.edu
(約翰霍普金斯大學機械工程系與生物醫學工程系王澤輝教授)


BIOGRAPHY