The 2014 EITA Conference on New Media and Biomedical Research

(EITA-New Media and Bio 2014)

"Recent Advances in New Media and Biomedical Research"

Conference Proceedings

The Whitaker Building and the Green Building
Massachusetts Institute of Technology

Cambridge, MA, U.S.A.

Thursday-Friday, July 31 - August 1, 2014

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Conference Themes

"Recent Advances in New Media and Biomedical Research"

The EITA-New Media and Bio 2014 conference consists of three parallel workshops and a young investigators workshop:

- **Workshop 1 (W1):** Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining
- **Workshop 2 (W2):** Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics
- **Workshop 3 (W3):** Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering
- **Young Investigators Workshops (YA, YB, YC):** New Media and Biomedical Research

Planning Committee

General Conference Chairs

Sy-Yen Kuo	(郭斯彥)	National Taiwan University

Conference Chairs

Yaoyu E Wang	(王耀煜)	Harvard University
Chen-Hsiang (Jones) Yu	(余禎祥)	Prentice Lab

Conference Organizers

Howard Chen	(陳浩)	IBM T.J. Watson Research Center (Retired)
Li-San Wang	(王立三)	University of Pennsylvania
Yi-Hsiang (Sean) Hsu	(許益祥)	Harvard University
Woei-Jyh (Adam) Lee	(李偉智)	University of Maryland, College Park
Chen-Hsiang (Jones) Yu	(余禎祥)	Prentice Lab
Nien-Tsu Huang	(黃念祖)	National Taiwan University

Project Manager

Nien-Tsu Huang	(黃念祖)	National Taiwan University

Program Committee

Workshop Track Co-Chairs

Workshop 1 (W1): Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Sao-Jie Chen	(陳少傑)	National Taiwan University

Workshop 2 (W2): Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

I-Chen Wu	(吳毅成)	National Chiao-Tung University
Li-San Wang	(王立三)	University of Pennsylvania

Workshop 3 (W3): Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Yaoyu E Wang	(王耀煜)	Harvard University

Yi-Hsiang (Sean) Hsu	(許益祥)	Harvard University

Young Investigators Workshops (YA, YB, YC): New Media and Biomedical Research

Woei-Jyh (Adam) Lee	(李偉智)	University of Maryland, College Park
Chen-Hsiang (Jones) Yu	(余禎祥)	Prentice Lab
Hsiang-Ying (Sherry) Lee	(李湘盈)	Massachusetts Institute of Technology

Conference Manager

<TBD>

Publication

Publication Committee Chair:

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

Conference Program:

Nien-Tsu Huang	(黃念祖)	National Taiwan University

Conference Proceedings:

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

Conference Treasurer

Chinese Institute of Engineers-GNYC

Local Management

The Republic of China Student Association of M. I. T.

On-Site Registration

The Republic of China Student Association of M. I. T.

Web Development

Michael Hwa-Han Wang	(王華漢)	EBMedia, LLC

Co-Organizing Associations - TSA

- The Republic of China Student Association of M. I. T.

Co-Organizing Associations

- Taipei Economic & Cultural Office in Boston
- Investment & Trade Office, Taipei Economic and Cultural Representative Office the U.S.
- Education Division, Taipei Economic & Cultural Office in Boston
- Commercial Division, Taipei Economic & Cultural Office in Boston

Co-Sponsors

- Taipei Economic & Cultural Office in Boston
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- Education Division, Taipei Economic & Cultural Office in Boston
- Commercial Division, Taipei Economic & Cultural Office in Boston
- Taiwan Trade Center, New York

Conference Program

Day 1 (Thursday, July 31, 2014)

7/31 (Thur) 8:30 am - 5:00 pm: Registration
Room: 56-154

7/31 (Thur) 9:30 am - 9:50 am: Opening Session
Chairs:
Dr. Yaoyu E. Wang, Associate Director, Center for Cancer Computational Biology, Dana-Farber Cancer Institute, Harvard University
(波士頓達納法伯癌症研究所王耀煜博士)
Dr. Chen-Hsiang (Jones) Yu, Founder and CEO, Prentice Lab
(Prentice Lab 余禎祥博士)
Room: 56-154

Welcome Remarks:

Ms. Anne Hung
Director General, Taipei Economic and Cultural Office in Boston
(駐波士頓台北經濟文化辦事處洪慧珠處長)

Dr. Sy-Yen Kuo
Dean, College of Electrical Engineering and Computer Science
Distinguished Professor, Department of Electrical Engineering
National Taiwan University
(台灣大學電資學院院長暨電機工程學系郭斯彥特聘教授)

Parallel Sessions:
7/31 (Thur) 9:50 am - 11:20 am: Plenary Session (1): New Media
Chair: **Dr. Chen-Hsiang (Jones) Yu**, Founder and CEO, Prentice Lab
(Prentice Lab 余禎祥博士)
Room: 56-154

"Light-weight tools for personal health monitoring"
Dr. Krzysztof Gajos
Associate Professor of Computer Science
School of Engineering and Applied Sciences
Harvard University

7/31 (Thur) 11:20 am - 11:35 am: Break

7/31 (Thur) 11:35 am – 1:05 pm: Plenary Session (2): Biomedical Research
Chair: **Dr. Yaoyu E. Wang**, Associate Director, Center for Cancer Computational Biology, Dana-Farber Cancer Institute, Harvard University
(波士頓達納法伯癌症研究所王耀煜博士)

Room: 56-154

"Molecular Pathological Epidemiology (MPE): Evolving Integrative Biomedical Health Science"
Dr. Shuji Ogino
Associate Professor of Pathology, Harvard Medical School
Associate Professor in the Department of Epidemiology, Harvard School of Public Health

7/31 (Thur) 1:05 pm - 2:35 pm: Lunch

Parallel Sessions:

7/31 (Thur) 2:35 pm – 4:05 pm: Technical Session D1-W1-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Chair: **Dr. Shanchieh Jay Yang,** Associate Professor & Department Head, Department of Computer Engineering, Rochester Institute of Technology
(羅徹斯特理工學院電腦工程學系主任楊善傑教授)
Room: 56-114

Dr. Li-Chun Wang
Distinguished Professor and Chairman, Department of Electrical and Computer Engineering
National Chiao-Tung University
(交通大學電信工程研究所兼電機工程學系系主任王蒞君特聘教授)

"AIS-based Knowledge Discovery and Service Provision to Improve Safety at Sea"
Dr. Shwu-Jing Chang
Associate Professor and Chair, Department of Communications, Navigation and Control Engineering
National Taiwan Ocean University
(台灣海洋大學通訊與導航工程學系主任張淑淨教授)

Dr. Steve H.L. Liang
Associate Professor, AITF-Microsoft Industry Chair in Open Sensor Web
Department of Geomatics Engineering
University of Calgary
(卡加利大學空間資訊工程系梁鴻翎教授)

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

7/31 (Thur) 2:35 pm – 4:05 pm: Technical Session D1-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. Li-San Wang,** Associate Professor, Department of Pathology and Laboratory Medicine, University of Pennsylvania Perelman School of Medicine
(賓州大學醫學院王立三教授)
Room: 56-154

"Exploiting Network Effects for Fraud and Malware Detection"
Dr. Duen Horng Polo Chau
Assistant Professor, School of Computational Science and Engineering
Georgia Institute of Technology

"Data Mining in Bioinformatics: Case Studies"
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)

"The Phenotype and Exposure Data"
Dr. Chun-Nan Hsu
Associate Professor of Medicine, Division of Biomedical Informatics
University of California, San Diego

Dr. Yu Cao
Assistant Professor, Department of Computer Science
University of Massachusetts, Lowell

7/31 (Thur) 2:35 pm – 4:05 pm: Technical Session D1-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Chair: **Dr. Yi-Hsiang (Sean) Hsu,** Assistant Professor, School of Medicine, Harvard University
(哈佛大學醫學院許益祥教授)
Room: 54-100

"Multifunctional Polymer Drug Nanocarriers for Targeted Cancer Therapy"
Dr. Shaoqin "Sarah" Gong
Professor, Department of Biomedical Engineering &
Wisconsin Institutes for Discovery
University of Wisconsin, Madison

"Robotizing Functional Nanoentities - for single-cell drug delivery, bioanalysis, and tunable biochemical release"
Dr. Donglei (Emma) Fan
Assistant Professor, Materials Science and Engineering Program
The Department of Mechanical Engineering
The University of Texas at Austin

Dr. Gang Logan Liu
Assistant Professor, Department of Electrical and Computer Engineering and Bioengineering
University of Illinois at Urbana-Champaign

"Molecular programming with DNA/RNA: nanofabrication, imaging, and sensing"
Dr. Peng Yin
Assistant Professor, Department of Systems Biology
Harvard Medical School

7/31 (Thur) 4:05 pm – 4:20 pm: Break

Parallel Sessions:

7/31 (Thur) 4:20 pm – 5:50 pm: Technical Session D1-W1-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Chair: **Dr. Sao-Jie Chen,** Professor, Department of Electrical Engineering, National Taiwan University

(台灣大學電機工程學系陳少傑教授)

Room: 56-114

"Morphing: a New Communication Way in New Media"
Dr. Heng Ji
Edward P. Hamilton Development Chair Associate Professor, Department of Computer Science
Director of BLENDER Lab
Rensselaer Institute for Data Exploration and Applications, and Center for Cognition, Communication & Culture
Rensselaer Polytechnic Institute

Dr. Jie Chi Yang
Head, Graduate Institute of Network Learning Technology
Professor, Department of Computer Science and Information Engineering
National Central University

(中央大學資訊工程學系暨網路學習科技研究所所長楊接期教授)

"Understanding Attack Behavior in the Mobile-Social-Internet Era"
Dr. Shanchieh Jay Yang
Associate Professor & Department Head
Department of Computer Engineering
Rochester Institute of Technology

(羅徹斯特理工學院電腦工程學系主任楊善傑教授)

7/31 (Thur) 4:20 pm – 5:50 pm: Technical Session D1-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. I-Chen Wu,** Professor, Department of Computer Science and Director, Institute of Multimedia Engineering, National Chiao-Tung University

(交通大學資訊工程系暨多媒體工程研究所所長吳毅成教授)

Room: 56-154

"MicroRNA Regulation in Human Protein Interaction Network"
Dr. Hsuan-Cheng Huang
Director and Professor, Institute of BioMedical Informatics
National Yang Ming University

(陽明大學生物醫學資訊研究所長黃宣誠教授)

Dr. Jingyi Jessica Li
Assistant Professor, Department of Statistics
University of California, Los Angeles

(加州大學洛杉磯分校統計系李婧翌教授)

Dr. Ming Hu
Assistant Professor, Department of Population Health

Division of Biostatistics
New York University School of Medicine

"Integrative modeling of multi-platform genomic data"
Dr. Yen-Tsung Huang
Assistant Professor, Department of Epidemiology
Brown University

7/31 (Thur) 4:20 pm – 5:50 pm: Technical Session D1-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Chair: **Dr. Hsueh-Fen Juan,** Professor, Institute of Biomedical Electronics and Bioinformatics, Institute of Molecular and Cellular Biology, and Department of Life Science, Center for Systems Biology and Bioinformatics, National Taiwan University
(台灣大學分子細胞生物學研究所阮雪芬教授)
Room: 54-100

"Vocal Fold-Mimetic Microenvironment for the Modulation of Stem Cell Behaviors"
Dr. Xinqiao Jia
Associate Professor, Biomedical Engineering Program
Department of Materials Science and Engineering
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)

"Citrate Biomaterial Design Strategies for Tissue Engineering, Drug Delivery, Medical Devices, and Bioimaging"
Dr. Jian Yang
Associate Professor, Department of Biomedical Engineering
Materials Research Institute
The Huck Institutes of the Life Sciences
The Pennsylvania State University

Dr. Rong Fan
Associate Professor, Department of Biomedical Engineering
Yale University
(耶魯大學生物醫學工程系樊榮教授)

"Capture and identification of circulating RNAs using tethered cationic lipoplex nanoparticles for lung cancer early detection"
Dr. Yun Wu
Assistant Professor, Department of Biomedical Engineering
University at Buffalo, State University of New York

Day 2 (Friday, August 1, 2014):

8/1 (Fri) 8:30 am - 12:45 pm: Registration
Room: 56-154

8/1 (Fri) 8:30 am - 9:50 am: Panel Discussions: Big Data Analytics for Biomedical Science
Moderator: **Dr. Yaoyu E. Wang**, Associate Director, Center for Cancer Computational Biology, Dana-Farber Cancer Institute, Harvard University
(波士頓達納法伯癌症研究所王耀煜博士)
Room: 56-154

Mr. Jason Stowe
CEO, Cycle Computing

Mr. Mick Correll
Chief Operating Officer, Genospace

"Observational Studies with Electronic Health Records"
Dr. Chun-Nan Hsu
Associate Professor of Medicine
Division of Biomedical Informatics
University of California, San Diego

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

Parallel Sessions:
8/1 (Fri) 9:50 am – 11:20 am: Technical Session D2-W1-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining
Chair: **Dr. Shanchieh Jay Yang,** Associate Professor & Department Head, Department of Computer Engineering, Rochester Institute of Technology
(羅徹斯特理工學院電腦工程學系主任楊善傑教授)
Room: 56-114

"Social Media Analytics for Big Data"
Dr. Yun Raymond Fu
Assistant Professor, Department of Electrical and Computer Engineering
Founding Director of SMILE Lab
Northeastern University

"Transcribing the Pitch Content of Polyphonic Music Audio"
Dr. Zhiyao Duan
Assistant Professor, Department of Electrical and Computer Engineering
University of Rochester

"From Web Page Enhancement to Mobile Reading and Learning"
Dr. Chen-Hsiang (Jones) Yu
Founder and CEO, Prentice Lab
(Prentice Lab 余禎祥博士)

8/1 (Fri) 9:50 pm – 11:20 am: Technical Session D2-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. Hsuan-Cheng Huang,** Director and Professor, Institute of BioMedical Informatics National Yang Ming University, (陽明大學生物醫學資訊研究所長黃宣誠教授)
Room: 56-154

"Dissecting the Human Protein-Protein Interaction Network via Phylogenetic Decomposition"
Dr. Hsueh-Fen Juan
Professor, Institute of Biomedical Electronics and Bioinformatics, Institute of Molecular and Cellular Biology, and
Department of Life Science, Center for Systems Biology and Bioinformatics
National Taiwan University
(台灣大學分子細胞生物學研究所與基因體與系統生物學學位學程阮雪芬教授)

Mr. Cho-Yi Chen
PhD Candidate, Genome and Systems Biology Degree Program
National Taiwan University
(台灣大學基因體與系統生物學學位學程陳卓逸)

“Developing and Using Bioinformatics Tools for Analysis of Big DNA Sequence Data”
Dr. Xiaoqiu Huang
Professor, Department of Computer Science
Iowa State University

"Secondary Use of Electronic Medical Records"
Dr. Hongfang Liu
Associate Professor, Mayo College of Medicine

"Personalize Treatment using evidence from data-mining and simulation studies"
Dr. Chih-Lin (Jake) Chi
Assistant Professor, School of Nursing & Institute for Health Informatics
University of Minnesota

8/1 (Fri) 9:50 pm – 11:20 am: Technical Session D2-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Chair: **Dr. Yaoyu E. Wang**, Associate Director, Center for Cancer Computational Biology, Dana-Farber Cancer Institute, Harvard University
(波士頓達納法伯癌症研究所王耀煜博士)
Room: 54-100

“Multiple mechanisms underlying acquired resistance to taxanes in selected docetaxel-resistant MCF-7 breast cancer cells”
Dr. Zhixiang Wang
Professor, Department of Medical Genetics
University of Alberta
(阿尔伯特大学医学遗传学系王智翔教授)

Dr. Xue Han
Assistant Professor, Biomedical Engineering
Boston University

"Fabrication of Nanostructured Constructs from Decellularized Tissue Using Bioskiving"
Dr. Qiaobing Xu
Assistant Professor, Department of Biomedical Engineering
Tufts University

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

8/1 (Fri) 11:20 am – 11:35 am: Break

Parallel Sessions:

8/1 (Fri) 11:35 am – 1:05 pm: Technical Session D2-W1-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Chair: **Dr. Sao-Jie Chen,** Professor, Department of Electrical Engineering, National Taiwan University
(台灣大學電機工程學系陳少傑教授)
Room: 56-114

Dr. Yaoyu E. Wang
Associate Director, Center for Cancer Computational Biology
Dana-Farber Cancer Institute
Harvard University
(波士頓達納法伯癌症研究所王耀煜博士)

Dr. Woei-jyh (Adam) Lee
Tyser Teaching Fellow of Information Systems, School of Business
University of Maryland, College Park and
National Institutes of Health
(馬里蘭大學學院市分校商學院及美國國家衛生研究院李偉智教授)

"DNA-Seq Analysis and Cloud Computing"
Dr. Chiao-Feng Lin
Senior Data Analyst, Department of Pathology and Laboratory Medicine
University of Pennsylvania Perelman School of Medicine
(賓州大學醫學院林嬌鳳博士)

8/1 (Fri) 11:35 am – 1:05 pm: Technical Session D2-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. Hsuan-Cheng Huang,** Director and Professor, Institute of BioMedical Informatics National Yang Ming University, (陽明大學生物醫學資訊研究所長黃宣誠教授)
Room: 56-154

Dr. Kechen Zhang
Assistant Professor of Biomedical Engineering and Neuroscience
Department of Biomedical Engineering
Johns Hopkins University School of Medicine

Dr. Jing Qian
Assistant Professor, Division of Biostatistics and Epidemiology
School of Public Health and Health Sciences
University of Massachusetts, Amherst

Dr. Gang Han
Associate Research Faculty
Department of Biostatistics
Yale University School of Public Health

"Mdmx: the choreographer of signal dynamics and cell fate"
Dr. Sheng-hong Chen
Research Fellow, Department of Systems Biology
Harvard Medical School

8/1 (Fri) 11:35 am – 1:05 pm: Technical Session D2-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

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

Room: 54-100

"MicroRNA-mediated Regulatory Network Driven by MYCN in Neuroblastoma"
Dr. Hsueh-Fen Juan
Professor, Institute of Biomedical Electronics and Bioinformatics, Institute of Molecular and Cellular Biology, and
Department of Life Science, Center for Systems Biology and Bioinformatics
National Taiwan University
(台灣大學分子細胞生物學研究所阮雪芬教授)

"Tapping into chemodiversity in plants: from natural product biosynthesis to mechanism-based herbal medicine"
Dr. Jing-Ke Weng
Assistant Professor, Whitehead Institute for Biomedical Research and
Department of Biology
Massachusetts Institute of Technology

"Development of flavivirus inhibitors"
Dr. Hongmin Li
Research Scientist, the Division of Genetics, Wadsworth Center, NYSDOH and
Associate Professor, Department of Biomedical Sciences
The State University of New York at Albany

"Population dynamics and synthetic biology in antibacterial treatment"
Dr. Cheemeng Tan
Assistant Professor, Department of Biomedical Engineering
Society in Science – Branco Weiss Fellow
University of California, Davis

8/1 (Fri) 1:05 pm - 2:35 pm: Lunch

Parallel Sessions:

8/1 (Fri) 2:35 pm – 4:05 pm: Technical Session D2-YA-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Chair: **Dr. Chen-Hsiang (Jones) Yu,** Founder and CEO, Prentice Lab
(Prentice Lab 余禎祥博士)
Room: 56-114

Ms. Lining (Lizzie) Yao
PhD Candidate, Tangible Media Group
MIT Media Lab
Massachusetts Institute of Technology

"MoveInk: an Interactive Gestural Pen Animation"
Ms. Sheng-Ying (Aithne) Pao
PhD Candidate, MIT Media Lab
Massachusetts Institute of Technology
(麻省理工學院媒體實驗室包盛盈)

"High-Performance Complex Event Processing for Decision Analytics"
Mr. Haopeng Zhang
PhD Candidate, School of Computer Science
University of Massachusetts Amherst
(马萨诸塞大学安默斯特分校计算机学院张浩鹏博士)

8/1 (Fri) 2:35 pm – 4:05 pm: Technical Session D2-YB-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. Woei-jyh (Adam) Lee,** Tyser Teaching Fellow of Information Systems, School of Business, University of Maryland, College Park and National Institutes of Health
(馬里蘭大學學院市分校商學院及美國國家衛生研究院李偉智教授)
Room: 56-154

Dr. Di Wu
Postdoctoral fellow, Department of Statistics
Harvard Medical School

"MAGeCK enables robust identification of essential genes from genome-scale CRISPR-Cas9 knockout screens"
Dr. Wei Li
Postdoctoral Research Fellow, Department of Biostatistics and Computational Biology
Dana-Farber Cancer Institute, Harvard School of Public Health

Dr. Ying Shen
Postdoctoral Associate, Computational Biomedicine
Department of Medicine
Boston University

"Molecular Organization of the GARP Vesicle Tethering Complex"
Dr. Hui-Ting Chou
Postdoctoral Fellow, Department of Cell Biology
Harvard Medical School

8/1 (Fri) 2:35 pm – 4:05 pm: Technical Session D2-YC-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Chair: **Dr. Hsiang-Ying (Sherry) Lee,** Postdoctoral Associate, Whitehead Institute for Biomedical Research, Massachusetts Institute of Technology
(麻省理工學院李湘盈博士)
Room: 54-100

"Epigenetics of Genetic Switches: Micro and Macro Views"
Dr. Jian Xu
Instructor in Pediatric Hematology-Oncology
Boston Children's Hospital, HHMI, Harvard Medical School

Dr. Yuyu Song
Postdoctoral Research Fellow, Howard Hughes Medical Institute
Yale University School of Medicine and
Visiting Research Fellow in Systems Biology, Howard Hughes Medical Institute
Harvard Medical School

"Humanization of an anti-CCR4 antibody and its functional role in cancer immunotherapy"
Dr. DeKuan Chang
Postdoctoral Fellow, Department of Cancer Immunology & AIDS
Dana-Farber Cancer Institute
Harvard Medical School

Dr. Sidi (Steve) Chen
Damon Runyon Cancer Research Fellow, Koch Institute for Integrative Cancer Research
Massachusetts Institute of Technology

8/1 (Fri) 4:05 pm – 4:20 pm: Break

Parallel Sessions:

8/1 (Fri) 4:20 pm – 5:50 pm: Technical Session D2-YA-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Chair: **Dr. Chen-Hsiang (Jones) Yu,** Founder and CEO, Prentice Lab
(Prentice Lab 余禎祥博士)
Room: 56-114

"Accountable HTTP"
Ms. Oshani Seneviratne
PhD Candidate, Computer Science and Artificial Intelligence Laboratory
Department of Electrical Engineering and Computer Science
Massachusetts Institute of Technology

"Loco-Radio - an Augmented-Reality Music Player for Mobile Users"
Dr. Wu-Hsi Li
MIT Media Lab

Massachusetts Institute of Technology
(麻省理工學院媒體實驗室李務熙博士)

"A newly designed selection method and its evaluation for camera-based mouse-replacement systems"
Ms. Wenxin Feng
PhD Student, The Computer Science Department
Boston University

8/1 (Fri) 4:20 pm – 5:50 pm: Technical Session D2-YB-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Chair: **Dr. Woei-jyh (Adam) Lee,** Tyser Teaching Fellow of Information Systems, School of Business, University of Maryland, College Park and National Institutes of Health
(馬里蘭大學學院市分校商學院及美國國家衛生研究院李偉智教授)
Room: 56-154

"Processing Vastly Growing Human Genomic Data"
Dr. Wan-Ping Lee
Senior Lead Scientist, R&D
Seven Bridges Genomics, Inc.
(Seven Bridges Genomics 李婉萍博士)

"Personalized Genomic Medicine - Current Strategies and Bioinformatics Pipelines"
Dr. Ellen Ay-Lun Tsai
Sr. Bioinformatician, Partners Healthcare
Research Fellow, Harvard Medical School and Brigham and Women's Hospital

Dr. Wen-Chi Chou
Postdoctoral Research Fellow, Hebrew SeniorLife
Harvard Medical School

"Identification of novel muscle secreted proteins (myokines) using RNAseq"
Dr. Chia-Ling Wu
Postdoctoral Research Associate, Whitaker Cardiovascular Institute
Boston University

8/1 (Fri) 4:20 pm – 5:50 pm: Technical Session D2-YC-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Chair: **Dr. Hsiang-Ying (Sherry) Lee,** Postdoctoral Associate, Whitehead Institute for Biomedical Research, Massachusetts Institute of Technology
(麻省理工學院李湘盈博士)
Room: 54-100

"Drug-Induced Ablation of Activated Pin1 Selectively in Cancer Cells Has Potent Anticancer Activity by Inhibiting Many Cancer-Driving Pathways"
Dr. Shuo (Dennis) Wei
Susan G. Komen Research Fellow, Beth Israel Deaconess Medical Center and
Harvard Medical School
(哈佛醫學院魏碩博士)

"Cells, Tissues, and Scaffolds: Seeing Them All – Photoacoustic Imaging in Regenerative Engineering"
Dr. Y. Shrike Zhang
Postdoctoral Research Fellow, Department of Medicine
Brigham and Women's Hospital, Harvard Medical School
Harvard-MIT Division of Health Sciences and Technology

"Real-Time Visualization of JC Virus Internalization"
Dr. Yi-ying Chou
Postdoctoral Fellow, Department of Cell Biology, Harvard Medical School and
Cellular and Molecular Medicine Program, Boston Children's Hospital
(哈佛醫學院周怡吟博士)

"Computational Design of a Peptide-based Self-assembling Nano-Cube"
Dr. Jian Zhang
Postdoctoral Associate, Department of Computer Science
Dartmouth College

Dr. Hsiang-Ying (Sherry) Lee
Postdoctoral Associate, Whitehead Institute for Biomedical Research
Massachusetts Institute of Technology
(麻省理工學院李湘盈博士)

Abstracts and Biographies

Day 1 (July 31, 2014)

Opening Session

Opening Speech and General Conference Chair

Sy-Yen Kuo

Distinguished Professor, Department of Electrical Engineering
Dean, College of Electrical Engineering and Computer Science
National Taiwan University
(台灣大學電資學院院長暨電機工程學系郭斯彥特聘教授)

BIOGRAPHY

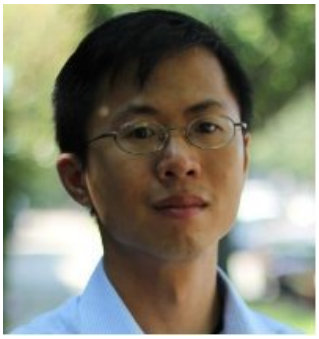
Opening Session

Conference Chair

Yaoyu E. Wang

Associate Director, Center for Cancer Computational Biology
Department of Biostatistics and Computational Biology
Dana-Farber Cancer Institute, 450 Brookline Ave SM822
Boston, MA, 02215 USA
Email: yewang@jimmy.harvard.edu
(波士頓達納法伯癌症研究所王耀煜博士)

BIOGRAPHY



Yaoyu Wang is Associate Director of the Center for Cancer Computational Biology at the Dana-Farber Cancer Institute. He received his B.S. in Biological Science and Computer Science from the Carnegie-Mellon University, and his Ph.D in Bioinformatics from the Boston University. He was a postdoctoral fellow in virology and immunology at the Ragon Institute of MGH, MIT, and Harvard. He currently leads the Center for Cancer Computational Biology (CCCB; http://cccb.dfci.harvard.edu), which provides broad-based genomic research technology platform to the community with high-throughput sequencing and bioinformatics support for collaborative research. The major focuses of the Center are developing novel NGS applications, such as extracellular RNA sequencing as well as computational tools for integrated analysis and visualization of multiple types of –omic data, including transcriptome, exome, whole genome, and targeted resequencing data.

Opening Session

Conference Chair

Chen-Hsiang (Jones) Yu

Founder and CEO, Prentice Lab
Email: jones.yu@prentice-lab.com
(Prentice Lab 余禎祥博士)

BIOGRAPHY

Jones Yu will be an Assistant Professor of Computer Science and Networking at Wentworth Institute of Technology (WIT) in September 2014. He earned B.E. and M.S. in Computer Science and Information Engineering (CSIE) from Tamkang University in 1998 and from National Taiwan University in 2000, respectively, and Ph.D. in Computer Science from MIT under Prof. Rob Miller's guidance in 2012. His research in Human-Computer Interaction (HCI) focuses on web customization and automation, and mobile learning.

He is founder and CEO of Prentice Lab, which is a startup company focusing on investigating mobile technologies and developing software for improving learning, including language learning and subject learning. In the past, he has worked for a few startup companies as Director of Mobile Engineering and User Experience, and developed mobile apps as products.

Opening Session

Welcome Remarks

Anne Hung

Director General, Taipei Economic and Cultural Office in Boston
(駐波士頓台北經濟文化辦事處洪慧珠處長)

BIOGRAPHY

Plenary Session (1)

Plenary Speaker

Light-weight tools for personal health monitoring

Krzysztof Gajos

Associate Professor of Computer Science
School of Engineering and Applied Sciences
Harvard University

BIOGRAPHY

Krzysztof Gajos is an associate professor of Computer Science at the Harvard School of Engineering and Applied Sciences. Krzysztof is broadly interested in interactive intelligent systems, a research area that bridges artificial intelligence, machine learning and human-computer interaction. Recent projects pursued by his group touched upon areas such as personalized adaptive user interfaces, computer accessibility, peer learning, creativity support tools, crowdsourcing, and tools and methods for engaging broader publics in research.

Prior to arriving at Harvard, Krzysztof was a postdoctoral researcher at Microsoft Research. He received his PhD from University of Washington and his M.Eng. and B.Sc. degrees from MIT. In the fall of 2005, he taught the first Artificial Intelligence course at the Ashesi University in Accra, Ghana. Krzysztof is a coeditor-in-chief of the ACM Transactions on Interactive Intelligent Systems. He is a recipient of a Sloan Research Fellowship.

Plenary Session (2)

Plenary Speaker

Molecular Pathological Epidemiology (MPE): Evolving Integrative Biomedical Health Science

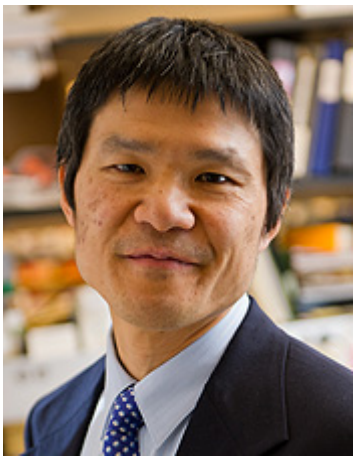
Shuji Ogino

Associate Professor of Pathology, Harvard Medical School
Associate Professor in the Department of Epidemiology, Harvard School of Public Health

ABSTRACT

This lecture introduces “Molecular Pathological Epidemiology (MPE)” (= Molecular Pathology + Epidemiology)” (Ogino et al. J Natl Cancer Inst 2010; Ogino et al. Nat Rev Clin Oncol 2011) as simply as possible. Any given human disease represents fundamentally heterogeneous process, as implicated by the "Unique Disease Principle" (Ogino et al. Expert Rev Mol Diagn 2012; Ogino et al. Mod Pathol 2013). MPE dissects complex interplay between environmental, dietary and lifestyle factors, molecular pathogenic alterations, and disease occurrence and progression. MPE is a logical next step of genome-wide association studies [“GWAS-MPE Approach” (Ogino et al. Gut 2011)]. MPE has proved itself to be a promising approach to identify biomarkers for precision medicine (Chan et al. NEJM 2007; Liao et al. NEJM 2012; Nishihara et al. NEJM 2013, etc.). It is increasingly possible to design MPE database worldwide using routine molecular testing data, as molecular pathology testing is becoming routine clinical practice. It is essential to build large-scale population-based databases including medication use, lifestyle factors, molecular pathology, and clinical outcome. Such databases can generate novel information on potential chemopreventive or therapeutic benefits of drugs, which can be further tested by experimental models and clinical trials. Because disease heterogeneity is a ubiquitous phenomenon, the MPE paradigm should become routine to advance epidemiology in the 21st century, and move us towards personalized prevention and treatment.

BIOGRAPHY



Shuji Ogino, MD, PhD, MS, is the only Harvard University faculty member who holds appointments in both Pathology (Harvard Medical School, HMS) and Epidemiology (Harvard School of Public Health, HSPH) (currently Associate Professor, and promotion to full professor in process). With his unique combination of expertise, Dr. Ogino conceptualized integrative interdisciplinary science of “Molecular Pathological Epidemiology (MPE)” (S Ogino et al. J Natl Cancer Inst 2010; Gut 2011; Nat Rev Clin Oncol 2011). Dr. Ogino has established The International MPE Meeting Series, and serves as Chairperson for The International MPE Meeting Series; the second meeting will be held in Boston on December 4 to 5, 2014. The MPE paradigm has internationally been accepted, and the use of the MPE term has become widespread. Dr. Ogino has also created a number of novel paradigms including “GWAS-MPE Approach” (2011), “Unique Tumor Principle” (2012), “Colorectal Continuum Model” (2012), “Unique Disease Principle”

(2013), and "Etiologic Field Effect" (2014). Dr. Ogino serves as Head of The MPE Laboratory, a multi-institutional research laboratory across Dana-Farber Cancer Institute (DFCI), Brigham and Women's Hospital (BWH), HMS, and HSPH. Recent highlights of his MPE research include two New England Journal of Medicine (NEJM) papers (X Liao et al. 2012; R Nishihara et al. 2013). Because of his effort and accomplishment of advancing the integrative MPE field, Dr. Ogino received Executive Officer's Award (2004) and Meritorious Service Award (2012) from Association for Molecular Pathology (AMP); Ramzi Cotran Young Investigator Award (2011) from United States and Canadian Academy of Pathology (USCAP); is recognized as "Most Influential Science Minds: 2014" by Thomson Reuters; and has been an elected member of an honorary society, American Society for Clinical Investigation (ASCI) since 2014.

Technical Session D1-W1-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Session Chair

Shanchieh Jay Yang

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(羅徹斯特理工學院電腦工程學系主任楊善傑教授)

BIOGRAPHY

S. Jay Yang received his BS degree in electronic engineering from the National Chiao-Tung University in Taiwan in 1995, and his MS and Ph.D. degrees in electrical and computer engineering from the University of Texas at Austin in 1998 and 2001, respectively.

He is currently an Associate Professor and the Department Head for the Department of Computer Engineering at Rochester Institute of Technology in Rochester NY, USA. Before joining RIT in 2002, he has worked as a Research Associate for Fujitsu Laboratory of America and NetQoS, and as an Intern for Bell Laboratory, Lucent Technologies. In summer 2005, he was selected as a Visiting Research Faculty for Air Force Research Laboratory, Rome NY. He has authored and co-authored more than 40 refereed papers in the areas of networking performance modeling and security, information fusion, and swarm robots. His current research interests focus on threat and impact assessments of cyber attacks with machine learning, information fusion and optimization techniques.

Prof. Yang is a Co-Director of the Networking and Information Processing (NetIP) Laboratory at RIT, and an active member of the Center for Multisource Information Fusion based in western New York. He is a member of IEEE, and was a Co-chair for IEEE Joint Communications and Aerospace Chapter in Rochester NY in 2005, when the chapter was recognized as an Outstanding Chapter of Region 1. He has participated in the development of two PhD programs at RIT. He received Norman A. Miles Award for Academic Excellence in Teaching in 2007. He has been on the organization committees for various conferences, including ISIF/IEEE International Conference on Information Fusion in 2009 and the International Conference on Social Computing, Behavioral-Cultural Modeling, & Prediction from 2011 to 2014. He has also been a TPC member or reviewer for numerous journals and conferences, including IEEE Transaction on Information Forensics and Security, IEEE ICCCN, IEEE MILCOM, IEEE GLOBECOM, and IEEE CNS.

Technical Session D1-W1-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Li-Chun Wang

Distinguished Professor and Chairman, Department of Electrical and Computer Engineering
National Chiao-Tung University
(交通大學電信工程研究所兼電機工程學系系主任王蒞君特聘教授)

ABSTRACT

BIOGRAPHY

Technical Session D1-W1-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

AIS-based Knowledge Discovery and Service Provision to Improve Safety at Sea

Shwu-Jing Chang

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(台灣海洋大學通訊與導航工程學系主任張淑淨教授)

ABSTRACT

Automatic Identification System is a cooperative type of electronic vessel tracking system and a wireless communication system for ship/ship and ship/shore information exchange. It is mandatory onboard vessels subject to the International SOLAS (Safety of Life At Sea) Convention. Shipborne AIS stations broadcast the vessels' static data and dynamic position reports on two maritime VHF channels at intervals varying from 2 seconds to several minutes. Besides vessel identification and tracking, AIS also provides mechanisms for binary application-specific messaging. Such data link and rapidly accumulated huge AIS data open up great opportunities leading to intelligent and green transportation.

This talk presents what we can and have achieved in AIS-based knowledge discovery, application and service provision, delivered in a series of government research projects. To be specific, we utilized real data collected from the coastal AIS receiving network of Taiwan since 2009 to analyze traffic pattern, vessel behavior and ship domain, detect near miss or anomalies, and investigate maritime casualties. Possible correlations with the marine environment are investigated by integrating the weather data as well as geospatial information retrieved from navigational charts. In response to the ever increasing cross-Taiwan Strait vessel traffic and operational activities in coastal waters, an internationally interoperable AIS weather information service is being implemented to improve safety at sea. This service is delivered with networked ICT infrastructure and shipboard smart applications platform. It not only broadcasts meteorological information to AIS-fitted vessels but also collects weather observation reports from ships to improve general weather services.

BIOGRAPHY

Shwu-Jing Chang received her B.S. (1986) degree in electronics engineering from National Chiao Tung University, Hsinchu, Taiwan, M.S. (1989) from University of Southern California, US, and Ph.D. (1993) degree in EE from National Chiao Tung University, Taiwan. In 1993, she joined the Department of Navigation, National Taiwan Ocean University, Keelung, Taiwan, as an associate professor and served as the department chair between 1997 and 2000. In 2000, she transferred to the Department of Communications, Navigation and Control Engineering, where she is currently a professor and the department chair. Her research interests include maritime application of information and communication technologies, geospatial information technology and

mobile location-based services. Prof. Chang has successfully implemented several systems at national level, including fishing vessel monitoring system, electronic navigational chart services and coastal network of Automatic Identification System. She has been a member of the Council of Marine Affairs Advancement, Executive Yuan (Cabinet), since 2004.

Technical Session D1-W1-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Steve H.L. Liang

Associate Professor, AITF-Microsoft Industry Chair in Open Sensor Web
Department of Geomatics Engineering
University of Calgary
(卡加利大學空間資訊工程系梁鴻翎教授)

ABSTRACT

BIOGRAPHY

Technical Session D1-W1-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Temporal and Spatial Denoising of Depth Maps

Sao-Jie Chen

Professor, Graduate Institute of Electronics Engineering and
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Email: csj@ntu.edu.tw
(台灣大學電機工程學系陳少傑教授)

ABSTRACT

This work presents a refinement procedure of depth map acquired by RGB Depth (RGB-D) cameras. With the release of many new structure-light RGB-D cameras, such as Microsoft Kincet or Asus Xtion PRO LIVE, it is very conventional and consumer-accessible to acquire high-resolution depth maps. These 3D depth information can be applied to many fields, like augmented reality, image processing, and 3D printer. However, RGB-D cameras suffered from problems such as undesired occlusion, inaccuracy of depth value, and temporal variation. To broaden its application, it is crucial to solve the above-mentioned problems.

This presentation, a novel algorithm based on the exemplar-based inpainting method to cope with the artifact in the depth maps of RGB-D cameras. This exemplar-based inpainting has been used to repair an object-removed image with missing information. The idea of this inpainting method is similar to the procedure of padding the occlusions of a depth map. Therefore, we enhance and adjust this inpainting method to fit and refine the image quality of depth maps in RGB-D cameras. For evaluating the experiment results, our proposed method will be tested on Tsukuba Stereo Dataset, which provides a 3D video with ground truth of depth maps, occlusion maps, and RGB images, PSNR, and computational time as evaluation metrics. Moreover, a set of self-shooting RGB-D depth maps and their refinement results will also be shown to prove the improvement of our performance compared with the original occluded depth maps.

BIOGRAPHY

Sao-Jie Chen received the B.S. and M.S. degrees in electrical engineering from the National Taiwan University, Taipei, Taiwan, ROC, in 1977 and 1982 respectively, and the Ph.D. degree in electrical engineering from the Southern Methodist University, Dallas, USA, in 1988.

Since 1982, he has been a member of the faculty in the Department of Electrical Engineering, National Taiwan University, where he is currently a full professor. During the fall of 2003, he held an academic visitor position in the Department of System Level Design, IBM Thomas J. Watson Research Center, Yorktown Heights, New York, USA. He obtained the “Outstanding Electrical Engineering Professor Award” by

the Chinese Institute of Electrical Engineering in December 2003 to recognize his excellent contributions to EE education. His current research interests include: VLSI physical design, SOC hardware/software co-design, Network-on-Chip, and Wireless LAN and Bluetooth IC design.

Dr. Chen is a member of the Chinese Institute of Engineers, the Chinese Institute of Electrical Engineering, the Institute of Taiwanese IC Design, a senior member of the IEEE Circuits and Systems and the IEEE Computer Societies.

Technical Session D1-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Workshop Co-chair and Session Chair

Li-San Wang

Associate Professor, Department of Pathology and Laboratory Medicine
University of Pennsylvania Perelman School of Medicine
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Email: lswang@mail.med.upenn.edu

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 Associate Professor of Pathology and Laboratory Medicine, and a faculty member of Institute for Biomedical Bioinformatics, University of Pennsylvania. Dr. Wang's research integrates bioinformatics, genomics, and genetics to study neurodegeneration and psychiatric disorders. He has authored more than seventy 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 chairs the data flow working group of the Alzheimer's Disease Sequencing Project (ADSP).

Technical Session D1-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Exploiting Network Effects for Fraud and Malware Detection

Duen Horng Polo Chau

Assistant Professor, School of Computational Science and Engineering
Georgia Institute of Technology
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Email: polo@gatech.edu

ABSTRACT

Graph mining is one of my primary research areas. I work with large graphs with billions of nodes and edges, to spot patterns and anomalies to help people gain insights into such huge datasets. In this talk, I will describe two major pieces of research that make impact to society. They share the common theme that both exploit network effects to combat and detect malicious behaviors.

1) The Polonium malware detection technology uses machine learning to unearth malware from 37 billion machine-file relationships. It is now patented and deployed by Symantec to protect more than 120 million machines worldwide.

2) The NetProbe system detects auction fraud on eBay and fingers bad guys by identifying their networks of suspicious transactions. This work appeared in Wall Street Journal, USA Today, and more.

BIOGRAPHY

Duen Horng (Polo) Chau is an Assistant Professor at Georgia Tech's School of Computational Science and Engineering of the College of Computing, and an Adjunct Assistant Professor at the College's School of Interactive Computing. He is the Associate Director of Georgia Tech Analytics Masters program.

His research bridges the fields of data mining and human-computer interaction (HCI). He develops tools that combine the best of both worlds to help people make sense of large graphs with billions of nodes and edges. He solves large-scale, real world problems that make impact to society. His NetProbe auction fraud detection system appeared on The Wall Street Journal, CNN, TV and radio. His patented Polonium malware detection technology (with Symantec) protects 120 million people worldwide.

Polo received his Ph.D. in Machine Learning and Masters in HCI from Carnegie Mellon (CMU). His PhD thesis work won CMU's School of Computer Science Distinguished Dissertation Award, Honorable Mention. Polo is the only two-time Symantec fellow. He received a Yahoo! Key Scientific Challenges Award. He contributes to the PEGASUS peta-scale graph mining that won an Open Source Software World Challenge Silver Award. His work on detecting fake reviews won a best paper award at SDM'14. Polo is also an award-winning designer. He designed Carnegie Mellon's ID card.

Technical Session D1-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Data Mining in Bioinformatics: Case Studies

Jason Tsong-Li Wang

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Email: 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 case studies for data mining in bioinformatics, with a focus on algorithms and software development.

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 over 120 refereed papers and seven 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 structural, network and systems biology.

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, and a Co-Chair of the 2006 IEEE ICDM Workshop on Data Mining in Bioinformatics and the IEEE ICDM Workshop on Biological Data Mining and its Applications in Healthcare (2011-2014).

Technical Session D1-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

The Phenotype and Exposure Data

Chun-Nan Hsu

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ABSTRACT

The ultimate goal of genomics is to understand the association between the genotypes and the phenotypes of individual organisms under various exposures from the environment and a large volume of research data has been collected and archived for reuse. One of the major obstacles for aggregating small data into Big Data is caused by data heterogeneity due to the use of non-standard terminologies, resulting in semantically equivalent data sources being mistakenly considered different. Tools for standardization have been successfully implemented to overcome this challenge for various –omics data, but this is much more challenging for phenotype and exposure data, where data values and metadata are frequently represented as short text strings. For example, a variable "TAKING HBP MED NOW" reported in a genome-wide association study (GWAS) is semantically equivalent to "Currently taking hypertension lowering medication" in another study. Matching semantically similar variables from different studies, a step known as semantic mapping in data harmonization, usually requires expensive human curation efforts because thousands of variables are involved from many studies on a wide variety of topics. Phenotype and exposure data are ubiquitous. The database of Genotypes and Phenotypes (dbGaP), a giant NCBI repository archives the results of studies that have investigated the interaction of genotype and phenotype, currently houses +3100 data sets from +480 studies and +149,000 phenotype and exposure variables (as of June, 2014). Standardization is challenging because the scope of phenotype and exposure is so broad and evolving that no one has been able to exhaustively organize all possible variables needed and create a comprehensive standard terminology acceptable by the research community.

This talk will present a suite of algorithms to solve these semantic mapping problems. These algorithms will share a common core idea that is to learn semantic similarity distance metrics of short text strings from big scientific and health data. It is challenging to measure the semantic similarity distance in biomedical domains. Previously, we have shown that simple string editing metrics, like the Levenshtein String Similarity Metric or Term Frequency Inverse Document Frequency (TFIDF), are not sufficient for biomedical data because the semantic similarity in biomedical domains cannot be easily defined. The problem is complicated further by the fact that few of the text strings that we need to deal with constitute grammatically valid sentences. Methods developed based on sentence parsing are not applicable.

The proposed approach is built on previous success in distance metric learning in Machine Learning. The proposed algorithms will learn distance metrics highly expressive to accurately model the semantic similarity in biomedical domains. The algorithms can reuse data annotated for data harmonization as the training examples. Moreover, these algorithms can be extended to be semi-supervised in the sense that they can take advantage of large volumes of unlabeled data to minimize the costs of annotating training examples.

Automated semantic mapping will enable us to create a comprehensive knowledge map of all phenotype and exposure variables in dbGaP. The resulting giant knowledge map will provide a holistic view that covers the entire scope of human phenotypes and exposures that have been studied and will serve as a valuable guidance toward a comprehensive standardization. This is a bottom-up and data-driven approach that is unprecedented and will complement previous approaches to standardization that are mostly top-down and knowledge-intensive.

BIOGRAPHY

Prof. Chun-Nan Hsu was born in Taipei, Taiwan. He earned his Ph.D. in computer science from the University of Southern California, Los Angeles, CA, USA.

He was Assistant Professor in computer science and engineering, Arizona State University, Tempe, AZ, USA before he joined Institute of Information Science, Academia Sinica, Taiwan, where he served as the project leader of the informatics group in the Advanced Bioinformatics Core, a core facility supported by the National Research Program of Genomics Medicine funded by the National Science Council, Taiwan, from 2005 to 2011. He joined the Information Sciences Institute, University of Southern California from 2009 to 2013 and moved to his current position at the Division of Biomedical Informatics, Department of Medicine, University of California, San Diego, La Jolla, CA, in November 2013. He has published nearly 100 peer-reviewed research articles in the fields of machine learning, data mining, and biomedical informatics. His team developed widely used software tools for biomedical sciences, including FASTSNP for functional analysis of gene variations, AIIAGMT for biological text mining, and various tools for cell image analysis. AIIAGMT is one of the world's most accurate gene mention tagging tools, ranked at the top in BioCreative international biological text mining challenges. FastSNP integrates 11 data sources in the public domain to facilitate prioritization of genetic markers in association studies. In 2006, the first medical product, Warfarin dosage prediction kit was commercialized. This kit is based on biomarkers identified with the use of FastSNP.

Prof. Hsu is a Senior Member of the Association of Computing Machinery and a professional member of the International Society of Computational Biology. He was elected as the President of the Taiwanese Association for Artificial Intelligence from 2009 to 2011. He won the IBM Faculty Award for his distinguished contributions to biomedical text mining in 2012.

Technical Session D1-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Yu Cao

Assistant Professor, Department of Computer Science
University of Massachusetts, Lowell

ABSTRACT

BIOGRAPHY

Technical Session D1-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Workshop Co-chair and Session Chair

Yi-Hsiang (Sean) Hsu

Assistant Professor, School of Medicine
Harvard University
(哈佛大學醫學院許益祥教授)

BIOGRAPHY

Technical Session D1-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Multifunctional Polymer Drug Nanocarriers for Targeted Cancer Therapy

Shaoqin "Sarah" Gong

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ABSTRACT

Multifunctional polymer drug nanocarriers have been extensively studied for targeted cancer therapy and diagnosis. Unimolecular micelles formed by individual multi-arm star amphiphilic block copolymers possess a number of unique characteristics including excellent in vivo stability and high drug loading levels that make them desirable for targeted cancer therapy. Moreover, various types of tumor-targeting ligands can be conveniently conjugated onto the unimolecular micelles thereby making them useful for a wide variety of cancer therapies. During this presentation, multifunctional unimolecular micelles conjugated with various types of tumor-targeting ligands including peptides, antibodies, and aptamers, and their utility in treating various types of cancers, will be discussed. Unimolecular micelles also show promise in vascular disease treatment and tissue engineering.

BIOGRAPHY

Prof. Gong received dual bachelor's degrees from Tsinghua University in Beijing, China, in 1991, in 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 a 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 200 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 boards of Biofabrication, Theranostics, and the Journal of Biobased Materials and Bioenergy. She has won a number of awards including the National Science Foundation CAREER award, National Institutes of Health Mentored Quantitative Research Career Development Award, the Vilas Associate Award at the University of Wisconsin–Madison, the University of Wisconsin–Milwaukee Outstanding Research Award, and the Society for Information Display Award.

Technical Session D1-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Robotizing Functional Nanoentities - for single-cell drug delivery, bioanalysis, and tunable biochemical release

Donglei (Emma) Fan

Assistant Professor, Materials Science and Engineering Program
The Department of Mechanical Engineering
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ABSTRACT

In this talk, I will discuss innovative concepts and approaches for robotizing functional nanoentities into highly controllable nanomotors for single-cell drug delivery, bioanalysis, and tunable biochemical release. Arrays of designed nanoparticles can be precisely transported along arbitrary trajectories, assembled, and actuated as various nanoelectromechanical (NEMS) devices (or nanomotors) by the electric tweezers — our recent invention. The nanomotors can deliver biosignals to a single live cell amidst many for signal transduction. Functionalized with plasmonics, they can analyze the composition of the membrane of a live cell. Assembled into rotary NEMS, they can precisely tune the release rate of biochemicals by the mechanical rotation. Here, the rotary nanomotors, with nanowires and nanomagnets as building blocks, are the smallest (all dimensions < 1 μm), fastest (18,000 rpm), and most durable rotary NEMS (continuously operate for 15 hours over 240,000 cycles). The innovations reported in this research, from concept, design, actuation, to application could be inspiring for NEMS, nanomedicine, microfluidics, and lab-on-a-chip architectures.

BIOGRAPHY

Dr. Fan received her bachelor's degree in chemistry from the Department of Intensive Instruction, an honor program for gifted undergraduate, in Nanjing University (NJU) in 1999, master's (2003) and doctorate (2007) degrees in Materials Science and Engineering from the Johns Hopkins University (JHU). She also obtained another master's degree in Electrical Engineering from JHU in 2005.

Dr. Fan is an Assistant Professor in the Department of Mechanical Engineering of the University of Texas at Austin, (Austin, TX) since 2010 after accomplishing a Postdoctoral Fellow at JHU in 2009. She received National Science Foundation CAREER award in 2012. She was one of 60 US and Europe young engineers, invited to attend the National Academy of Engineering (NAE) 2013 EU-US Frontier of Engineering Symposium in France. She was honored as a Recognized Mentor by the Siemens Foundation in 2012, a finalist of the Beckman Young Investigator Award (24 finalists nationwide). Prof. Fan's work has spurred a series of publications on leading journals including Nature Nanotechnology, Nature Communications, the Proceedings of National Academy of Sciences, Nano Today, Physical Review Letters, Advanced Materials, Advanced Functional Materials, ACS Nano, Applied Physics Letters, as well as a few pending patents.

Technical Session D1-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Gang Logan Liu

Assistant Professor, Department of Electrical and Computer Engineering and Bioengineering
University of Illinois at Urbana-Champaign

ABSTRACT

BIOGRAPHY

Technical Session D1-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Molecular programming with DNA/RNA: nanofabrication, imaging, and sensing

Peng Yin

Assistant Professor, Department of Systems Biology
Harvard Medical School

ABSTRACT

I will discuss my lab's research on engineering synthetic, nucleic acid-based nanostructures and their applications in biosensing, imaging, nanofabrication, and tissue engineering.

We have recently invented a general framework for programming the self-assembly of short synthetic nucleic acid strands into prescribed target shapes or demonstrating their prescribed dynamic behavior. Using short DNA strands, we have demonstrated the modular construction of sophisticated 1D (Science, 321:824, 2008), 2D (Nature, 485:623-626, 2012) and 3D (Science, 338:1177, 2012) structures on the 100-nanometer scale with nanometer precision. Using reconfigurable DNA hairpins, we have demonstrated diverse, dynamic behavior such as catalytic circuits, triggered assembly, and autonomous locomotion (Nature, 451:318, 2008).

By interfacing these synthetic, nucleic acid nanostructures with functional molecules, we are developing diverse applications. In bioimaging, we have engineered geometrically encoded fluorescent barcodes for highly multiplexed single-molecule imaging (Nature Chemistry, 4:832-839, 2012) and dynamic fluorescent probes for highly multiplexed 3D super-resolution cellular imaging (Nature Methods, 11:313, 2014; Science, 334:65, 2014). In biosensing, we have constructed robust and ultraspecific probes for detecting single-base changes in a single-stranded DNA/RNA target (Nature Chemistry, 4:208-214, 2012). In nanofabrication, we have collaboratively developed a versatile framework for producing inorganic materials (e.g. graphene [Nature Communications, 4:1663, 2013], silicon dioxides [JACS, 135:6778, 2013], silver, gold) with arbitrarily prescribed nanometer scale shapes. In tissue engineering, we have developed a general strategy to engineer DNA directed self-assembly of biocompatible hydrogel bricks into complex architectures (Nature Communications, 4:2275, 2013).

See our lab's work at http://molsys.net.

BIOGRAPHY

Peng Yin is an Assistant Professor of Systems Biology at Harvard Medical School and a Core Faculty Member at Wyss Institute for Biologically Inspired Engineering at Harvard University. He directs the Molecular Systems Lab at Harvard. His research interests lie at the interface of information science, molecular engineering, and biology. The current focus is to engineer information directed self-assembly of nucleic acid (DNA/RNA) structures and devices, and to exploit such systems to do useful molecular work, e.g. probing and programming biological processes for bioimaging and therapeutic applications. He is a recipient of a 2010 NIH Director's New Innovator Award, a 2011 NSF CAREER Award, a 2011 DARPA Young Faculty Award, a 2011 ONR Young Investigator Program

Award, a 2013 NSF Expedition in Computing Award, and a 2013 NIH Director's Transformative Research Award. See his lab's work at http://molecular-systems.net

Technical Session D1-W1-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Workshop Co-chair and Session Chair

Sao-Jie Chen

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BIOGRAPHY

Sao-Jie Chen received the B.S. and M.S. degrees in electrical engineering from the National Taiwan University, Taipei, Taiwan, ROC, in 1977 and 1982 respectively, and the Ph.D. degree in electrical engineering from the Southern Methodist University, Dallas, USA, in 1988.

Since 1982, he has been a member of the faculty in the Department of Electrical Engineering, National Taiwan University, where he is currently a full professor. During the fall of 2003, he held an academic visitor position in the Department of System Level Design, IBM Thomas J. Watson Research Center, Yorktown Heights, New York, USA. He obtained the "Outstanding Electrical Engineering Professor Award" by the Chinese Institute of Electrical Engineering in December 2003 to recognize his excellent contributions to EE education. His current research interests include: VLSI physical design, SOC hardware/software co-design, Network-on-Chip, and Wireless LAN and Bluetooth IC design.

Dr. Chen is a member of the Chinese Institute of Engineers, the Chinese Institute of Electrical Engineering, the Institute of Taiwanese IC Design, a senior member of the IEEE Circuits and Systems and the IEEE Computer Societies.

Technical Session D1-W1-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Morphing: a New Communication Way in New Media

Heng Ji

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ABSTRACT

The information in traditional media such as newspaper is usually explicitly expressed. However, in some certain conditions (e.g., the existence of censorship) in new media, users need to create new ways to communicate sensitive subjects in order to maximize communicative success and expressive power. One of the most innovative linguistic forms in social media is Morphing [Huang et al., 2013; Zhang et al., 2013]. Morph is a special case of alias to hide the original objects (e.g., sensitive entities and events) for different purposes, including avoiding censorship, expressing strong sentiment, emotion or sarcasm, and making descriptions more vivid. For example, in Chinese social media, users often use the entity morph ``方便面 (Instant Noodles)'' to refer to ``周永康 (Zhou Yongkang)" because it shares one character ``康 (Kang)" with the well-known brand of instant noodles ``康师傅 (Master Kang)".

We study this problem in the following two opposite yet complementary directions. (1). Morph Decoding: Identify morphs and resolve each morph to its real target; (2) Morph Encoding: Develop a wide variety of novel approaches to automatically encode proper and interesting morphs, which can effectively pass decoding tests. We believe that successful decoding and encoding is a crucial step for automated understanding of the fast evolving language in new media, social media marketing, dark web, as well as hidden networks discovery and mining.

BIOGRAPHY

Heng Ji is Edward P. Hamilton Development Chair Associate Professor in Computer Science Department of Rensselaer Polytechnic Institute. She received her B.A. and M.A. in Computational Linguistics from Tsinghua University in 2000 and 2002 respectively, and her M.S. and Ph.D. in Computer Science from New York University in 2005 and 2007 respectively.

Her research interests include Natural Language Processing, Data Mining, Information Networks and Social Networks, and Security.

She received Google Research Awards in 2009 and 2014, NSF CAREER award in 2009, Sloan Junior Faculty Award and IBM Watson Faculty Award in 2012, PACLIC2012 Best Paper Runner-up, "Best of SDM2013" paper, "Best of ICDM2013" paper and "AI's 10 to Watch" Award by IEEE Intelligent Systems in 2013. She coordinated the NIST TAC Knowledge Base Population task in 2010, 2011 and 2014, served as the vice Program Committee Chair for IEEE/WIC/ACM WI2013, the Information Extraction area chair for NAACL2012, ACL2013, EMNLP2013 and NLPCC2014, and the Local Co-chair for IJCAI2016.

Technical Session D1-W1-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Jie Chi Yang

Head, Graduate Institute of Network Learning Technology
Professor, Department of Computer Science and Information Engineering
National Central University
(中央大學資訊工程學系暨網路學習科技研究所所長楊接期教授)

ABSTRACT

BIOGRAPHY

Technical Session D1-W1-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Understanding Attack Behavior in the Mobile-Social-Internet Era

Shanchieh Jay Yang

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ABSTRACT

The prevalence of Internet-enabled services, social media and mobile devices has opened up new avenues for malicious attacks and privacy intrusion. While hardware platforms, software infrastructure, and network configurations can and should be continuously hardened, it is critical to advance research in understanding adversary behavior to reveal malicious effects that are not known previously. This talk will begin with discussing some of the new adversary activities via social media and mobile platforms. This discussion will lead to some of the new research directions, including obfuscation modeling, information cascade estimation, semi-supervised learning of asset-centric attack behavior, and moving target defense modeling. Preliminary results will provide insights on how much one can do in comprehending attack strategies and anticipating their effects.

BIOGRAPHY

S. Jay Yang received his BS degree in electronic engineering from the National Chiao-Tung University in Taiwan in 1995, and his MS and Ph.D. degrees in electrical and computer engineering from the University of Texas at Austin in 1998 and 2001, respectively. He is currently an Associate Professor and the Department Head for the Department of Computer Engineering at Rochester Institute of Technology in Rochester NY, USA. He is a Co-Director of the Networking and Information Processing (NetIP) Laboratory at RIT, and an active member of the Center for Multisource Information Fusion based in western New York. He has authored and co-authored more than 40 papers in the areas of cyber situation awareness and threat assessment, networking performance modeling, and swarm robots. His current research interests focus on network attack modeling with machine learning, information fusion and optimization techniques, and has developed several systems to synthesize, simulate, and predict complex attack strategies.

Prof. Yang is a member of IEEE, and was a Co-chair for IEEE Joint Communications and Aerospace Chapter in Rochester NY in 2005, when the chapter was recognized as an Outstanding Chapter of Region 1. He has participated in the development of two PhD programs at RIT. He received Norman A. Miles Award for Academic Excellence in Teaching in 2007. He

has been on the organization committees for various conferences, including ISIF/IEEE International Conference on Information Fusion in 2009 and the International Conference on Social Computing, Behavioral-Cultural Modeling, & Prediction from 2011 to 2014. He has also been a TPC member or reviewer for numerous journals and conferences, including IEEE Transaction on Information Forensics and Security, IEEE ICCCN, IEEE MILCOM, IEEE GLOBECOM, and IEEE CNS.

Technical Session D1-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Workshop Co-chair and Session Chair

I-Chen Wu

Professor, Department of Computer Science and
Director, Institute of Multimedia Engineering
National Chiao-Tung University
(交通大學資訊工程系暨多媒體工程研究所所長吳毅成教授)

BIOGRAPHY

Technical Session D1-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

MicroRNA Regulation in Human Protein Interaction Network

Hsuan-Cheng Huang

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ABSTRACT

MicroRNAs are small non-coding RNAs, which regulate the protein encoding genes at post-transcriptional level. Topological and dynamic features of protein-protein interaction network provide insights of biological processes. We have performed topological analysis to elucidate the global correlation between microRNA regulation and protein interaction network in human. The results showed that microRNA targets tend to be hubs and bottlenecks in the network. While proteins directly regulated by microRNA might not form a network module themselves, the microRNA targets and their interacting proteins jointly show significantly higher network density and modularity. We also found that microRNAs may engage in a wider diversity of biological processes by coordinating with transcription factors, and this kind of cross-layer co-regulation may have higher specificity than intra-layer co-regulation. We further investigated the combinatorial regulatory effects of transcription factor and microRNA pairs on the protein interaction network and observed significant crosstalk between non-overlapping targets of co-regulators through protein-protein interactions. With gene expression profiles in different biological states, we have examined the dynamic structure of microRNA-regulated networks, and developed a network-based method, Mirin, to identify active microRNAs and reveal their functional roles in specific biological condition. Mirin is freely available at http://mirin.ym.edu.tw/. Applying the analysis to gastric cancer, we found a key microRNA that plays an important role in tumor suppression and elaborated its regulatory mechanism in cancer cells.

BIOGRAPHY

Hsuan-Cheng Huang received his B.A., M.A., and Ph.D. degrees in physics from National Taiwan University in 1992, 1994 and 1998, respectively. He was engaged in experimental high-energy physics research at Taiwan and at High Energy Accelerator Research Organization, Japan, and awarded NSC Distinguished Postdoctoral Fellowship in 2003. Encouraged by the emerging of systems biology, Dr. Huang joined National Yang-Ming University in 2004 and is currently a Professor and the Director of the Institute of Biomedical Informatics, also affiliated with the Center for Systems and Synthetic Biology. In 2007, he received the NSC Wu Ta-You Memorial Award, an honor for excellent young investigators in Taiwan. He also serves as an Associate Editor and Deputy Section Editor of BMC Systems Biology. His research interests include bioinformatics, computational and systems biology, and network biology. Currently, Dr. Huang endeavors his

research efforts to computational analysis and modeling of biological networks, and applies them to unravel molecular mechanisms of cancer cell response, microRNA and lncRNA regulation, as well as other biological processes.

Technical Session D1-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Jingyi Jessica Li

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University of California, Los Angeles
(加州大學洛杉磯分校統計系李婧翌教授)

ABSTRACT

BIOGRAPHY

Technical Session D1-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Ming Hu

Assistant Professor, Department of Population Health
Division of Biostatistics
New York University School of Medicine

ABSTRACT

BIOGRAPHY

Technical Session D1-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Integrative modeling of multi-platform genomic data

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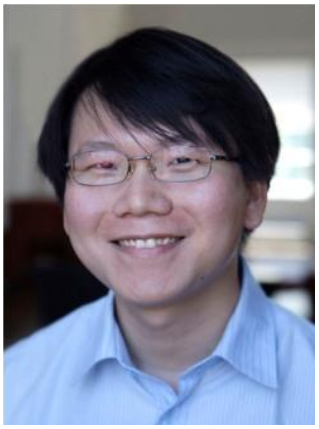
ABSTRACT

Given the availability of genomic data, there have been emerging interests in integrating multi-platform data. Here we propose to model genetics (single nucleotide polymorphism (SNP)), epigenetics (DNA methylation) and gene expression data as a biological process to delineate phenotypic traits under the framework of causal mediation modeling. We propose a regression model for the joint effect of SNPs, methylation, gene expression and their non-linear interactions on the outcome, and study three path-specific effects: the direct effect of SNPs on the outcome, the effect mediated through expression and the effect through methylation. We characterize correspondences between the three path-specific effects and coefficients in the regression model, which are influenced by causal relations among SNPs, DNA methylation and gene expression. To assess path-specific effects, we develop a score test for variance components of regression coefficients. The test statistic under the null follows a mixture of chi-square distributions, which can be approximated using a characteristic function inversion method or a perturbation procedure. We construct tests for candidate models determined by different combinations of SNPs, DNA methylation, gene expression and interactions, and further propose an omnibus test to accommodate different models. We illustrate the utility of our method in two genomic studies and numerical simulation studies.

BIOGRAPHY



Yen-Tsung Huang was born in Kaohsiung, Taiwan in 1978. He earned a Doctor of Medicine degree from the National Taiwan University, Taipei, Taiwan in 2003. Dr. Huang went to Harvard University, MA, USA for Master of Public Health concentrating on quantitative methods (2006) and Master of Science in biostatistics (2009). He earned Dual Degree of Doctor of Science in Epidemiology and Biostatistics at Harvard in 2012.

He served in military for one and half years as a Medical Officer in Taiwan after graduating from National Taiwan University. He worked in Dr. David Christiani's lab as a Postdoctoral Research Fellow at Harvard in 2006-2007. He is currently an Assistant Professor in Brown University, Providence, RI (2012-). His research interests focus on cancer genomics, high-dimensional statistics, and molecular/genetic epidemiology.

Dr. Huang is a member of American Statistical Association (ASA), Eastern North American Region of International Biometric Society, American Society of Human Genetics, and American

Association of Cancer Research. Dr. Huang is a recipient of ASA Byar Travel Award (2012) and Brown's Salomon Research Award (2013).

Technical Session D1-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Session Chair

Hsueh-Fen Juan

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BIOGRAPHY

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

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

Prof. Juan has developed a number of novel methods to advance systems-biology research and applied such approach for drug discovery and elucidating molecular mechanism of drug responses in cancer cells. She has published more than 75 journal papers and edited a scientific book entitled as Systems Biology: Applications in cancer-related research (2012). She is now the editor of Computational and Mathematical Methods in Medicine (Hindawi Publishing Corporation). She also serves as the reviewer of 37 various journals such as Drug Discovery Today, Molecular and Cellular Proteomics (ASBMB), Journal of Proteome Research (ACS), Proteomics (Wiley-VCH), Bioinformatics (Oxford), and has organized several international systems biology and bioinformatics symposiums. She is one of the founders of Center for Systems Biology (NTU), and currently the Council Member of four societies, the Taiwan Society for Biochemistry and Molecular Biology, Taiwan Proteomics Society, Taiwan Bioinformatics and Systems Biology Society, and Taiwan Society of Evolution and Computational Biology. Since Dr. Juan made significant contributions through systems biology approach to development of methodology and cancer therapy; she received the awards “Taiwan's Ten Outstanding Young Persons” (2008), FY2011 JSPS Invitation Fellowship Program for Research in Japan (2011), K. T. Li Breakthrough Award by Institute of Information and Computing Machinery (2012), and National Science Council (NSC) Award for Special Talents of the Colleges (2010-2014).

Technical Session D1-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Vocal Fold-Mimetic Microenvironment for the Modulation of Stem Cell Behaviors

Xinqiao Jia

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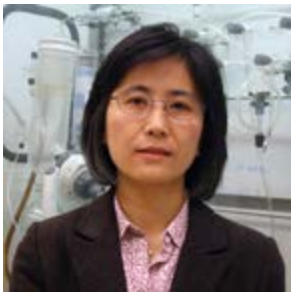
ABSTRACT

Voice is produced when vocal folds are driven into a wave-like motion by the air from the lung. Numerous mechanical and pathological factors can damage the tissue, giving rise to a variety of voice-related disorders with symptoms ranging from hoarseness to inability to phonate. Impaired voice production holds significant implications for individual health and wellness, social and occupational function, and societal productivity. Successful engineering of vocal fold tissues relies on a strategic combination of therapeutic cells, biomimetic scaffolds, physiologically relevant mechanical and biochemical factors. Specifically, high frequency vibratory stimulations and soluble connective tissue growth factor (CTGF), separately or in combination, were introduced to mesenchymal stem cells (MSCs) cultured on a poly(ε-caprolactone) (PCL)-derived fibrous scaffold. Introduction of CTGF to the cultured MSCs led to an enhanced cell proliferation, an increased expression of fibroblastic markers and an elevated synthesis of essential vocal fold extracellular matrix (ECM) components. Physiologically relevant vibratory stimulations also have a profound effect on MSC functions. A 1 h-on-1h-off sinusoidal vibration at 200 Hz was found to foster the cellular production of ECM components, such as elastin, HA, and matrix metalloproteinase-1. Finally, vibratory stresses and CTGF signals cooperatively coaxed MSCs toward a vocal fold fibroblast-like phenotype and accelerated the synthesis and remodeling of vocal fold-like matrices. Overall, the combination of multipotent stem cells, biomimetic scaffold, soluble factors and a vibratory culture device offers an exciting opportunity for the engineering of vocal fold lamina propria.

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

designing biomimetic synthetic matrices and mechano-culture devices for the engineering of functional tissues. Her research activities are currently supported by National Science Foundation and National Institutes of Health. She received the 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 Delaware 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 60 peer reviewed scientific papers since she started her MS thesis work in 1998.

Technical Session D1-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Citrate Biomaterial Design Strategies for Tissue Engineering, Drug Delivery, Medical Devices, and Bioimaging

Jian Yang

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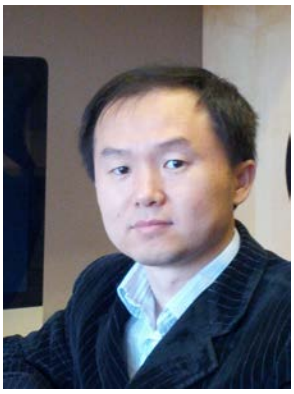
ABSTRACT

Dr. Yang will discuss a methodology of citrate-based biomaterial design for tissue engineering, drug delivery, medical devices, and cancer bioimaging. This methodology embraces biomimicking strategies and novel chemistry design to develop a family of novel biodegradable polymers. Specific topics to be covered in this seminar include nanoparticle scaffolds for in situ endothelium regeneration, osteoinductive polymers for orthopedic devices and bone regeneration, bioglues for wound healing, and theranostic nanoparticles for cancer imaging and drug delivery.

BIOGRAPHY



Dr. Yang was born in Wanzai, Jixangxi Province, P. R. China. He received his PhD in Polymer Chemistry and Physics in 2002 from the Chinese Academy of Sciences in China. After completing his PhD, he joined the Department of Biomedical Engineering at Northwestern University as a postdoctoral fellow in 2003-2006.

He was then recruited to the Department of Bioengineering at University of Texas at Arlington (UTA) as an assistant professor in 2006 and obtained an early promotion to associate professor with tenure in 2011. In 2012, Dr. Yang joined the Department of Biomedical Engineering at the Pennsylvania State University as a tenured associate professor.

Dr. Yang has published 67 peer-reviewed journal articles, 7 issued patents, and 6 book chapters. He was a recipient of NSF CAREER Award (2010) and Outstanding Young Faculty Award of College of Engineering at UTA (2011). Dr. Yang is a member of Biomedical Engineering Society, Society for Biomaterials, and American Heart Association. Dr. Yang services a frequent panel reviewer for NSF and NIH (BMBI, SBIR, etc). Dr. Yang is an Associate Editor for “Frontiers in Biomaterials”, a section of “Frontiers in Bioengineering and Biotechnology” and “Frontiers in Materials”. Dr. Yang’s lab is currently funded by 3 NIH R01 grants and 2 NSF grants. Dr. Yang’s major research interest lies in novel biomaterial design for tissue engineering, drug delivery and medical devices.

Selected Publications (* corresponding author)

1. Jian Yang*, Santosh Gautam, Li Liu, Jagannath Dey, Wei Chen, Ralph Mason, Liping Tang. Development of aliphatic biodegradable photoluminescent polymers. Proc. Natl. Acad. Sci. USA, 2009 106:10086-10091. (Highlighted in “In This Issue” of PNAS)
2. Jinshan Guo, Zhiwei Xie, Richard T. Tran, Denghui Xie, Dadi Jin, Xiaochun Bai, Jian Yang*. Click chemistry played a dual role in biodegradable polymer design. Advanced Materials 2014, 26: 1906-1911. NIHMSID #553927. (Back cover)
3. Zhiwei Xie, Yi Zhang, Li Liu, Hong Weng, Ralph P. Mason, Liping Tang, Kytai T. Nguyen, Jer-Tsong Hsieh, Jian Yang*. Development of Intrinsically Photoluminescent and Photostable Polylactones. Advanced Materials 2014 DOI: 10.1002/adma.201306070. NIHMSID #584801

Technical Session D1-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Rong Fan

Associate Professor, Department of Biomedical Engineering
Yale University
(耶魯大學生物醫學工程系樊榮教授)

ABSTRACT

BIOGRAPHY

Technical Session D1-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Capture and identification of circulating RNAs using tethered cationic lipoplex nanoparticles for lung cancer early detection

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ABSTRACT

Lung cancer is the leading cause of cancer deaths worldwide with a disappointing 15% overall 5-year survival rate. A patient-friendly early detection method would substantially reduce the mortality in this serious disease. Non-invasive 'liquid biopsy' relying on the detection of extracellular circulating RNAs (microRNAs and mRNAs) in patient blood samples has great potential to achieve this goal. Circulating RNAs carried by cell-secreted, vesicular 'nanoparticles' (i.e. exosomes) have emerged as promising diagnostic and prognostic cancer biomarkers because of their presence and remarkable stability in body fluids. Because over-diagnosis and false positives present significant problems in lung cancer diagnosis, development of circulating RNA-based non-invasive 'liquid biopsy' detection methods can be tremendously important for high-risk patient screening and early detection of lung cancer.

Circulating RNAs in serum/plasma samples are typically quantified using a workflow that involves isolation of RNA from the blood samples followed by analyte-specific quantitative reverse transcription (qRT)-PCR of RNA. However, this RNA isolation-qRT-PCR workflow cannot distinguish circulating RNAs secreted by cancer cells from those released physiologically and ubiquitously by all other, non-tumor cells of the body, making it potentially less sensitive or incapable of detecting cancer-specific RNA biomarkers.

We recently developed a novel and simple tethered cationic lipoplex nanoparticle (tCLN) biochip to capture and detect cancer-specific RNAs carried by exosomes in human serum samples. Serum was applied directly on the tCLN biochip. Molecular detection probes, such as molecular beacons (MBs), were encapsulated in the cationic lipoplex nanoparticles which can capture negatively charged circulating exosomes via electric static interactions to form a larger nanoscale complex. This lipoplex-exosome fusion lead to the mixing of RNAs and molecular beacons (MBs) within the nanoscale confinement near the biochip interface, and thus generated fluorescence signals. Total internal reflection fluorescence (TIRF) microscopy, which is capable of detecting a single biomolecule and measures signals <300 nm near the interface, was used to measure the intensity of fluorescence signals generated by the circulating RNAs. In tCLN biochip, the exosomal RNAs were confined within the lipoplex-exosome complex, which provided a "focusing" effect. Each lipoplex-exosome cluster was quantitatively and individually evaluated. The tCLN biochip can better distinguish cancer cell-derived exosomes from their non-tumor counterparts because the former is more likely to contain many copies of target RNAs leading to a strong local fluorescence signal. The in situ detection of target RNAs without diluting the sample leads to very high detection sensitivity not achievable by existing methods such as the traditional serum RNA isolation-qRT-PCR workflow. We have demonstrated the feasibility of the tCLN biochip in detecting microRNA miR-21 and Thyroid Transcription Factor-

1 (TTF-1) mRNA in serum of lung cancer patients. The tCLN biochip successfully distinguished early stage
lung cancer patients from normal healthy controls, whereas the serum RNA isolation-qRT-PCR workflow was found to be completely ineffective for the task.

This simple, fast and low-cost method with high sensitivity in identifying tumor-relevant RNAs may serve as routine pre-screening that could complement more invasive and expensive testing for clinical use.

BIOGRAPHY

Dr. Yun Wu was born in Hubei province, China. She received her B.S. and M.S. degrees from Harbin Institute of Technology, Harbin, China in 2000 and 2002, respectively, majoring in polymer materials and engineering. She received her Ph.D. from the Department of Chemical and Biomolecular Engineering at the Ohio State University, Columbus, Ohio, USA in 2009.

After completion of her Ph.D. degree, she worked in the NSF Nanoscale Science and Engineering Center at the Ohio State University as a Postdoctoral Research Associate. In 2013 she joined the Department of Biomedical Engineering at State University of New York at Buffalo, Buffalo, New York, USA as an Assistant Professor. She has published 1 book chapter and 24 peer-reviewed papers. She has more than 25 presentations at national and international conferences. Her research interests are focused on the development of multifunctional nanoparticles based therapeutics and diagnostics for cancer imaging, therapy and early detection.

Dr. Wu is a member of Biomedical Engineering Society (BMES) and American Institute of Chemical Engineers (AICHE). She also serves as reviewers for more than 10 scientific journals such as Journal of Controlled Release, Lab on a Chip, Chemical Communications, and Molecular Pharmaceutics etc. She was the recipient of the Biomedical Engineering Society Innovation and Career Development Award in 2013.

Day 2 (August 1, 2014)

Panel Discussions: Big Data Analytics for Biomedical Science

Moderator

Yaoyu E. Wang

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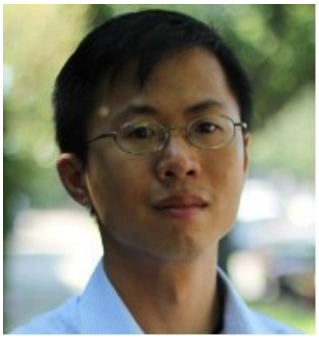
BIOGRAPHY



Yaoyu Wang is Associate Director of the Center for Cancer Computational Biology at the Dana-Farber Cancer Institute. He received his B.S. in Biological Science and Computer Science from the Carnegie-Mellon University, and his Ph.D in Bioinformatics from the Boston University. He was a postdoctoral fellow in virology and immunology at the Ragon Institute of MGH, MIT, and Harvard. He currently leads the Center for Cancer Computational Biology (CCCB; http://cccb.dfci.harvard.edu), which provides broad-based genomic research technology platform to the community with high-throughput sequencing and bioinformatics support for collaborative research. The major focuses of the Center are developing novel NGS applications, such as extracellular RNA sequencing as well as computational tools for integrated analysis and visualization of multiple types of –omic data, including transcriptome, exome, whole genome, and targeted resequencing data.

Panel Discussions: Big Data Analytics for Biomedical Science

Panelist

Jason Stowe

CEO, Cycle Computing

BIOGRAPHY

Panel Discussions: Big Data Analytics for Biomedical Science

Panelist

Mick Correll

Chief Operating Officer, Genospace

BIOGRAPHY

Panel Discussions: Big Data Analytics for Biomedical Science

Observational Studies with Electronic Health Records

Chun-Nan Hsu

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ABSTRACT

The observational study is a new paradigm of study-design for the Big Data era. In contrast of the randomized controlled trial that have been the standard research methodology for nearly a century in biomedical sciences, an observation study reuses data from existing repositories like the data archives of electronic health records to replace a random sample obtained by recruiting new study subjects as in the randomized controlled trial. Whether this difference creates more advantages over the randomized controlled trial or more unreliable, irreproducible results is an open question.

BIOGRAPHY

Prof. Chun-Nan Hsu was born in Taipei, Taiwan. He earned his Ph.D. in computer science from the University of Southern California, Los Angeles, CA, USA.

He was Assistant Professor in computer science and engineering, Arizona State University, Tempe, AZ, USA before he joined Institute of Information Science, Academia Sinica, Taiwan, where he served as the project leader of the informatics group in the Advanced Bioinformatics Core, a core facility supported by the National Research Program of Genomics Medicine funded by the National Science Council, Taiwan, from 2005 to 2011. He joined the Information Sciences Institute, University of Southern California from 2009 to 2013 and moved to his current position at the Division of Biomedical Informatics, Department of Medicine, University of California, San Diego, La Jolla, CA, in November 2013. He has published nearly 100 peer-reviewed research articles in the fields of machine learning, data mining, and biomedical informatics. His team developed widely used software tools for biomedical sciences, including FASTSNP for functional analysis of gene variations, AIIAGMT for biological text mining, and various tools for cell image analysis. AIIAGMT is one of the world's most accurate gene mention tagging tools, ranked at the top in BioCreative international biological text mining challenges. FastSNP integrates 11 data sources in the public domain to facilitate prioritization of genetic markers in association studies. In 2006, the first medical product, Warfarin dosage prediction kit was commercialized. This kit is based on biomarkers identified with the use of FastSNP.

Prof. Hsu is a Senior Member of the Association of Computing Machinery and a professional member of the International Society of Computational Biology. He was elected as the President of the Taiwanese Association for Artificial Intelligence from 2009 to 2011. He won the IBM Faculty Award for his distinguished contributions to biomedical text mining in 2012.

Panel Discussions: Big Data Analytics for Biomedical Science

Panelist

Li-San Wang

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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 Associate Professor of Pathology and Laboratory Medicine, and a faculty member of Institute for Biomedical Bioinformatics, University of Pennsylvania. Dr. Wang's research integrates bioinformatics, genomics, and genetics to study neurodegeneration and psychiatric disorders. He has authored more than seventy 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 chairs the data flow working group of the Alzheimer's Disease Sequencing Project (ADSP).

Technical Session D2-W1-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Session Chair

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BIOGRAPHY

S. Jay Yang received his BS degree in electronic engineering from the National Chiao-Tung University in Taiwan in 1995, and his MS and Ph.D. degrees in electrical and computer engineering from the University of Texas at Austin in 1998 and 2001, respectively.

He is currently an Associate Professor and the Department Head for the Department of Computer Engineering at Rochester Institute of Technology in Rochester NY, USA. Before joining RIT in 2002, he has worked as a Research Associate for Fujitsu Laboratory of America and NetQoS, and as an Intern for Bell Laboratory, Lucent Technologies. In summer 2005, he was selected as a Visiting Research Faculty for Air Force Research Laboratory, Rome NY. He has authored and co-authored more than 40 refereed papers in the areas of networking performance modeling and security, information fusion, and swarm robots. His current research interests focus on threat and impact assessments of cyber attacks with machine learning, information fusion and optimization techniques.

Prof. Yang is a Co-Director of the Networking and Information Processing (NetIP) Laboratory at RIT, and an active member of the Center for Multisource Information Fusion based in western New York. He is a member of IEEE, and was a Co-chair for IEEE Joint Communications and Aerospace Chapter in Rochester NY in 2005, when the chapter was recognized as an Outstanding Chapter of Region 1. He has participated in the development of two PhD programs at RIT. He received Norman A. Miles Award for Academic Excellence in Teaching in 2007. He has been on the organization committees for various conferences, including ISIF/IEEE International Conference on Information Fusion in 2009 and the International Conference on Social Computing, Behavioral-Cultural Modeling, & Prediction from 2011 to 2014. He has also been a TPC member or reviewer for numerous journals and conferences, including IEEE Transaction on Information Forensics and Security, IEEE ICCCN, IEEE MILCOM, IEEE GLOBECOM, and IEEE CNS.

Technical Session D2-W1-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Social Media Analytics for Big Data

Yun Raymond Fu

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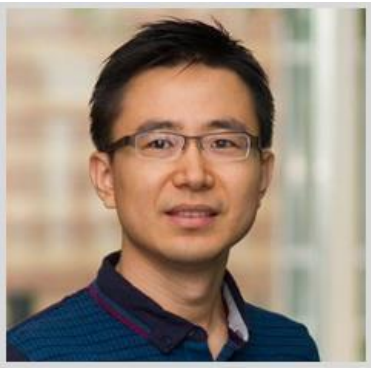
ABSTRACT

Social media analytics is an emerging research area involving multi-interdisciplinary fields, such as computer vision, machine learning, and social network analysis. In this talk, Dr. Fu will mainly present their recent research and envision future trend in this area especially for large scale analytics and robust inference. In particular, a manifold learning based framework with low-rank formulations will be presented.

BIOGRAPHY



Dr. Fu is an interdisciplinary faculty member affiliated with College of Engineering and the College of Computer and Information Science at Northeastern University. He received the B.Eng. degree in information engineering and the M.Eng. degree in pattern recognition and intelligence systems from Xi'an Jiaotong University, China, respectively, and the M.S. degree in statistics and the Ph.D. degree in electrical and computer engineering from the University of Illinois at Urbana-Champaign, respectively. Prior to joining the Northeastern faculty, he was a Scientist working at BBN Technologies, Cambridge, MA, during 2008-2010. He holds a Part-Time Lecturer position in the Department of Computer Science, Tufts University, Medford, MA, in 2009. He was a tenure-track Assistant Professor of the Department of Computer Science and Engineering, State University of New York, Buffalo, during 2010-2012.

Dr. Fu's research interests are Interdisciplinary research in Machine Learning and Computational Intelligence, Social Media Analytics, Human-Computer Interaction, and Cyber-Physical Systems. He has extensive publications in leading journals, books/book chapters and international conferences/workshops. He serves as associate editor, chairs, PC member and reviewer of many top journals and international conferences/workshops. Dr. Fu is the recipient of 5 best paper awards (SIAM SDM 2014, IEEE FG 2013, IEEE ICDM -LSVA 2011, IAPR ICFHR 2010, IEEE ICIP 2007), 3 young investigator awards (2014 ONR Young Investigator Award, 2014 ARO Young Investigator Award, 2014 INNS Young Investigator Award), 2 service awards (2012 IEEE TCSVT Best Associate Editor, 2011 IEEE ICME Best Reviewer), the 2011 IC Postdoctoral Research Fellowship Award, the 2010 Google Faculty Research Award, the 2008 M. E. Van Valkenburg Graduate Research Award, the 2007-2008 Beckman Graduate Fellowship, 2007 Chinese Government Award for Outstanding Self-Financed Students Abroad, the 2003 Hewlett-Packard Silver Medal and Science Scholarship, Edison Cups of the 2002 GE

Fund Edison Cup Technology Innovation Competition, and the 2002 Rockwell Automation Master of Science Award. He is currently an Associate Editor of the IEEE Transactions on Neural Networks and Leaning Systems (TNNLS), and IEEE Transactions on Circuits and Systems for Video Technology (TCSVT). His research is broadly supported by NSF, DOD, DARPA, IARPA, ONR, AFOSR, ARL/ARO, NGA, IC, Samsung and Google. He is a Senior Member of IEEE, Lifetime Member of ACM, AAAI, SPIE, and Institute of Mathematical Statistics, member of INNS and Beckman Graduate Fellow during 2007-2008.

Technical Session D2-W1-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Transcribing the Pitch Content of Polyphonic Music Audio

Zhiyao Duan

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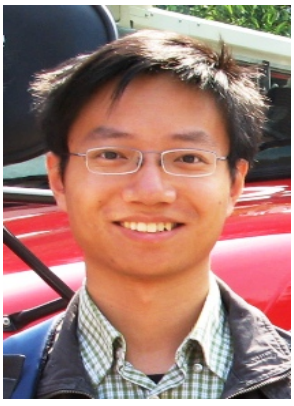
ABSTRACT

Polyphonic music transcription (i.e. converting music audio to musical score) is an extraordinary capability of talented musicians. Having computers to automatically transcribe music audio is called automatic music transcription, which is a fundamental problem in music information retrieval research with many applications. In this talk I will present our system to automatically transcribe the pitch content of polyphonic music audio. This system takes a piece of music audio as input and figures out what pitches are played by each instrument and when they are played. This approach consists of two stages. In the first stage, it estimates pitches (and the number of pitches) in each time frame of the music audio. This is done in a maximum likelihood framework modeling the relationship between pitches and the magnitude spectrum of the audio signal. In the second stage, it streams the pitch estimates in different time frames into pitch trajectories, where each trajectory corresponds to an instrument. This is done by clustering the pitch estimates using timbre information with constraints modeling pitch location relations. This system achieves promising results not only on polyphonic music, but also on multi-talker speech mixtures.

BIOGRAPHY



Zhiyao Duan received his B.S. and M.S. in Automation from Tsinghua University, China, in 2004 and 2008, respectively, and received his Ph.D. in Computer Science from Northwestern University in 2013. He is currently an assistant professor in the Electrical and Computer Engineering Department at the University of Rochester. His research interest is in the broad area of computer audition, i.e. designing computational systems that are capable of analyzing and processing sounds, including music, speech, and environmental sounds. This is an emerging and interdisciplinary area that involves signal processing, machine learning, acoustics, and music theory. Specific problems that he has been working on include automatic music transcription, multi-pitch analysis, music audio-score alignment, sound source separation, and speech enhancement.

Technical Session D2-W1-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

From Web Page Enhancement to Mobile Reading and Learning

Chen-Hsiang (Jones) Yu

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(Prentice Lab 余禎祥博士)

ABSTRACT

The Web is a convenient platform to deliver information, but reading web pages is challenging. My research interests focus on investigating techniques to enhance web pages on desktop and mobile browsers, and extend them to create useful products. In this talk, I will summarize my previous work in this field, including web page readability enhancement, skimmability support and mobile continuous reading. In addition, I will present a new mobile system, which is an extension to my previous work, and discuss a few interesting research directions I am working on now.

BIOGRAPHY

Jones Yu will be an Assistant Professor of Computer Science and Networking at Wentworth Institute of Technology (WIT) in September 2014. He earned B.E. and M.S. in Computer Science and Information Engineering (CSIE) from Tamkang University in 1998 and from National Taiwan University in 2000, respectively, and Ph.D. in Computer Science from MIT under Prof. Rob Miller's guidance in 2012. His research in Human-Computer Interaction (HCI) focuses on web customization and automation, and mobile learning.

He is founder and CEO of Prentice Lab, which is a startup company focusing on investigating mobile technologies and developing software for improving learning, including language learning and subject learning. In the past, he has worked for a few startup companies as Director of Mobile Engineering and User Experience, and developed mobile apps as products.

Technical Session D2-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Session Chair

Hsuan-Cheng Huang

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BIOGRAPHY

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

Technical Session D2-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Dissecting the Human Protein-Protein Interaction Network via Phylogenetic Decomposition

Hsueh-Fen Juan

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ABSTRACT

In network biology, the protein-protein interaction (PPI) network offers a conceptual framework for better understanding the functional organization of the proteome. However, difficulties may arise in the process of systematic analysis due to the intricacy of network complexity. Here, we adopted a phylogenic grouping method combined with force-directed graph simulation in the topological space, effectively decomposing the human PPI network in a multi-dimensional manner. This network model enabled us to associate the network topological properties with evolutionary and biological implications, and to address the question whether proteins from different age groups play different roles in a PPI network. First, we found that ancient proteins occupy the core of the network, whereas young proteins tend to reside on the periphery. Topological analysis also revealed a positive correlation between protein age and network centrality. Second, the scale-free and hierarchical properties of the PPI network are ubiquitous across age groups, whereas each group still contributes dependently to the global properties. Third, the presence of age homophily was revealed in the PPI network, suggesting a possible selection pressure may have acted on the duplication and divergence process during the network evolution, in which proteins with higher centrality were selected to avoid perturbation. Lastly, functional analysis revealed that each age group possesses high specificity of enriched biological processes and pathway engagements, which could correspond to their evolutionary roles in eukaryotic cells. More interestingly, the network landscape closely coincides with the subcellular localization of proteins. Together, these findings suggest the potential of using conceptual frameworks to mimic the true functional organization in a living cell.

BIOGRAPHY

Hsueh-Fen Juan was born in 1969, Miao-Li, Taiwan. She received her BS and MS degree in Botany and PhD in Biochemical Sciences from National Taiwan University (NTU) in 1999. She

worked as a research scientist in the Japan International Research Center for Agricultural Sciences (Tsukuba, Japan) during 2000-2001 and a postdoctoral research fellow in the Institute of Biological Chemistry, Academia Sinica (Taipei, Taiwan) during 2001-2002.

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

Prof. Juan has developed a number of novel methods to advance systems-biology research and applied such approach for drug discovery and elucidating molecular mechanism of drug responses in cancer cells. She has published more than 75 journal papers and edited a scientific book entitled as Systems Biology: Applications in cancer-related research (2012). She is now the editor of Computational and Mathematical Methods in Medicine (Hindawi Publishing Corporation). She also serves as the reviewer of 37 various journals such as Drug Discovery Today, Molecular and Cellular Proteomics (ASBMB), Journal of Proteome Research (ACS), Proteomics (Wiley-VCH), Bioinformatics (Oxford), and has organized several international systems biology and bioinformatics symposiums. She is one of the founders of Center for Systems Biology (NTU), and currently the Council Member of four societies, the Taiwan Society for Biochemistry and Molecular Biology, Taiwan Proteomics Society, Taiwan Bioinformatics and Systems Biology Society, and Taiwan Society of Evolution and Computational Biology. Since Dr. Juan made significant contributions through systems biology approach to development of methodology and cancer therapy; she received the awards “Taiwan's Ten Outstanding Young Persons” (2008), FY2011 JSPS Invitation Fellowship Program for Research in Japan (2011), K. T. Li Breakthrough Award by Institute of Information and Computing Machinery (2012), and National Science Council (NSC) Award for Special Talents of the Colleges (2010-2014).

BIOGRAPHY

Mr. Cho-Yi Chen was born in Taipei, Taiwan. He received his BS and MS degrees in Computer Science and Bioinformatics from National Taiwan University in 2007 and 2009, respectively. He is currently a PhD candidate in the Genome and Systems Biology Degree Program at National Taiwan University.

In 2009-2012, he worked as a Research Assistance at Academia Sinica for R&D alternative military service. He was delegated to represent Taiwan as an athlete in several international sporting events, including Asian Games and Summer Olympic Games. In 2013, he was awarded a Study Abroad Grant from the National Science Council. He is now a visiting graduate student in the Department of Biostatistics at the University of Pittsburgh, PA.

Mr. Cho-Yi Chen was a founding member of Taiwan Society of Evolution and Computational Biology (TaiwanSECB). His research interests include bioinformatics and computational systems biology. During his graduate studies in the Systems Biology Laboratory led by Prof. Hsueh-Fen Juan and Prof. Hsuan-Cheng Huang, he developed a functional network model to

infer potential microRNA regulation and its cooperation with transcription factors in transcriptional networks. This work was selected as an oral presentation in APBC2011 bioinformatics conference and later published in BMC Bioinformatics. In another comparative genomic study, he found a striking exponential expansion of post-transcriptional regulatory circuit in parallel with the increase of morphological complexity in animal evolution. This study was published in Bioinformatics. Both of these works have been selected as Highly Cited Paper by the ESI. He is now developing a new meta-analysis framework for differential coexpression module detection in breast cancer and major depressive disorder under the guidance of Prof. George C. Tseng at the University of Pittsburgh.

Technical Session D2-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Developing and Using Bioinformatics Tools for Analysis of Big DNA Sequence Data

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ABSTRACT

Recent advances in next-generation sequencing technology provide an opportunity to develop and use bioinformatics tools for analysis of big DNA sequence data in order to further our understanding of living systems at the molecular level. In this talk, I will describe my recent work in developing and using bioinformatics tools to further our understanding of how genetic variation is generated in an asexual plant pathogen.

BIOGRAPHY

Xiaoqiu Huang was born on January 13, 1961, in Harbin, China. He received, in 1990, his Ph.D. in computer science from Pennsylvania State University, State College, Pennsylvania, USA. His research area is bioinformatics.

He is a professor of computer science at Iowa State University. His previous research interests include development of computer algorithms and software for reconstruction of genome sequences and for finding genes and other functional elements in genomes. He is currently interested in understanding evolutionary processes by applying these computer programs to big data sets of genomic DNA sequences.

Professor Huang is a member of the American Association for the Advancement of Science. He is the author of a widely used

CAP3 assembly program. He and his collaborators have developed a whole-genome assembly program named PCAP. PCAP has been used by Washington University Genome Center in chimpanzee and chicken genome projects.

Technical Session D2-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Secondary Use of Electronic Medical Records

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ABSTRACT

The rapid adoption of electronic health records (EHRs) has enabled the use of the EHR data for secondary purposes, such as care process, clinical decision support, outcomes improvement, biomedical research, and epidemiologic monitoring of the nation's health. However, a prerequisite of meaningful, secondary use of the EHR data is syntactic and semantic interoperability across heterogeneous sources to ensure unambiguous data representation, interpretation, and exchange. Data normalization aims for syntactic and semantic interoperable data. In this talk, I will focus on multiple past and current data normalization efforts for secondary use of EHR including i) the data normalization effort under Mayo Strategic Health IT Advanced Research Project area four (SHARPn) project, ii) the open health natural language processing (OHNLP) effort which aims to improve availability, usability, and interoperability among clinical natural language processing systems, and iii) Mayo big data effort which aims to support late-binding normalization for practical clinical applications using EHR.

BIOGRAPHY

Dr. Liu received her undergraduate training in Mathematics/Statistics from University of Science and Technology of China from 1990 to 1994. She then continued her Master and PhD education at Fordham University and Graduate Center of City University of New York respectively. Her PhD training was directed by Dr. Carol Friedman, a pioneer in clinical natural language processing (NLP). Her PhD research focused on two foci: one is to apply advanced machine learning techniques and sublanguage analysis for building NLP systems and the other is to bring NLP to end users through advanced visualization. Her PhD thesis work on applying distant supervision on resolving ambiguity in concept mapping was its first application in the clinical informatics field. Her work on visualization has yielded an approach to review NLP results dynamically with tree visualization.

After PhD graduation, Dr. Liu accepted a tenure-track assistant professor appointment at University of Maryland in 2003. She received her first federal grant funding from the National Science Foundation ($800k for three years) on the use of distant supervision for concept-mention detection and normalization. In 2006, she relocated to Georgetown University to pursue close collaboration with Protein Information Resource (PIR), one of the consortium sites of UniProtKB (the most comprehensive protein database resource), and the Laboratory of Molecular Pharmacology at the National Cancer Institute in the field of Bioinformatics and System Biology. She has contributed to the field of bioinformatics with multiple tools and resources including: BioThesaurus, BioTagger, SpliceCenter, SpliceMiner, GOMiner,

RedundancyMiner, CellMiner, iProLINK, DynGO and dbOGAP. In 2011, she joined Mayo Clinic as Senior Associate Consultant, directing Mayo NLP program. At Mayo, she has dedicated to the use of Electronic Medical Records (EMRs) for individualized prevent care of diseases and adverse events.

Dr. Liu is a member of several professional societies, including the American Medical Informatics Association (AMIA) and the International Society for Computational Biology (ISCB). Dr. Liu currently leads the community-wide effort on open health national language processing (OHNLP) which aims to promote open source and interoperable NLP for clinical and translational research. Dr. Liu is the Vice- Chair Elect of the AMIA Natural Language Processing (NLP) Work Group.

Technical Session D2-W2-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Personalize Treatment using evidence from data-mining and simulation studies

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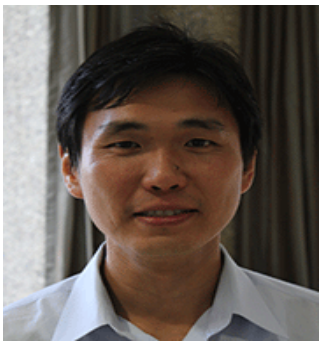
ABSTRACT



Clinical heterogeneity influences treatment efficacy and, subsequently, results in outcome variations across individuals in one-treatment-fit-all settings. On the other hand, there is an opportunity to improve outcomes while reduce costs by currently existing treatments when we understand how clinical heterogeneity influences treatment efficacy and how much difference exists among treatment options. Specifically, when we successfully capture the relationships among patient characteristics, treatment options, and outcomes from electronic health records, such relationships enable us to understand which treatment option most improves outcomes for a particular type of patients.

In this presentation, we will demonstrate two most recent studies to show the abovementioned personalized health management studies. (1) Identifying evidence of personalized nursing intervention for patients with oral health problems. In this study, we identify such evidence from public-health nursing data with Omaha System. We will show overall outcome improvement in simulated settings. (2) We will also demonstrate the project of personalized warfarin treatment plan. In this project, clinical and genotypic data are used to identify the personalized treatment plan that minimize thrombosis and stroke risks when receiving warfarin treatment.

These examples show two take-home messages. (1) Instead of inventing a new treatment that requires investment of years of efforts and millions (if not, billions) of dollars, there is another opportunity to improve outcome using currently existing treatment when we understand how to assign treatment options to particular type of individuals based on their characteristics and (2) Evidence of personalized treatment for particular patient characteristics can be derived from clinical data, omics data, or integrated data (clinical and omics data) depending on our data availability. The key point is if we can get a clear pattern from data to predict the optimal treatment. We anticipate personalized health management studies will provide another avenue to improve outcomes leveraging big-data analysis.

BIOGRAPHY

Dr. Chih-Lin Chi is assistant professor in School of Nursing and Institute for Health Informatics at the University of Minnesota. He was a research associate at the laboratory for personalized medicine in Center for Biomedical Informatics at Harvard Medical School. He received his PhD degree of Health Informatics at the University of Iowa and MBA degree at Feng

Chia University in Taiwan. He has developed many integrative computational approaches (including machine learning, data mining, modeling and simulation, optimization, and artificial intelligence) to analyze medical data and extract evidence of personalized health management.

Technical Session D2-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Workshop Co-chair and Session Chair

Yaoyu E. Wang

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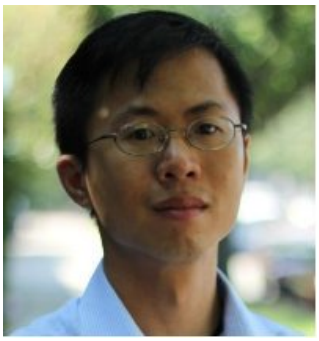
BIOGRAPHY



Yaoyu Wang is Associate Director of the Center for Cancer Computational Biology at the Dana-Farber Cancer Institute. He received his B.S. in Biological Science and Computer Science from the Carnegie-Mellon University, and his Ph.D in Bioinformatics from the Boston University. He was a postdoctoral fellow in virology and immunology at the Ragon Institute of MGH, MIT, and Harvard. He currently leads the Center for Cancer Computational Biology (CCCB; http://cccb.dfci.harvard.edu), which provides broad-based genomic research technology platform to the community with high-throughput sequencing and bioinformatics support for collaborative research. The major focuses of the Center are developing novel NGS applications, such as extracellular RNA sequencing as well as computational tools for integrated analysis and visualization of multiple types of –omic data, including transcriptome, exome, whole genome, and targeted resequencing data.

Technical Session D2-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Multiple mechanisms underlying acquired resistance to taxanes in selected docetaxel-resistant MCF-7 breast cancer cells

Zhixiang Wang

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ABSTRACT

Chemoresistance is a major factor involved in a poor response and reduced overall survival in patients with advanced breast cancer. Although extensive studies have been carried out to understand the mechanisms of chemoresistance, many questions remain unanswered. In this research, we used two isogenic MCF-7 breast cancer cell lines selected for resistance to doxorubicin (MCF-7DOX) or docetaxel (MCF-7TXT) and the wild type parental cell line (MCF-7CC) to study mechanisms underlying acquired resistance to taxanes in MCF-7TXT cells. Cytotoxicity assay, immunoblotting, indirect immunofluorescence and live imaging were used to study the drug resistance, the expression levels of drug transporters and various tubulin isoforms, apoptosis, microtubule formation, and microtubule dynamics.

We showed that MCF-7TXT cells were cross resistant to paclitaxel, but not to doxorubicin. MCF-7DOX cells were not cross-resistant to taxanes. We also showed that multiple mechanisms are involved in the resistance to taxanes in MCF-7TXT cells. Firstly, MCF-7TXT cells express higher level of ABCB1. Secondly, the microtubule dynamics of MCF-7TXT cells are weak and insensitive to the docetaxel treatment, which may partially explain why docetaxel is less effective in inducing M-phase arrest and apoptosis in MCF-7TXT cells in comparison with MCF-7CC cells. Moreover, MCF-7TXT cells express relatively higher levels of β2- and β4-tubulin and relatively lower levels of β3-tubulin than both MCF-7CC and MCF-7DOX cells. The subcellular localization of various β-tubulin isoforms in MCF-7TXT cells is also different from that in MCF-7CC and MCF-7DOX cells.

In conclusion, multiple mechanisms are involved in the resistance to taxanes in MCF-7TXT cells. The high expression level of ABCB1, the specific composition and localization of β-tubulin isoforms, the weak microtubule dynamics and its insensitivity to docetaxel may all contribute to the acquired resistance of MCF-7TXT cells to taxanes.

BIOGRAPHY

Education:

Sept. 1989-June 1993 Department of Biological Sciences
Simon Fraser University, Vancouver, Canada

	Ph.D. Biochemistry
Sept. 1982-June 1985	Institute of Zoology, Academia Sinica, Beijing, China M.Sc. Zoology
Sept. 1978-July 1982	Department of Biology, Beijing University, Beijing, China B.Sc. Biology

After obtained his PhD, Dr. Wang did his postdoctoral training at University of Toronto supported by various scholarships including CIHR (MRC) Centennial Fellowship, Charles H. Best Postdoctoral Fellowship and NSERC Postdoctoral Fellowship. He started his first independent research position as a Career Scientist at Northeastern Ontario Cancer Centre in 1996 and as an Assistant Professor at University of Ottawa in 1997. He moved to the Department of Cell Biology, University of Alberta as an Assistant Professor. He is now a Full Professor at the Department of Medical Genetics, University of Alberta. His research has focused on ErbB receptor-mediated cell signaling, receptor endocytosis, and human cancer. ErbB receptors including EGFR/ErbB1, ErbB2, ErbB3 and ErbB4 lie at the head of a complex signal transduction cascade that modulates cell proliferation, survival, adhesion, migration and differentiation. While ErbB receptor signaling is essential for many normal cell functions, the aberrant activity of ErbB receptors has been shown to play a key role in the development of many cancers. ErbB receptors are overexpressed in many cancers especially in breast cancer, ovarian cancer, small cell lung cancer and skin cancer. ErbB receptor overexpression correlates to poor prognosis, drug resistance, cancer metastasis and lower survival rate. All these make ErbB receptor the top choice as a target for developing cancer therapies. To date, monoclonal antibodies (mAbs) and synthetic inhibitors of tyrosine kinase have taken central stage. The central theme of my research is to understand how the activation of EGFR regulate cell signaling, how the signaling is terminated through EGFR endocytosis, trafficking and degradation, how the breakdown of this regulation contributes to cancer development, and how an intervention can be provided.

Dr. Wang's recent publications:

Wang H, Vo T, Hajar A, Li S, Chen X, Parissenti AM, Brindley DN, Wang Z: Multiple mechanisms underlying acquired resistance to taxanes in selected docetaxel-resistant MCF-7 breast cancer cells.
BMC Cancer 2014, 14:37.

Tong, J., Li, L., Ballermann, B. and Wang, Z. (2013) Phosphorylation of Rac1 T108 by ERK in response to EGF: A novel mechanism to regulate Rac1 function.
Mol. Cell. Biol. 33:4538-4551.

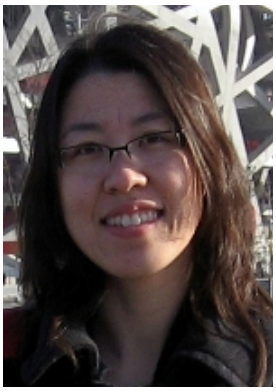
Technical Session D2-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Xue Han

Assistant Professor, Biomedical Engineering
Boston University

ABSTRACT

BIOGRAPHY



Technical Session D2-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Fabrication of Nanostructured Constructs from Decellularized Tissue Using Bioskiving

Qiaobing Xu

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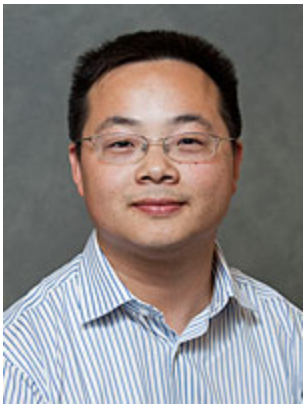
ABSTRACT

My lab has pioneered the use of nature-derived nanostructured tissue as a source of biomaterials and works to engineer these materials through a combination of tissue sectioning, multilayer stacking and rolling into structures with innovative biomedical functions. Many biological specimens have extremely well-defined shapes and chemical activities, such as collagen fibers in tendon, muscle fibers in muscle, cornea, bone, diatoms, wood. Tendon for example, comprises bundles of well-aligned of collagen nanofibers. Recently, we have used decellularized tendon as a substrate for sectioning, and demonstrated the fabrication of novel 2D and 3D nanostructured constructs using a combination of sectioning, stacking and rolling, a process as we call “Bioskiving”. These tendon-derived constructs are biocompatible, biodegradable and have excellent mechanical properties. More importantly, they provide nanotopographic cues which could offer contact guidance for oriented cell growth. These novel structures are being explored for applications, including nerve and blood vessel regeneration.

BIOGRAPHY



Dr. Qiaobing Xu was born in Nanjing, Jiangsu, China in 1977. He obtained his B.S. in 1999, and M.Sc. in 2002, both from Department of Chemistry, Jilin University, Changchun, China. From 2002-2007, he pursued his PhD degree in chemistry under the guidance of Prof. George Whitesides at Harvard University where he invented “Nanoskiving”, a novel technology to fabricate functional nanomaterials. From 2007-2010, he was a Cancer Center for Nanotechnology Excellence postdoctoral fellow with Prof. Robert Langer at MIT, where he worked on developing novel nanomaterials for drug delivery applications.

He joined Tufts in September, 2010. He is currently an assistant professor in Department of Biomedical Engineering at Tufts University. He also holds adjunction assistant professor position in Department of Chemical and Biological Engineering and School of Medicine at Tufts University. He is also a member of Program in Cell, Molecular and Developmental Biology, Sackler School of graduate biomedical science, Tufts University. His current research interests lie at the intersection of material science engineering, specifically micro/nanoscience, and biomedical application.

His work involves using combinatorial method to develop novel materials for the delivery of therapeutic biomacromolecules and using nanotechnology to develop novel biomaterials for tissue engineering. He has published about 40 peer reviewed scientific paper and 7 patents

either filed or pending.

Dr. Xu is a member of Society for Biomaterials, Biomedical Engineering Society. He received Charlton Award from Tufts University School of Medicine in 2012 and named the Pew Scholar for Biomedical Sciences from Pew Charitable Trusts in 2013.

Technical Session D2-W3-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Yi-Hsiang (Sean) Hsu

Assistant Professor, School of Medicine
Harvard University
(哈佛大學醫學院許益祥教授)

ABSTRACT

BIOGRAPHY

Technical Session D2-W1-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Workshop Co-chair and Session Chair

Sao-Jie Chen

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BIOGRAPHY

Sao-Jie Chen received the B.S. and M.S. degrees in electrical engineering from the National Taiwan University, Taipei, Taiwan, ROC, in 1977 and 1982 respectively, and the Ph.D. degree in electrical engineering from the Southern Methodist University, Dallas, USA, in 1988.

Since 1982, he has been a member of the faculty in the Department of Electrical Engineering, National Taiwan University, where he is currently a full professor. During the fall of 2003, he held an academic visitor position in the Department of System Level Design, IBM Thomas J. Watson Research Center, Yorktown Heights, New York, USA. He obtained the "Outstanding Electrical Engineering Professor Award" by the Chinese Institute of Electrical Engineering in December 2003 to recognize his excellent contributions to EE education. His current research interests include: VLSI physical design, SOC hardware/software co-design, Network-on-Chip, and Wireless LAN and Bluetooth IC design.

Dr. Chen is a member of the Chinese Institute of Engineers, the Chinese Institute of Electrical Engineering, the Institute of Taiwanese IC Design, a senior member of the IEEE Circuits and Systems and the IEEE Computer Societies.

Technical Session D2-W1-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Yaoyu E. Wang

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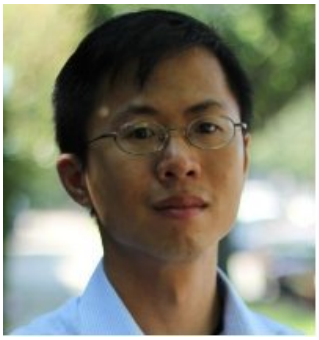
BIOGRAPHY



Yaoyu Wang is Associate Director of the Center for Cancer Computational Biology at the Dana-Farber Cancer Institute. He received his B.S. in Biological Science and Computer Science from the Carnegie-Mellon University, and his Ph.D in Bioinformatics from the Boston University. He was a postdoctoral fellow in virology and immunology at the Ragon Institute of MGH, MIT, and Harvard. He currently leads the Center for Cancer Computational Biology (CCCB; http://cccb.dfci.harvard.edu), which provides broad-based genomic research technology platform to the community with high-throughput sequencing and bioinformatics support for collaborative research. The major focuses of the Center are developing novel NGS applications, such as extracellular RNA sequencing as well as computational tools for integrated analysis and visualization of multiple types of –omic data, including transcriptome, exome, whole genome, and targeted resequencing data.

Technical Session D2-W1-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Woei-jyh (Adam) Lee, PhD

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(馬里蘭大學 學院市分校 史密斯商學院 李偉智教授)

ABSTRACT

BIOGRAPHY

Dr. Woei-jyh (Adam) Lee received BSE degree from the National Taiwan University, MS degree from the Courant Institute at New York University, and PhD degree from the University of Maryland at College Park (UMD). He worked on distributed objects and fault tolerance at the AT&T Labs - Research in 1997. He focused on network software and management at the Bell Laboratories Research from 1998 to 2000. He visited the University of Southern California specializing in continuous media streaming and multimedia networking from 2002 to 2003.

He contributed in protein domain parsing and boundary prediction at the National Cancer Institute (NCI), National Institutes of Health (NIH) from 2004 to 2005. He was a fellow focusing on human genetics and genomics at the National Center for Biotechnology Information, National Library of Medicine, NIH from 2009 to 2012. He became a special volunteer working on computational modeling for cancer progression and metastatic at the NCI, NIH from 2012 to 2013. He was also affiliated with the Center for Bioinformatics and Computational Biology and the Institute for Advanced Computer Studies at UMD.

He is currently a faculty of Information Systems at the Robert H. Smith School of Business at UMD since 2012. His research interests include information integration, data management and mining, literature-based discovery, performance simulation and evaluation, bioinformatics and computational biology, human genomics and genetics, and cancer biology. He has two US Patents and is a member of the ISCB, the IAENG, and the CAPA.

Technical Session D2-W1-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

DNA-Seq Analysis and Cloud Computing

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ABSTRACT

The wide adoption of Next Generation Sequencing (NGS) creates unquenchable demands for computing capacity to process and analyze sequencing data as well as constant struggles for data storage. The "bottomless" cloud computing is a crucial, if not the only, solution. I will talk about our experience of using the DNA Resequencing Analysis Workflow (DRAW) software to process >800 samples, our strategy to use Amazon EC2 effectively for DNA-Seq analysis, and moreover, how we will extend from these and take on the challenge of processing and managing Whole Genome/Exome sequencing data of >11,000 samples.

BIOGRAPHY

Chiao-Feng Lin received her B.S. (1992) in Electronic Engineering from Chung-Yuan Christian University, Chung-Li, Taiwan. She received her Master degree in Library and Information Science (2000) from the University of Texas at Austin and Ph.D. in Biology (2008) from the Pennsylvania State University. She was a postdoctoral fellow at the University of Pennsylvania between 2008 and 2011. Currently she is Senior Data Analyst of the National Institute on Aging Genetics of Alzheimer's Disease Data Storage Site (NIAGADS) and a member of Li-San Wang's lab at the Department of Pathology and Laboratory Medicine. Her work is focused on biomedical informatics, including variant prioritization and tool/resource development with particular emphasis on large-scale DNA sequencing. She co-built and published a DNA-seq pipeline (DRAW+SneakPeek), used it to process 150 human exomes, and oversaw production of ~700 exomes. Machine image (AMI) of DRAW is available on Amazon Elastic Cloud Computing.

Technical Session D2-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Session Chair

Hsuan-Cheng Huang

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(陽明大學生物醫學資訊研究所長黃宣誠教授)

BIOGRAPHY

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

Technical Session D2-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

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Johns Hopkins University School of Medicine

ABSTRACT

BIOGRAPHY

Technical Session D2-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

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University of Massachusetts, Amherst

ABSTRACT

BIOGRAPHY

Technical Session D2-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

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Associate Research Faculty, Department of Biostatistics
Yale University School of Public Health

ABSTRACT

BIOGRAPHY

Technical Session D2-W2-T2: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Mdmx: the choreographer of signal dynamics and cell fate

Sheng-hong Chen

Research Fellow, Department of Systems Biology
Harvard Medical School

ABSTRACT

BIOGRAPHY

Technical Session D2-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Workshop Co-chair and Session Chair

Yi-Hsiang (Sean) Hsu

Assistant Professor, School of Medicine
Harvard University
(哈佛大學醫學院許益祥教授)

BIOGRAPHY

Technical Session D2-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

MicroRNA-mediated Regulatory Network Driven by MYCN in Neuroblastoma

Hsueh-Fen Juan

Professor, Institute of Biomedical Electronics and Bioinformatics, Institute of Molecular and Cellular Biology, Department of Life Science, Center for Systems Biology and Bioinformatics, National Taiwan University, Taipei, Taiwan
No. 1, Sec. 4, Roosevelt Road, Taipei, 10617 Taiwan
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ABSTRACT

Neuroblastoma (NB) is the most common extracranial solid tumor of childhood, and MYCN, an oncogenic transcription factor of the Myc family, is a major driver of NB tumorgenesis. Approximately 20–25% of NB tumors showed amplification of the MYCN gene which was associated an ultra-high risk of death and treatment failure. Recent studies revealed that a number of MicroRNAs (miRNAs), small non-coding RNA molecules, play critical roles in NB tumorigenesis and disease progression. Uncovering the regulations between MYCN and miRNAs can assist us to understand the pathogenesis of NB. In our study, we performed ChIP-Seq and miRNA-Seq on SK-N-BE (2), a MYCN-amplified NB cells, and identified 32 potential miRNAs mediated by MYCN, with 17 and 15 miRNAs being activated and repressed by MYCN, respectively. A total of 1,392 feed-forward loops (FFLs) with 26 miRNAs and 342 co-regulated genes were subsequently identified. We further elucidated the miRNA-mediated regulatory network driven by MYCN in NB. Our results not only help researchers to understand the complex regulatory mechanism in NB but also provide in-depth information on the impact and importance for NB therapeutical strategy.

BIOGRAPHY

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

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

integrating transcriptomics, proteomics and bioinformatics for biomarker and drug discovery.

Prof. Juan has developed a number of novel methods to advance systems-biology research and applied such approach for drug discovery and elucidating molecular mechanism of drug responses in cancer cells. She has published more than 75 journal papers and edited a scientific book entitled as Systems Biology: Applications in cancer-related research (2012). She is now the editor of Computational and Mathematical Methods in Medicine (Hindawi Publishing Corporation). She also serves as the reviewer of 37 various journals such as Drug Discovery Today, Molecular and Cellular Proteomics (ASBMB), Journal of Proteome Research (ACS), Proteomics (Wiley-VCH), Bioinformatics (Oxford), and has organized several international systems biology and bioinformatics symposiums. She is one of the founders of Center for Systems Biology (NTU), and currently the Council Member of four societies, the Taiwan Society for Biochemistry and Molecular Biology, Taiwan Proteomics Society, Taiwan Bioinformatics and Systems Biology Society, and Taiwan Society of Evolution and Computational Biology. Since Dr. Juan made significant contributions through systems biology approach to development of methodology and cancer therapy; she received the awards “Taiwan's Ten Outstanding Young Persons” (2008), FY2011 JSPS Invitation Fellowship Program for Research in Japan (2011), K. T. Li Breakthrough Award by Institute of Information and Computing Machinery (2012), and National Science Council (NSC) Award for Special Talents of the Colleges (2010-2014).

Technical Session D2-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Tapping into chemodiversity in plants: from natural product biosynthesis to mechanism-based herbal medicine

Jing-Ke Weng

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Department of Biology, Massachusetts Institute of Technology
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ABSTRACT

Metabolic pathways are often considered “perfected” or at least predictable as substrates efficiently rearrange into products through the intervention of an optimized enzyme. Moreover, single catalytic steps link up, forming a myriad of metabolic circuits that are often modeled with a high degree of certainty. However, on closer examination, most enzymes are not precise with respect to their activity, using not just one substrate but often a variety and producing not just one product but a diversity. Hence, the metabolic systems assembled from enzymes possessing varying degrees of what can be termed catalytic promiscuity are not clear-cut and restrictive; rather, they may at times operate stochastically in the intracellular milieu. This “messiness” complicates our understanding of normal and aberrant cellular behavior, while paradoxically sowing the seeds for future advantageous metabolic adaptations for host organisms.

In this talk, I will discuss the evolutionary implication of catalytic promiscuity widely observed in plant specilized metabolic systems and how the systems-level promiscuity in plant metabolism could be harnessed through synthetic biology approaches to generate new natural product chemical libraries. I will also disuss new frontiers in elucidating mechanisms of action underlying traditional herbal medicine.

BIOGRAPHY

Jing-Ke Weng received his B.S. (2003) in Biotechnology from Zhejiang University, Hangzhou, China. He received his Ph.D. (2009) in Biochemistry from Purdue University, and was a pioneer postdoctoral fellow at the Salk Institute for Biological Studies and Howard Hughs Medical Institute between 2009 and 2013. Currently he is a member of the Whitehead Institue for Biomedical Research, and an Assistant Professor of Biology at Massachusetts Institute of Technology.

Dr. Weng's research focuses on understanding the origin and evolution of plant specialized metabolism at enzyme, pathway, and systems levels, as well as how plants exploit discrete small molecules to interact with their surrounding biotic and abiotic environments. In addition, he utilizes plant as a unique model system to study human diseases, including metabolic syndromes and protein-misfolding diseases. He is also interested in elucidating the molecular mechanisms underlying the "matrix effect" known from many traditional herbal remedies used for thousands of years.

Dr. Weng is a member of the American Society of Plant Biologists, and has won numerous awards in his career, including Pew Scholar in the Biomedical Sciences (2014), American Society of Plant Biologists Early Career Award (2014), and Tansley Medal for Excellence in Plant Science (2013).

Technical Session D2-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Development of flavivirus inhibitors

Hongmin Li

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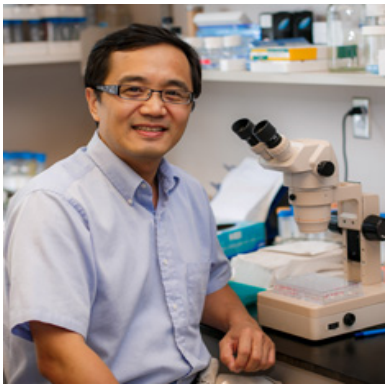
ABSTRACT

Flavivirus family includes many human pathogens such as Dengue virus, West Nile virus, and Yellow fever virus. Two enzymes encoded by flavivirus, the methyltransferase and protease, are essential for flavivirus life cycle. The flavivirus NS5 methyltransferase (MTase) sequentially methylates the N7 and 2'-O positions of the viral RNA cap (GpppA-RNA®m7GpppA-RNA®m7GpppAm-RNA), using S-adenosyl-L-methionine (SAM) as a methyl donor. The NS2B/NS3 protease functions to cleave the viral polypeptide to the mature form of individual protein. Therefore, both the flavivirus MTase and protease are attractive targets for therapeutic invention. Here we report the identification and characterization of several potential MTase and protease inhibitors. Through structure-based in silico screening of compound library, we identified several MTase inhibitors with the IC50 value as low as 0.7 mM, and protease inhibitors with IC50 in low micromolar range. The cytotoxicity and anti-viral abilities of these compounds have been evaluated. Our study also indicated that these compounds exert a broad spectrum of antiflavivirus activity. Thus, these compounds can serve as novel lead inhibitors for development of therapies to treat flavivirus-associated disease. This research was partially supported by grant AI094335 from the National Institute of Health (NIH).

BIOGRAPHY



Birth Place: Hegang, Heilongjiang Province, China

Birth Year: 1968

Education:

7/86-7/1990 B.Sc. Major in biophysics & physiology, Department of Biology, Beijing University, Beijing, China

9/90-7/1993 M.Sc. in molecular biology, Institute of Biophysics, Chinese Academy of Sciences, Beijing, China.

7/93-7/1995 Ph.D. in molecular biology, Institute of Biophysics, Chinese Academy of Sciences, Beijing, China.

Professional Experience:

10/1995-9/2000 Postdoctoral Associate, Center for Advanced Research in Biotechnology (CARB), University of Maryland Biotechnology Institute (UMBI), Rockville, MD.

9/2000-10/2002 Research Scientist III (Research Assistant Professor equivalent), Wadsworth Center, Health Research Inc, Albany, NY

10/2002-1/2008 Research Scientist IV (Tenure-track Assistant Professor equivalent), Wadsworth Center, New York State Department of Health (NYSDOH), Albany, NY

1/2003-12/2014 Assistant Professor (Volunteer), Department of Biomedical Sciences, School of Public Health (SPH), University at Albany, State University of New York, Albany, NY

12/2014-present Associate Professor (Volunteer), Department of Biomedical Sciences, School of Public Health (SPH), University at Albany, State University of New York, Albany, NY

1/2008-present Research Scientist V (Tenured Associate Professor equivalent), Wadsworth Center, NYSDOH, Albany, NY

Current Research Interests:

Dr. Li's research focuses on the molecular structure, function, and mechanism of proteins or complexes related to bacterial or viral infection and host response, using crystallography, biochemistry, and molecular biology. Current projects include bacterial and viral superantigens, signaling proteins involved in apoptosis and stem cell regulation, and rational drug design against key viral enzymes.

Professional Affiliations:

1998-Present Member, American Crystallography Association

2008-present Member, Biophysical Society

2013-present Member, American Society of Biochemistry and Molecular Biology

2014-present Member, American Society of Virology

2014-present Member, American Society of Microbiology

Technical Session D2-W3-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Population dynamics and synthetic biology in antibacterial treatment

Cheemeng Tan

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ABSTRACT

Antibiotics are important therapeutic agents in antibacterial treatment. However, the efficacy of existing antibiotics is diminished by the rise and subsequent spread of resistant bacteria. The crisis of resistant bacteria highlights the critical need to understand bacterial population dynamics during antibiotic treatment and to develop new antibiotics. I will first describe my work in understanding density-dependency of bacterial populations during antibacterial treatment. Specifically, the efficacy of some antibiotics is known to decrease with increasing bacterial density (inoculum effect). I discovered that the inoculum effect can be explained by bistable growth inhibition: for a given concentration of antibiotic, a bacterial population survives only if its initial density is sufficiently high. I further demonstrated that the inoculum effect has profound implications for periodic treatment of bacteria by antibiotics. Next, I will discuss our preliminary work toward controlling artificial cellular systems, which would establish a foundation toward integrating synthetic cellular components of biological circuits and artificial cells for biotechnological applications.

BIOGRAPHY

Cheemeng Tan received his B.Eng. degree (first class honors) from National University of Singapore and his M.S. degree in High Performance Computing from Singapore-MIT Alliance. In 2005, he started his doctoral research in the Department of Biomedical Engineering at Duke University, where he evolved into a hybrid computational and microbial biologist. After his Ph.D., he worked in the Lane Center in Carnegie Mellon University as a Lane Fellow and Branco-Weiss Fellow. During this time, he established a multi-scale method to study dynamics of artificial cellular systems. He published his research in journals such as Nature Chemical Biology, Molecular Systems Biology, and Nature Nanotechnology. He was awarded the Medtronic Fellowship, the Lane Fellowship, and the Society-in-Science: Branco Weiss Fellowship. His lab at UC Davis is interested in the engineering of synthetic biological systems for therapeutic treatment. The Tan Lab approaches this issue through two fundamental directions. To improve the control of synthetic cellular systems, the lab harnesses functioning mechanisms in natural cells to control dynamics of synthetic cells and organisms. In parallel, the lab investigates how heterogeneous cellular populations respond to drug treatment. The Tan Lab strives to create new frontiers in synthetic biology by synergizing ideas from different fields.

Technical Session D2-YA-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Workshop Co-chair and Session Chair

Chen-Hsiang (Jones) Yu

Founder and CEO, Prentice Lab
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(Prentice Lab 余禎祥博士)

BIOGRAPHY

Jones Yu will be an Assistant Professor of Computer Science and Networking at Wentworth Institute of Technology (WIT) in September 2014. He earned B.E. and M.S. in Computer Science and Information Engineering (CSIE) from Tamkang University in 1998 and from National Taiwan University in 2000, respectively, and Ph.D. in Computer Science from MIT under Prof. Rob Miller's guidance in 2012. His research in Human-Computer Interaction (HCI) focuses on web customization and automation, and mobile learning.

He is founder and CEO of Prentice Lab, which is a startup company focusing on investigating mobile technologies and developing software for improving learning, including language learning and subject learning. In the past, he has worked for a few startup companies as Director of Mobile Engineering and User Experience, and developed mobile apps as products.

Technical Session D2-YA-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Lining (Lizzie) Yao

PhD Candidate, Tangible Media Group
MIT Media Lab
Massachusetts Institute of Technology

ABSTRACT

BIOGRAPHY

Technical Session D2-YA-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

MoveInk: an Interactive Gestural Pen Animation

Sheng-Ying (Aithne) Pao

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ABSTRACT

The process of creation itself is an art, however, this process is usually non-visible in the completion of the final form. What if there was a way to engage the audience and the artists to revisit this missing mistery of creation? What if we were given an opportunity to interact with the static final form of creation as a function of time? In this talk, I will present one of my recent projects, MoveInk. MoveInk acts simultaneously in physical and virtual realms, transforming a pen into a gestural wand that converts a user's static drawing on paper to an animated digital creation. It provides the artists as well as the audience to transform sketches on paper into dynamic, interactive experiences, giving static artwork vivacious perspectives. I will talk about the design metaphore, the engineering challenges behind the scene, and the process of brining this project to the real world.

More information available at http://paoshengying.com

BIOGRAPHY

Sheng-Ying Pao (包盛盈 Aithne Pao) is an interdisciplinary researcher, designer, and entrepreneur. Her award-winning design introduces new platforms that transform natural elements into dynamic forms of expressive media. For example, LightByte — which won the 2014 iF Design Award, selected from 4,615 competitive entries from 55 countries, augments sunlight and shadows to become a new communication medium. Another series of gesture-sensing innovation, one of which presented at SIGGRAPH 2013 and won the 2013 ACM student research competition, transform analog creations into animated facsimiles through gestures and augments physical environments.

Pao is currently a PhD candidate in the MIT Media Lab. She was selected as an MIT Arts Scholar in 2013, and named MIT Cisco Fellow for two consecutive years. With backgrounds in interaction design, biomedical engineering, and international marketing, she was also the Center for Future Banking Fellow in 2010. Prior to that, Pao received a M.S. in media arts and sciences from MIT, a M.S. in biomedical engineering from National Taiwan University, and was certified in international trading and marketing by the Taiwan External Trade Development Council.

Enabling intuitive interactions in both pragmatic and poetic ways, Pao's work has been featured in museum and gallery exhibitions in New York, Barcelona, Hamburg, Cambridge, Boston, Taipei, Singapore, and Shanghai. She has taught "Interactive Technology Design" and

"MIT Living Labs" in MIT. Her designs have led to start-ups launched by entrepreneurial teams selected finalists in MIT 100K Entrepreneurship Competition and the IDEAS Global Challenge.

Technical Session D2-YA-T1: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

High-Performance Complex Event Processing for Decision Analytics

Haopeng Zhang

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(张浩鹏)

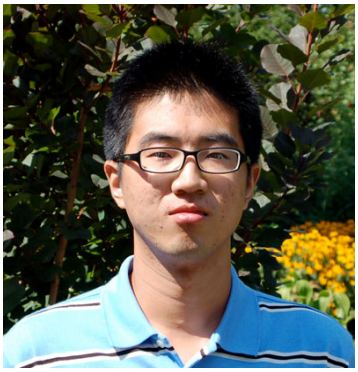
ABSTRACT

Complex Event Processing (CEP) systems are becoming increasingly popular in domains for decision analytics such as financial services, transportation, cluster monitoring, supply chain management, business process management, and health care. These systems collect or create high volumes of events, which form an event stream and the stream often needs to be processed in real-time. CEP queries are applied for filtering, correlation, aggregation, and transformation, to derive high-level, actionable information.

As a new stream-processing paradigm that addresses the above information needs of monitoring applications, CEP extends relational stream processing with a sequence-based model (in contrast to the traditional set-based model), and hence considers a wide range of pattern queries that address temporal correlations of events. Prior research has shown that such pattern queries are more expressive than selection-join-aggregation queries and regular languages. This thesis addresses challenges arising in the context of complex event processing.

In the talk, some motivating applications will first be presented, then some research problems regarding data quality and performance of CEP systems will be discussed briefly.

BIOGRAPHY



Haopeng Zhang was born in Hebei, China, in 1985. He received the B.S. degree in software engineering from the Beihang University, Beijing, in 2008, and the M.S. degree in computer science in University of Massachusetts Amherst, in 2011. He is expected to receive his Ph.D. degree in computer science from University of Massachusetts Amherst, in 2014. He is currently available in the job market and open to both academia jobs and industrial positions.

In 2008, he joined the School of Computer Science, University of Massachusetts Amherst, in Amherst MA, as a Research Assistant. He worked as Research Intern in NEC Labs America, in Cupertino CA, in 2011. His selected publications include Recognizing Patterns over Streams with Imprecise Timestamps, VLDB 2010 and On Complexity and Optimization of Expensive

Queries in Complex Event Processing in SIGMOD 2014. His current research interests include complex event processing, data stream processing and data analytics.

Mr. Zhang is a reviewer of ACM Transactions on Database Systems. He is also an external reviewer for Distributed and Parallel Databases and VLDB.

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

Workshop Co-chair and Session Chair

Woei-jyh (Adam) Lee, PhD

Tyser Teaching Fellow of Information Systems, Robert H. Smith School of Business
University of Maryland, College Park, Maryland 20742
(馬里蘭大學 學院市分校 史密斯商學院 李偉智教授)

BIOGRAPHY

Dr. Woei-jyh (Adam) Lee received BSE degree from the National Taiwan University, MS degree from the Courant Institute at New York University, and PhD degree from the University of Maryland at College Park (UMD). He worked on distributed objects and fault tolerance at the AT&T Labs - Research in 1997. He focused on network software and management at the Bell Laboratories Research from 1998 to 2000. He visited the University of Southern California specializing in continuous media streaming and multimedia networking from 2002 to 2003.

He contributed in protein domain parsing and boundary prediction at the National Cancer Institute (NCI), National Institutes of Health (NIH) from 2004 to 2005. He was a fellow focusing on human genetics and genomics at the National Center for Biotechnology Information, National Library of Medicine, NIH from 2009 to 2012. He became a special volunteer working on computational modeling for cancer progression and metastatic at the NCI, NIH from 2012 to 2013. He was also affiliated with the Center for Bioinformatics and Computational Biology and the Institute for Advanced Computer Studies at UMD.

He is currently a faculty of Information Systems at the Robert H. Smith School of Business at UMD since 2012. His research interests include information integration, data management and mining, literature-based discovery, performance simulation and evaluation, bioinformatics and computational biology, human genomics and genetics, and cancer biology. He has two US Patents and is a member of the ISCB, the IAENG, and the CAPA.

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

Di Wu

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ABSTRACT

A gene set test is a differential expression analysis in which a P-value is assigned to a set of genes as a unit. Gene set tests are valuable for increasing statistical power, organizing and interpreting results and for relating expression patterns across different experiments. Most existing methods are based on permutation. Methods that rely on permutation of sample are limited by sample size, while those that rely on permutation of probes unrealistically assume independence of genes.

We present ROMER, a statistically rigorous gene set test that allows for gene-wise correlation to test the so-called competitive null hypothesis that the genes in the gene-set are no more differentially expressed than the randomly chosen genes of the same set size in the array platform. Rank of log fold change or moderated t was used to represent the differential expression level of a gene. ROMER is not limited by sample size. It is for any experimental design that can be expressed as a linear model, and can also incorporate array weights and correlated samples. ROMER can test for uni- or bi-direction regulation. This is particularly important when testing multiple pathway gene sets, in which case the genes in a pathway may not be regulated in the same direction.

Instead of permutation, ROMER uses rotation of residuals of a linear model for all samples. The rotation step is a Monte Carlo technology for multivariate regression. Due to usage of rotation, ROMER has a the flavor to test a combination of the self-contained and competitive hypotheses.

The power and size of the ROMER procedure is demonstrated in a simulation study, by comparing to other representative competitive methods and one rotation-based self-contained gene set testing method.ROMER is designed to test a battery of gene sets.

ROMER has been used in the data analysis of at least six publications. Here, we used ROMER to find the important pathways in the different breast cancer molecular subtypes, and to find the pathways differently affected by two HDACI drugs in the long term treatment.

BIOGRAPHY

Di received her PhD in statistical bioinformatics at Melbourne University, based in the Walter and Eliza Hall Institute, Australia, in 2011. She works on statistical gene set testing methods, genomic data integration and drug repurposing.

She has been a postdoctoral fellow at Harvard Statistics Department at Boston, since 2011. Di's most three publications include

1. Okada Y, Wu D, Trynka G, et al., Plenge R. 2013. Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature. doi:10.1038/nature12873. Epub 2013 Dec 25.
2. Wu D, Pang Y, Wilkerson MD, Wang D, Hammerman PS and Liu JS. 2013. Gene expression data integration for squamous cell lung cancer subtypes reveals drug sensitivity. British Journal of Cancer. doi: 10.1038/bjc.2013.452. Epub 2013 Sep 3.
3. Wu D, Hu Y, Tong S, Williams BRG, Smyth GK and Gantier MP. 2013. The use of miRNA microarrays for the analysis of cancer samples with global miRNA decrease. RNA. 19(7):876-88.

Her recent research interests are focusing on developing drug repurpose for cancer types, as well as statistical methods in RNAseq data analysis and data integration.

Dr Wu has held the Australia NHMRC fellowship from 2012-2014.

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

MAGeCK enables robust identification of essential genes from genome-scale CRISPR-Cas9 knockout screens

Wei Li

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ABSTRACT

We propose Model-based Analysis of Genome-wide CRISPR-Cas9 Knockout (MAGeCK) for genome-scale CRISPR-Cas9 knockout (GeCKO) screens. MAGeCK prioritizes individual single-guided RNA (sgRNA) between conditions using a negative binomial model, and combines multiple sgRNAs per gene with robust rank aggregation to identify essential genes. MAGeCK demonstrates good control of false discovery rate and better performance comparing with existing computational methods for analyzing RNA interference (RNAi) screens. Furthermore, MAGeCK identifies both positively- and negatively-selected genes simultaneously, and reports robust results across different sequencing depths and numbers of sgRNAs per gene. Using public GeCKO datasets, MAGeCK identified biologically meaningful new essential genes from the initial studies, including EGFR in vemurafenib treated A375 cell line harboring BRAF mutation. It also detected cell-specific essential genes by comparing different leukemia cell lines, including BCR and ABL1 in KBM7 bearing BCR-ABL fusion, and IGF1R in HL60 which depends on insulin signaling pathway for proliferation. MAGeCK is freely available at http://mageck.sourceforge.net.

BIOGRAPHY

Dr. Li is currently a postdoctoral research fellow in the Department of Biostatistics and Computational Biology at Dana-Farber Cancer Institute and Harvard School of Public Health. He received his B.S. (2006) and M.S. (2008) in Computer Science from Tsinghua University, Beijing, China, and Ph.D. (2012) in Computer Science and Engineering from University of California, Riverside, USA. Dr. Li's research interest includes developing computational methodology for processing, integrating and interpreting high-throughput genomic data (especially next-generation sequencing data like CRISPR-Cas9 screening, ChIP-Seq, RNA-Seq), and its applications in biomedical and cancer research. He has published several peer-reviewed publications about ribosomal RNA fingerprinting, RNA-Seq transcriptome assembly, expression level estimation and bias correction in top computational biology conferences and journals, including RECOMB, Journal of Computational Biology, Bioinformatics, etc.

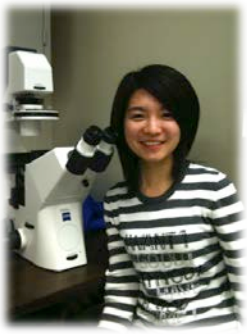
Technical Session D2-YB-T1: Machine Learning and Big Data, Biostatistics, In Silico Research and Biomedical Informatics

Ying Shen

Postdoctoral Associate, Computational Biomedicine
Department of Medicine
Boston University

ABSTRACT

BIOGRAPHY



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

Molecular Organization of the GARP Vesicle Tethering Complex

Hui-Ting Chou

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Email: Hui-Ting_Chou@hms.harvard.edu

ABSTRACT

The steps in intracellular trafficking include vesicle budding, movement, tethering and fusion with the target membrane. The first physical interaction between a transport vesicle and its target membrane is mediated by tethering factors, which are recruited to the membrane by Rab GTPases and facilitate the assembly of SNARE complexes. These three components determine the specificity and efficiency of vesicle fusion. Here, we focus on GARP (Golgi- associated retrograde protein), the multisubunit tethering complexes (MTCs) on the trans-Golgi membrane tethering the vesicles derived from endosomes. GARP contains 4 subunits (Vps51, Vps52, Vps53 and Vps54) and its association with the Golgi apparatus is mediated by the Rab GTPase, Ypt6. GARP is a member of the CATCHR subfamily of MTCs, which also includes the Dsl1, COG and Exocyst complexes. GARP mutants/deletions are lethal in mice and plants. In mice, the point mutant L967Q in Vps54 can cause degeneration of motor neurons, resulting in progressive muscle weakness, atrophy and contractures similar to the human disease amyotrophic lateral sclerosis (also known as Lou Gehrig's disease). Crystal structures show that the C-terminal domains of Vps53 (residue 554-822) and Vps54 (residue 836-974) form elongated a-helical bundles, similar to the subunits of Dsl1, COG and exocyst. We are using single-particle electron microscopy to study the structure and molecular organization of GARP in an effort to understand how each subunit contributes to tethering, GTPase binding and SNARE complex assembly.

BIOGRAPHY

Hui-Ting Chou was born in Taipei, Taiwan and got her B.S. degree in 1999 and M.S. degree in 2002 in Department of Physics at National Taiwan University. In 2003, she moved to University of California at Davis and obtained her PhD degree in biophysics in 2010.

She was a summer student in Institute of Astronomy & Astrophysics at Academia Sinica in Taiwan in 1998 and a research assistant in Institute of Biomedical Sciences at Academia Sinica in 2002-2003. She is currently a postdoctoral fellow in Department of Cell Biology at Harvard Medical School and studying the structures of protein complexes involved in membrane trafficking since 2010. Dr. Chou was a structural biologist with an interest in using biophysical tools such as electron microscope and NMR to study protein structures. She wrote the chapter, Electron Crystallography of Membrane Proteins, in the book, Electron Microscopy Methods and Protocols (2nd ed., NJ, USA: Humana Press, 2007) and was the 2nd author of the paper, the Fold of α-Synuclein Fibrils, in the journal, Proceedings of the National Academy of Sciences of the United States of America (2008). Her work in 1999-2003 was focused on NMR spectroscopy

and protein dynamics of LBD (lipoic acid-bearing domain) and SBD (subunit binding domain) of human mitochondrial BCKD (branched-chain alpha-ketoacid dehydrogenase) complex in the hope of better understanding its physiological function. Since 2003, her interest was switched to single-particle electron microscope and conducted several projects including the pH-dependent behavior of bacterial chloride-proton transporter (ClC-ec1), the oligomeric state of xylulose kinase and the aggregation of α-synulcein.

Dr. Chou is a board member of Postdoctoral Association at Harvard Medical School and Boston Taiwanese Biotechnology Association. She received IUCr Yong Scientist Travel Fellowship in First K.H. Kuo Summer School of Electron Microscope and Crystallography as well as traveling award in Luc Bossuyt/Bristol-Myers Squibb Scholarship Fund in 2008.

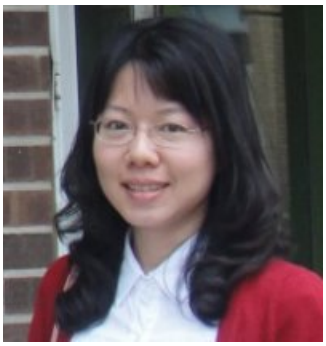
Technical Session D2-YC-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Workshop Co-chair and Session Chair

Hsiang-Ying (Sherry) Lee

Postdoctoral Associate, Whitehead Institute for Biomedical Research
Massachusetts Institute of Technology
(麻省理工學院李湘盈博士)

BIOGRAPHY



Technical Session D2-YC-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Epigenetics of Genetic Switches: Micro and Macro Views

Jian Xu

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ABSTRACT

Gene expression and cell fate decisions are controlled by both tissue-specific and broadly expressed transcription factors acting in concert with epigenetic regulators. Many questions remain unanswered regarding how specialized transcriptional programs are established and maintained, and how perturbations of genetic networks influence cellular phenotypes during lineage programming, reprogramming and cancer progression.

My laboratory investigate the genetic and epigenetic control of disease-associated genes and gene networks in hematopoietic development and disorders, focusing on both single gene ('micro') and genomic ('macro') levels. In a micro view, we study the transcriptional regulation of the clinically important genetic switch of the human β-globin gene cluster. In a macro view, we systematically characterize the contribution of both cis-acting (non-coding genomic elements such as transcriptional enhancers) and trans-acting (Polycomb regulators) elements in blood stem cell function and cancer.

By comparing the ontogeny of gene regulatory networks in normal and malignant hematopoiesis, we aim to understand how the functional genomic elements, lineage-specifying regulators, epigenetic modulators and environmental signals cooperate to control developmental potency, and how aberration may lead to cancer development.

BIOGRAPHY

Dr. Jian Xu received his Bachelor's degree in Biochemistry from Fudan University in Shanghai in 2000, and his PhD in Molecular Biology from UCLA in 2008. Currently he is an Instructor in Pediatric Hematology-Oncology in Dr. Stuart Orkin's laboratory at Boston Children's Hospital, Harvard Medical School. From September he will join the Children's Research Institute at UT-Southwestern as an Assistant Professor of Pediatrics. Dr. Xu's primary research interest is developmental gene regulation with a focus on genetic and epigenetic control of normal and malignant hematopoiesis. He was awarded the Helen Hay Whitney Fellowship in 2008, the American Society of Hematology (ASH) Merit Award in 2008 and 2009, and an NIH Career Development Award in 2011.

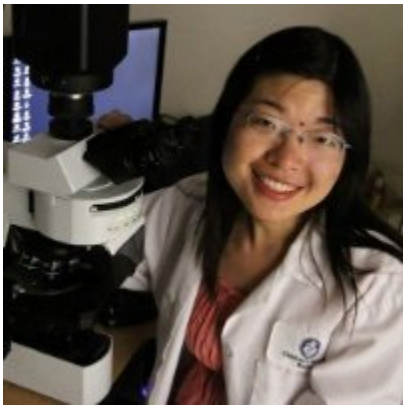
Technical Session D2-YC-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Yuyu Song

Postdoctoral Research Fellow, Howard Hughes Medical Institute
Yale University School of Medicine and
Visiting Research Fellow in Systems Biology, Howard Hughes Medical Institute
Harvard Medical School

ABSTRACT

BIOGRAPHY



Technical Session D2-YC-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Humanization of an anti-CCR4 antibody and its functional role in cancer immunotherapy

DeKuan Chang

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Email: De-Kuan_Chang@dfci.harvard.edu

ABSTRACT

Cutaneous T-cell lymphoma (CTCL) is the second most common extranodal non–Hodgkin lymphoma in adults, characterized by primary accumulation of clonally derived malignant CD4+ T cells in the skin. Although CTCL usually has indolent clinical behavior, in advanced stages, it can progress into an aggressive phenotype with poor prognosis and survival with severe immunodeficiency characteristically developing during disease progression. Therefore, disease-specific and more effective therapeutics that can decrease toxicity profiles and induce durable responses will greatly benefit patients with CTCL.

Normal skin-homing CD4+ T cells express cutaneous lymphocyte–associated antigen and CC chemokine receptors (CCR) CCR4, CCR6, CCR7, and CCR10. Among these, only CCR4 is universally expressed at high levels on the malignant skin-homing T cells, and its surface expression is closely associated with the enhanced skin-homing characteristics of CTCL cells and unfavorable disease outcome. Thus, the high-level expression of CCR4 on CTCL cells and its preferential expression on Tregs make CCR4 a potential ideal therapeutic target for CTCLs.

This talk is an overview of characterization and humanization of a mouse anti-CCR4 monoclonal antibody that recognizes both the N-terminal (NT) and the extracellular domains of CCR4. The antibody exhibited potent antitumor effects in a CTCL mouse model and its mechanism(s) of action were elucidated by a number of in vitro studies. The humanized anti-CCR4 antibody was further improved in affinity and showed stronger CDC and ADCC activities against CCR4+ tumor cells.

BIOGRAPHY

DeKuan Chang received his B.S. (2003) in Life Science from the Catholic Fu-Jen University and M.S. (2005) and Ph.D. (2009) in Pathology from the National Taiwan University. He starts his postdoctoral fellow at the Harvard Medical School at 2011. Dr. Chang's research integrates oncology, immunology, animal model, antibody engineering and targeted therapy to study tumor immunology and tumor therapy. He has patented four anti-cancer biomaterials and published many peer-reviewed papers on these topics.

Technical Session D2-YC-T1: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Sidi (Steve) Chen

Damon Runyon Cancer Research Fellow, Koch Institute for Integrative Cancer Research
Massachusetts Institute of Technology

ABSTRACT

BIOGRAPHY

Technical Session D2-YA-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Workshop Co-chair and Session Chair

Chen-Hsiang (Jones) Yu

Founder and CEO, Prentice Lab
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(Prentice Lab 余禎祥博士)

BIOGRAPHY

Jones Yu will be an Assistant Professor of Computer Science and Networking at Wentworth Institute of Technology (WIT) in September 2014. He earned B.E. and M.S. in Computer Science and Information Engineering (CSIE) from Tamkang University in 1998 and from National Taiwan University in 2000, respectively, and Ph.D. in Computer Science from MIT under Prof. Rob Miller's guidance in 2012. His research in Human-Computer Interaction (HCI) focuses on web customization and automation, and mobile learning.

He is founder and CEO of Prentice Lab, which is a startup company focusing on investigating mobile technologies and developing software for improving learning, including language learning and subject learning. In the past, he has worked for a few startup companies as Director of Mobile Engineering and User Experience, and developed mobile apps as products.

Technical Session D2-YA-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Accountable HTTP

Oshani Seneviratne

PhD Candidate, Computer Science and Artificial Intelligence Laboratory
Department of Electrical Engineering and Computer Science
Massachusetts Institute of Technology

ABSTRACT

I will describe an infrastructure that enables data transparency and accountability on appropriate usages of data. This infrastructure is encapsulated in a web protocol called HTTPA (HTTP with Accountability) and powered by the decentralized Provenance Tracking Network (PTN). HTTPA enables data consumers and data producers to agree to specific usage restrictions, while the PTN is used to preserve the provenance of data transferred from one entity to another. Using this infrastructure, the data subject can derive an audit trail for a data item and determine if there has been any usage restriction violations. We have evaluated the protocol with two reference accountable systems implementations: (1) Transparent Health: an electronic healthcare records system for patients to mark data items as sensitive and determine the access and usage of those data items, and (2) PhotoRM: a decentralized photo sharing and editing application that allows a content creator to see how her content has been reused on the Web.

BIOGRAPHY

Oshani is a PhD candidate at MIT CSAIL advised by Tim Berners-Lee. Her research is on social systems on the Web augmented with provenance, policy expressions and Linked Data. She is also working on using MIT App Inventor to make disaster management applications. For more information, please see: http://people.csail.mit.edu/oshani/

Technical Session D2-YA-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

Loco-Radio - an Augmented-Reality Music Player for Mobile Users

Wu-Hsi Li

Founder/CEO, CharmPI.com
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(麻省理工學院媒體實驗室李務熙博士)

ABSTRACT

The journeys in everyday mobility are considered mundane, repetitive, yet inevitable. Therefore, many mobile users listen to music in order to free their minds in the constrained space and time. However, the isolated auditory bubbles make them become further disconnected from the world. Can sound be used to connect mobile users to the environments? Can music be played to enhance their awareness of the surroundings? How can we deal with the traffic of information and prevent the mixture of sounds from becoming noise?

This talk presents Loco-Radio, an augmented-reality (AR) auditory environment for car drivers, bikers, and pedestrians. The mobile user is able to tune in and listen to the surroundings, and the GPS-based system renders audio according to the user's location and mobility state. Nearby places are augmented with localized audio streams and the user is immersed within a soundscape as he/she moves. To improve the auditory experience in high-density audio environments, I introduce auditory spatial scaling, a set of techniques that dynamically adjust the spatial density of perceived sounds based on context. A geo-tagged audio database is created by attaching genre-matching songs to all restaurants around the MIT campus. As users move in the city, they encounter a series of music and the perception enhances their awareness of the numbers, styles, and locations of restaurants.

BIOGRAPHY

Dr. Wu-Hsi Li was born in Taipei, Taiwan. He received his M.S. (2008) and Ph.D. (2013) in media arts and sciences from the Media Laboratory at Massachusetts Institute of Technology, MA, USA. During the time, he worked with Prof. Barry Vercoe in Music Mind Machine group and Dr. Chris Schmandt in Speech + Mobility group. He is the CEO/founder of CharmPI, a startup that provides solutions for collecting, curating, and real-time managing event photos in an interactive broadcasting experience.

His works involve augmented-reality (AR) audio, interaction design on time and space, and user experience design of music players. At a time when the culture of media consumption is all about on-demand, he explores ways to create serendipitous musical encounters. Loco-Radio allows mobile users to run into an interactive soundscape on the street. Radioish revives the lost art of channel surfing from the old analog radio tuner. He is the inventor of Musicpainter, an ongoing One-Laptop-per-Child project, which empowers users to create music by painting on the digital canvas and encourages them to share and collaborate with others.

Technical Session D2-YA-T2: Broadband, Wireless Computing, Communication and Applications, New Media and Multimedia Systems, Web, Cloud Computing and Data Mining

A newly designed selection method and its evaluation for camera-based mouse-replacement systems

Wenxin Feng

PhD Student, The Computer Science Department
Boston University

ABSTRACT

Severe paralysis caused by a traffic accident, a stroke, or a degenerative disease can drastically change a person's life. Video-based mouse-replacement system, requiring no more than a computer and a webcam, is useful technologies for nonverbal users with severe impairments. This system tracks the user's movements with a video camera and translates them into the movements of the mouse pointer on the screen. The interface interprets a pointer that has not moved for a certain period of time (dwell time) as a left mouse click.

Our research work focuses on the interface design and evaluation for camera-based mouse-replacement system. We proposed a selection method, “target reverse crossing”, based on goal-crossing design, and evaluated this method by comparing it to dwell-time clicking. Our results showed that target reverse crossing is more efficient than dwell-time clicking, while its one-time success accuracy is lower. We found that target directions have effects on the accuracy of reverse crossing. We also show that increasing the target size improves the performance of reverse crossing significantly, which provides future interface design implications for the selection method.

BIOGRAPHY

Wenxin Feng joined the Image and Video Computing group of Boston University in 2012, and is advised by Prof. Margrit Betke. Her research interest lies in human-computer interaction, and focuses on human-computer interface design and human behavior study for people with impairments. She graduated from Renmin University of China and received her B.E. degree in Information Systems in 2012.

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

Workshop Co-chair and Session Chair

Woei-jyh (Adam) Lee, PhD

Tyser Teaching Fellow of Information Systems, Robert H. Smith School of Business
University of Maryland, College Park, Maryland 20742
(馬里蘭大學 學院市分校 史密斯商學院 李偉智教授)

BIOGRAPHY

Dr. Woei-jyh (Adam) Lee received BSE degree from the National Taiwan University, MS degree from the Courant Institute at New York University, and PhD degree from the University of Maryland at College Park (UMD). He worked on distributed objects and fault tolerance at the AT&T Labs - Research in 1997. He focused on network software and management at the Bell Laboratories Research from 1998 to 2000. He visited the University of Southern California specializing in continuous media streaming and multimedia networking from 2002 to 2003.

He contributed in protein domain parsing and boundary prediction at the National Cancer Institute (NCI), National Institutes of Health (NIH) from 2004 to 2005. He was a fellow focusing on human genetics and genomics at the National Center for Biotechnology Information, National Library of Medicine, NIH from 2009 to 2012. He became a special volunteer working on computational modeling for cancer progression and metastatic at the NCI, NIH from 2012 to 2013. He was also affiliated with the Center for Bioinformatics and Computational Biology and the Institute for Advanced Computer Studies at UMD.

He is currently a faculty of Information Systems at the Robert H. Smith School of Business at UMD since 2012. His research interests include information integration, data management and mining, literature-based discovery, performance simulation and evaluation, bioinformatics and computational biology, human genomics and genetics, and cancer biology. He has two US Patents and is a member of the ISCB, the IAENG, and the CAPA.

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

Processing Vastly Growing Human Genomic Data

Wan-Ping Lee

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Seven Bridges Genomics, Inc.
(Seven Bridges Genomics 李婉萍博士)

ABSTRACT

There are about three billion nucleotides/basepairs in human genome and one person differs from another by millions of variations. The current revolution in genomics has made it feasible to identify a person's unique variations, and many of those unique variations affect susceptibility to disease and response to treatments. Therefore, greater understanding of individual genomes is a key to enable scientists and physicians to begin to personalize medicine based on each patient's unique genome.

The current technology sequences a genome by generating millions or billions of short DNA sequences (reads) that range from 50 to several hundred basepairs in length. Then, short-read mapping algorithms utilize human genome reference sequences to align reads from a newly sequenced person. Many reads fail to map or are incorrectly mapped because each new genome typically contains many genetic variations not captured by the reference sequence. As a result, while it is possible to detect single-nucleotide polymorphism (SNP) and short insertion/deletion (INDEL) variants using such mappings, longer/structural variant alleles and more complex variations are often missed. Furthermore, undetected structural variants in a newly genome often cause mismappings that lead to false positive variant predictions.

As lots of novel variants are discovered by high profile projects, accounting for those novel variants when aligning newly reads becomes imperative and vastly improves sensitivity. This is based on the fact that most of variants found in a single individual are shared in that species. We thus develop a novel whole-genome read mapper that can take into account known variations, in addition to the genome reference, for mapping reads more accurately. Our approach is to construct a directed acyclic graph (DAG) representing the reference sequence and the allelic alternates. Our mapper works in two phases. In a first read localization step, we identify regions where a read is likely to map in the DAG. In a second local alignment step, we align the read against the DAG, using a graph-aware extension of the Smith-Waterman optimal alignment algorithm.

We demonstrate the power of this new read mapper for the detection of mobile element insertions (MEIs) in a human sample. When constructing a DAG using known MEI sites in YRI population in the 1000 Genomes Project, we are able to detect >95% of such sites present in a simulated genome. Similar results are achieved when detecting MEIs in NA12878. Moreover, using our mappings considering known MEIs, we are able to eliminate >95% of falsely called SNPs and INDELs at or near the MEI insertion sites in traditionally mapped sequence alignments. These false positives are almost always caused by mismapping reads containing the MEI sequences in the sample but that are not present in the reference genome. Our mapper, accounting for these insertions within the DAG, is able to correctly align the reads.

These initial results indicate that read mapping that accounts for known variations can

substantially improve read placement and supports vast improvements in variant calling accuracy.

BIOGRAPHY

Dr. Wan-Ping Lee is a senior lead scientist in R&D at Seven Bridges Genomes Inc. She joined Seven Bridges Genomics in June 2014. Prior to that, Wan-Ping was a senior research associate at Boston College in the Department of Biology in the laboratory of Dr. Gabor Marth where she was a postdoctoral research associate when she started the position at Boston College in 2009. Wan-Ping's expertise currently lies in Bioinformatics, specifically in next-generation sequencing (NGS) data analysis.

Before Wan-Ping joined the Marth lab as a bioinformatics researcher, Wan-Ping received her Ph.D. in Electronics Engineering from National Taiwan University in 2009 and M.S. in Computer Science from National Sun Yat-sen University in 2004. She was trained in electronic design automation (EDA) and vary large scale integrated circuit (VLSI) design. In 2008 Wan-Ping spent a year as a visiting scholar in Electrical and Computer Engineering at Carnegie Mellon University.

Wan-Ping got in the college in 1997 and she went to Chung Yuan Christian University. Wan-Ping majored in business and earned her Bachelor of Business Administration (B.B.A.) there after four years. Wan-Ping is multidisciplinary trained in bioinformatics, electrical engineering, computer science, and commerce.

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

Personalized Genomic Medicine - Current Strategies and Bioinformatics Pipelines

Ellen Ay-Lun Tsai

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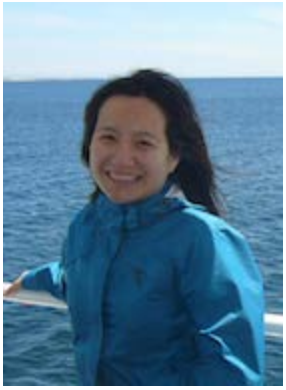
ABSTRACT

Next-generation sequencing (NGS) is a fast and efficient tool that has enabled geneticists access to sequencing data for tens to tens of thousands of genes in search of pathogenic mutations that cause the patient's clinical disorder. Prior to NGS methods being established in the laboratory, gene panels using Sanger sequencing technology required many hours of experimental work as well as manual analysis of sequence traces to deliver a clinical report summarizing the findings on just a handful of genes. The transition of NGS from the research community into the clinical setting not only reduces the sequencing time, but it enables geneticists access to genes outside of the ordered genetic test panels.

The Laboratory for Molecular Medicine (LMM) is a CLIA-certified clinical diagnostic laboratory of Partners Healthcare Personalized Medicine. At this center, we have migrated our sequencing efforts of gene panels from Sanger sequencing to NGS. We are looking to expand our genetic testing further by moving from targeted NGS panels to exome sequencing using the custom capture Medical Exome kit developed as a collaboration between Partners Healthcare, Children's Hospital of Philadelphia, and Emory University. This talk will summarize the development of clinical exome sequencing at this center. It will also overview the current bioinformatics pipeline that supports the clinical operations at the LMM.

BIOGRAPHY



Ellen Tsai received her B.S. (2008) in Bioengineering (Biotechnology) from the University of California, San Diego. From her undergraduate coursework in genetics, she was inspired to pursue the field further and obtained a Ph.D. (2013) in Genomics and Computational Biology from the University of Pennsylvania studying the genetic underpinnings of pediatric liver diseases. She is currently a Research Fellow at Harvard Medical School and Brigham and Women's Hospital, working on standards for clinical sequencing and on identifying causal changes that confer disease in patients. Her current interests are in copy number variation, genome and exome sequencing, as well as methods to infer pathogenicity from variants identified from DNA-sequencing.

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

Wen-Chi Chou

Postdoctoral Research Fellow, Hebrew SeniorLife
Harvard Medical School

ABSTRACT

BIOGRAPHY

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

Identification of novel muscle secreted proteins (myokines) using RNAseq

Chia-Ling Wu

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Email: clwu@bu.edu

ABSTRACT

Resistance training induced muscle hypertrophy is beneficial for various metabolic parameters associated with aging, obesity and type II diabetes. However, little is known about its underlying cellular and molecular mechanisms. Emerging evidence suggests that skeletal muscles secret cytokines and other peptides, referred to as myokines, which target distant metabolic organs and affect whole-body metabolism. To identify novel myokines in hypertrophic muscles, we analyzed the transcriptome profiles of mouse skeletal muscle with or without hypertrophy. Next-generation sequencing of poly(A)+ tail mRNA was performed on gastrocnemius muscles from control and MyoMouse. In the MyoMouse model, constitutively-active Akt1 is conditionally activated in skeletal muscle and promote growth in type II fast/ glycolytic fibers, thus resembling the muscle hypertrophy phenotype observed in anaerobic/ resistance exercise. We found >28,000 known isoforms expressed in skeletal muscle transcriptome and major changes in genes mediating metabolic pathways and inflammation in hypertrophic muscles. In silico analysis identified ~280 transcripts encoding for known or inferred secreted proteins from hypertrophic muscles of MyoMouse. Gene ontology analysis suggested that most of these muscle secreted proteins were involved in cell-to-cell communication, immune function and metabolic processes. Our data provide an extensive deep sequencing of transcriptome during glycolytic myofiber hypertrophy and contribute important information for novel myokine identification at genome-wide level.

BIOGRAPHY

Chia-Ling (Leslie) Wu is born and raised up in Taipei, Taiwan. She was first trained as physical therapist at Kaohsiung Medical University, Taiwan. After completion of internship and working at National Taiwan University, she realized the paucity of evidence-based practice in rehabilitation sciences, which is in sharp contrast to the vast needs of patients. She became determined to better understand the pathophysiology of muscle diseases. She first came to the States to obtain a Master's degree in exercise physiology at University of Buffalo at New York. In 2007, she went on pursuing her doctoral degree in applied anatomy and physiology at Boston University, MA. Trained as a muscle biologist in Dr. Susan Kandarian's lab, Dr. Wu's doctoral dissertation identified target genes of a NF-κB transcription factor and its coactivator, p50 and Bcl-3, during disuse muscle atrophy. Combining gene expression profiling and ChIP-seq technologies, her dissertation was the first study to identify target genes of transcription factors required for muscle atrophy at a genome-wide level.

Dr. Wu is currently a postdoctoral research associate in Dr. Ken Walsh's lab at Boston University School of Medical. Her research interests focus on understanding the cellular and molecular mechanisms of skeletal muscle adaptations in health or diseases. She has published several papers on identifying target gene networks and dysregulated signaling pathways in disuse muscle atrophy and cancer cachexia. She is also an active member in American Physiological Society, American College of Sports Medicine, and Association for Woman in Science.

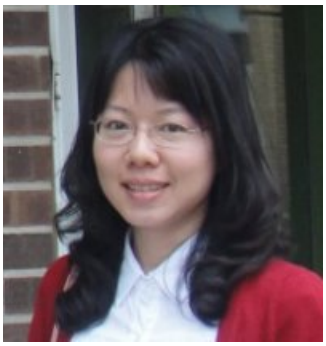
Technical Session D2-YC-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Workshop Co-chair and Session Chair

Hsiang-Ying (Sherry) Lee

Postdoctoral Associate, Whitehead Institute for Biomedical Research
Massachusetts Institute of Technology
(麻省理工學院李湘盈博士)

BIOGRAPHY



Technical Session D2-YC-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Drug-Induced Ablation of Activated Pin1 Selectively in Cancer Cells Has Potent Anticancer Activity by Inhibiting Many Cancer-Driving Pathways

Shuo (Dennis) Wei

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(哈佛醫學院魏碩博士)

ABSTRACT

Targeted therapy has transformed cancer treatment, but blocking a single pathway is often ineffective against solid tumors, especially aggressive or drug-resistant ones, because genetic or non-genetic changes have activated oncogenes and/or inactivated tumor suppressors to turn on a range of interactive and/or redundant pathways during tumorigenesis. Thus major challenges remain in the struggle to inhibit multiple oncogenic pathways either using a cocktail of targeted drugs or by targeting some common mechanism.

A common and central signaling mechanism in the oncogenic pathways is Pro-directed phosphorylation (pSer/Thr-Pro). Proline uniquely adopts cis and trans conformations, whose isomerization is catalyzed by prolyl isomerases (PPIases). A major advance in the understanding of the conformational regulation after Pro-directed phosphorylation was our identification of the unique PPIase Pin1. Using its WW domain, Pin1 binds to specific pSer/Thr-Pro motif, thus targeting Pin1 close to its substrates, where its PPIase domain catalyzes cis-trans isomerization of certain pSer/Thr-Pro motifs, which can be detected by cis and trans-specific antibodies.

Pin1 plays a pivotal role in tumorigenesis. For example, Pin1 is commonly overexpressed and/or activated in human cancers, which correlates with poor outcomes. In contrast, the Pin1 polymorphisms that reduce Pin1 expression are associated with lower cancer risk. Moreover, Pin1 knockout prevents tumorigenesis, even induced by activated oncogenes such as HER2 or Ras, whereas Pin1 overexpression disrupts cell cycle coordination, leading to centrosome amplification, chromosome instability and cancer development in vitro and in vivo. Significantly, Pin1 activates ~25 oncogenes/growth enhancers and also inactivates ~19 tumor suppressors/growth inhibitors. Thus, Pin1 amplifies oncogenic pathways through positive and negative feedback mechanisms to turn on oncogenes and/or turn off tumor suppressors at the same time. Thus, Pin1 inhibitors may have the unique and desirable ability to block multiple cancer-driving pathways at once. However, the available Pin1 inhibitors have lacked the required specificity and/or potency, or cannot enter cells.

Using mechanism-based high throughput screening, we identified five chemotypes of Pin1 inhibitors that strongly and selectively bind to the Pin1 active site taking advantage of the substrate phosphate- and proline-binding pockets, and causes degradation of active Pin1 selectively in cancer cells. Such drugs-induced Pin1 ablation exerts potent anticancer activity against both APL and aggressive triple negative breast cancer by turning off oncogenes

including PML-RARα, cyclin D1, HER2, Akt, NFkB/p65 and turning on tumor suppressors, like Smad and SMRT simultaneously. Thus Pin1 inhibitors effectively block multiple cancer-driving pathways at once, a unique property desirable for treating aggressive or drug-resistant tumors. Our results also provide a rationale for developing more potent and specific Pin1-targeted inhibitory derivatives for cancer treatment.

BIOGRAPHY

Shuo Wei was born in Taipei, Taiwan. He obtained his pharmacy Ph.D from The Ohio State University, Columbus OH, at 2009 in Dr. Ching-Shih Chen's laboratory.

He worked as a postdoctoral research fellow in Kun Ping Lu's laboratory at Beth Israel Deaconess Medical Center and Department of Medicine of Harvard Medical School, Boston MA, from 2010 until present.

Dr. Wei's research focuses on 1) repositioning old drugs by dissecting unknown mechanism and 2) identifying new class of anti-cancer and anti-lupus drugs via high throughput screening. Dr. Wei received Albert H. Soloway OSU Graduate Student Award at Ohio State University sequentially at 2008 and 2009. Dr. Wei has a total 16 publications with 7 papers with him as the first author published in prestige journals. He has been a member in the American Association for Cancer Research. Dr. Wei's discovery on developing potent and selective Pin1 inhibitors has led him to be recognized and supported by a fellowship award from Susan G. Komen for the Cure, the breast cancer foundation. As an inventor of Pin inhibitors, Dr. Wei holds three US patents, by which his effort has successfully built up the scientific basis for a biotech start-up, Pinteon, aiming to develop next generation Pin1-targeted therapy against cancer.

Technical Session D2-YC-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Cells, Tissues, and Scaffolds: Seeing Them All – Photoacoustic Imaging in Regenerative Engineering

Y. Shrike Zhang

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ABSTRACT

At the intersection of life sciences, materials science, engineering, and medicine, regenerative engineering stands out as a highly interdisciplinary field that aims at retaining, restoring, or augmenting tissue/organ functions to promote the human welfare. While the field of regenerative engineering has witnessed tremendous progress over the past three decades, challenges remain. For example, it is always highly desired not only to visualize the morphologies but also assess the functions of engineered tissue/organ constructs, particularly when three-dimensional structures are involved. Fortunately, recent advances in biomedical imaging have offered better tools to examine these tissue/organ constructs and their microenvironment at different length scales and functionality levels, greatly accelerating the field of regenerative engineering.

This talk will focus on photoacoustic microscopy, a recently developed volumetric and quantitative imaging modality based on the photoacoustic effect, that is, the production of ultrasonic waves by an optically absorbing agent through transient thermoelastic expansion upon pulsed or intensity-modulated laser irradiation. Since its invention about a decade ago, photoacoustic microscopy has been widely used in biomedicine in imaging blood vessels and melanomas, and in cancer theranostics in tracking dye-loaded or metal nanoparticles. Only in the past few years has it witnessed the application of photoacoustic microscopy in the field of regenerative engineering as pioneered by the speaker and co-workers. Morphological and functional analyses of critical parameters in regenerative engineering extending from cell distribution, proliferation, and tissue formation all the way to scaffold degradation and post-culture histology assessment have been demonstrated, both in vitro and in vivo.

BIOGRAPHY

Yu Shrike Zhang was born in Nanjing, Jiangsu, China. He received his B.S. in Biomedical Engineering from Southeast University in 2008, after which he came to the U.S. to pursue his Ph.D. degree in Biomedical Engineering with Prof. Younan Xia at Washington University in St. Louis and Georgia Institute of Technology/Emory University School of Medicine (2013). Currently he is a postdoctoral research fellow in Prof. Ali Khademhosseini's group at Harvard Medical School, Brigham and Women's Hospital, and Harvard-MIT Health Sciences and Technology. Dr. Zhang has authored 34 peer-reviewed journal articles, and his researches span across a wide spectrum including biomaterials, tissue engineering and regenerative

medicine, biomedical imaging, drug delivery, nanomedicine, cancer theranostics, organ-on-a-chip, and developmental biology. More details can be found on his personal website: http://shrikezhang.weebly.com

Technical Session D2-YC-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Real-Time Visualization of JC Virus Internalization

Yi-ying Chou

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(哈佛醫學院周怡吟博士)

ABSTRACT

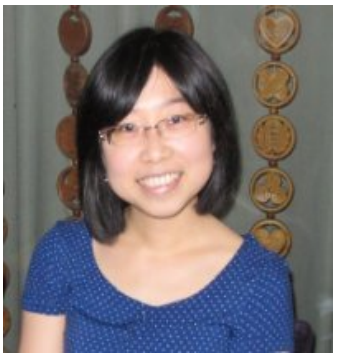
JC virus (JCV) is a non-enveloped polyomavirus that infects 70-90% of humans. The virus reactivates in immunodeficiency or immunosuppressed patients and infection of the oligodendrocytes leads to the fatal demyelinating progressive multifocal leukoencephalopathy (PML) disease.

It is known that for successful infection, JCV is first internalized from the plasma membrane, and then sequentially reach the endosomal compartment and the endoplasmic reticulum (ER). It is also known that the DNA genome needs to reach the nucleus for genome replication and virus particle assembly. It is unknown, however, how, where and when the membrane barrier is breached to allow virus (and genome) to penetrate into the cytosol and the nucleus.

To study how JCV virus penetrates, we are developing a real-time fluorescence microscopy visualization platform with single-virus particle sensitivity to follow the infectious route of single JCV particles. Since it is not practical to use intact virus to track in real-time virus entry and penetration, we have established a reconstitution system that allows the generation of biochemical amounts of non-infectious recombinant JC particles composed of all the viral capsid proteins but devoid of the viral genome. We found that these particles are indistinguishable from JCV by negative staining electron microscopy. These particles can be labeled with fluorescent dyes and they follow the same entry route as intact JCV. We have also established gene-edited human fetal glial SVG-A cells expressing markers for membrane-bound organelles at physiological levels, including GFP-Rab5A for early endosomes, GFP-Rab7A for late endosomes, GFP-Sec61beta for the ER and GFP-Nup133 for the nuclear pore complex on the nuclear membrane.

Here we present real-time visualization data of SVG-A gene-edited cells obtained in 3D using fast spinning disc confocal microscopy showing the tracking of fluorescently labeled recombinant JC particles at different time points after inoculation. We found particles colocalized with Rab5-EGFP/ early endosomes within 1 hr post inoculation followed by their accumulation in Rab7-EGFP / late endosomes within 4 hrs. Associations of the recombinant JC particles with the ER was observed ~ 20 hr post inoculation. At this time we also observed many immobile particles in proximity to the nuclear membrane whereas none were ever observed within the nucleus. Visualization of fixed cells simultaneously exposed to fluorescently tagged recombinant JC particles and intact JCV confirmed equivalent intracellular traffic by showing their colocalization in the same intracellular compartments.

BIOGRAPHY



Yi-ying Chou was born in Taipei, Taiwan, 1985. She received her B.S. (2007) in Life Science from the National Taiwan University. She performed her graduate study in Dr. Peter Palese's lab focusing on influenza virus researches and later earned her Ph.D. (2013) in Biomedical Science from Icahn School of Medicine at Mount Sinai, New York City. Currently, Yi-ying is a postdoctoral research fellow in Dr. Tom Kirchhausen's lab in the Department of Cell Biology at Harvard Medical School. Dr. Chou's researches focus on molecular virology and the study of virus-host interactions using various imaging technology. She has co-authored nine peer-reviewed journal papers and serve as ed hoc reviewer for The Journal of Virology from 2009-2010. She serves on the programs and organizing committees of various associations, such as Association for Women in Science, Boston Taiwanese Biotechnology Association. She is an honor member for the Phi Tau Phi Scholastic Honor Society and member of The New York Academy of Science and the American Society of Microbiology.

Technical Session D2-YC-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

Computational Design of a Peptide-based Self-assembling Nano-Cube

Jian Zhang

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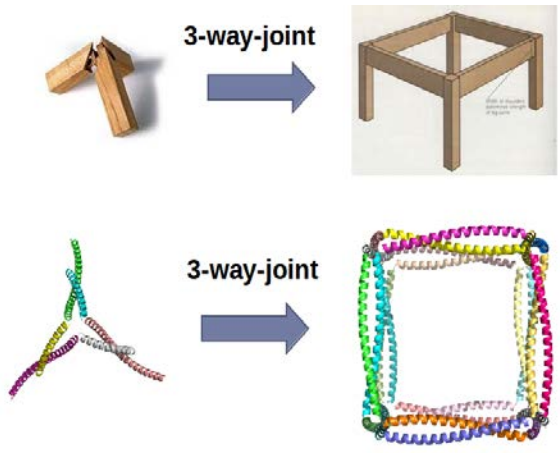
ABSTRACT

The rational design of self-assembling biomolecule-based nanostructures of defined 2D and 3D shapes remains a challenging problem. Currently, DNA is the widely used building block because it is predictable and programmable. The use of peptide- or protein-based systems, however, has potential advantages due to their richer chemistries, structures and functions. Here we present a strategy to design a polypeptide nano-cube, based on self-assembling coiled-coil segments. The target nano-cube is self-assembled from 8 three-way-joint building blocks. Each three-way-joint is assembled from 3 single-chain polypeptides. The vertex of three-way-joint is further enforced with a metal-binding site. The major driving force ensuring the correct self-assembly of this system is the specificity of coiled-coil interactions, designed using the previously published CLASSY approach. We explicitly take into account the correct associations leading to the nano-cube structure (desired state) along with all possible incorrect coiled-coil associations (undesired states). To this end, the molecular-mechanics energies of the target and all undesired states are first converted into sequence-based expressions, containing constant, single-residue and residue-pair terms via Cluster Expansion. Next, the space of trade-offs between target-state stability and its specificity relative to undesired states is explored using Integer Linear Programming. Our fully automated computational design platform provides a new route for constructing peptide-based assemblies and biomaterials.

Figure 1. Illustration of peptide-based self-assembly nano-cube.



BIOGRAPHY

Jilin City, Jilin Province, China.

2005–2008 PhD in Chemical Engineering, North Carolina A&T State University, Greensboro, NC, USA.

2002–2005 M.S. in Biochemical Engineering, Zhejiang University, Hangzhou, Zhejiang, China.

1998–2002 B.S. in Bioengineering, Zhejiang University, Hangzhou, Zhejiang, China.

2011–current, Department of Computer Science, Dartmouth College, Post-doctoral Research Associate, Hanover, NH, USA.

Computational design and experimental characterization of protein-protein and protein-fullerene (graphene,C60,carbon nanotube) self-assembly nano system Develop a fast 3D structural motif search engine (MaDCaT)

2008–2011, Center for Computational Medicine and Bioinformatics, University of Michigan, Post-doctoral Fellow, (Lab moved from Kansas), Ann Arbor, MI, USA.
Protein structure prediction I-TASSER server (Best server in CASP9);
High-resolution protein structure refinement using hybrid molecular dynamics and bioinformatics approach FG-MD; Structural modeling of all putative G-protein coupled receptors (GPCR) in humane genome (GPCRRD);

Development of a statistical poteintial using random walk chain model as reference state (RW potential).

Dr. Jian Zhang is a member of Protein Society. He won the first place in the 9th international competition on the Critical Assessment of Structure Prediction (CASP9)

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Technical Session D2-YC-T2: Medicine and Life Sciences, Biomaterials, Biomedical Sciences and Engineering

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ABSTRACT

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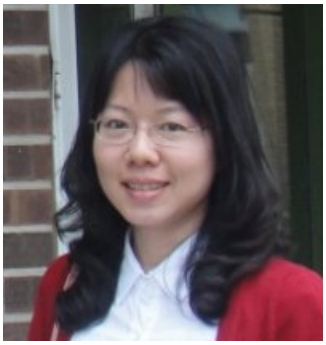

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