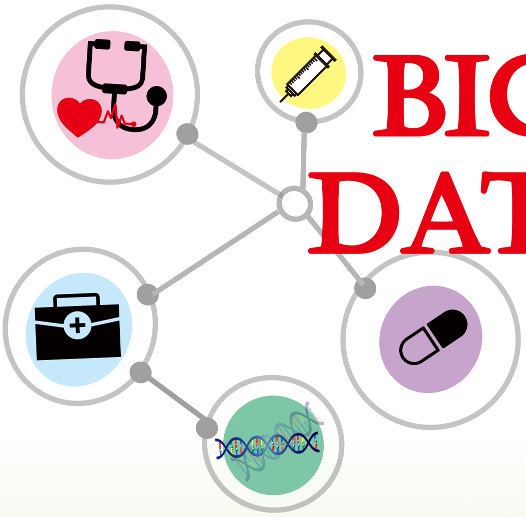


BIG DATA in Health Sciences

Innovations for health care, medical product development and regulatory science

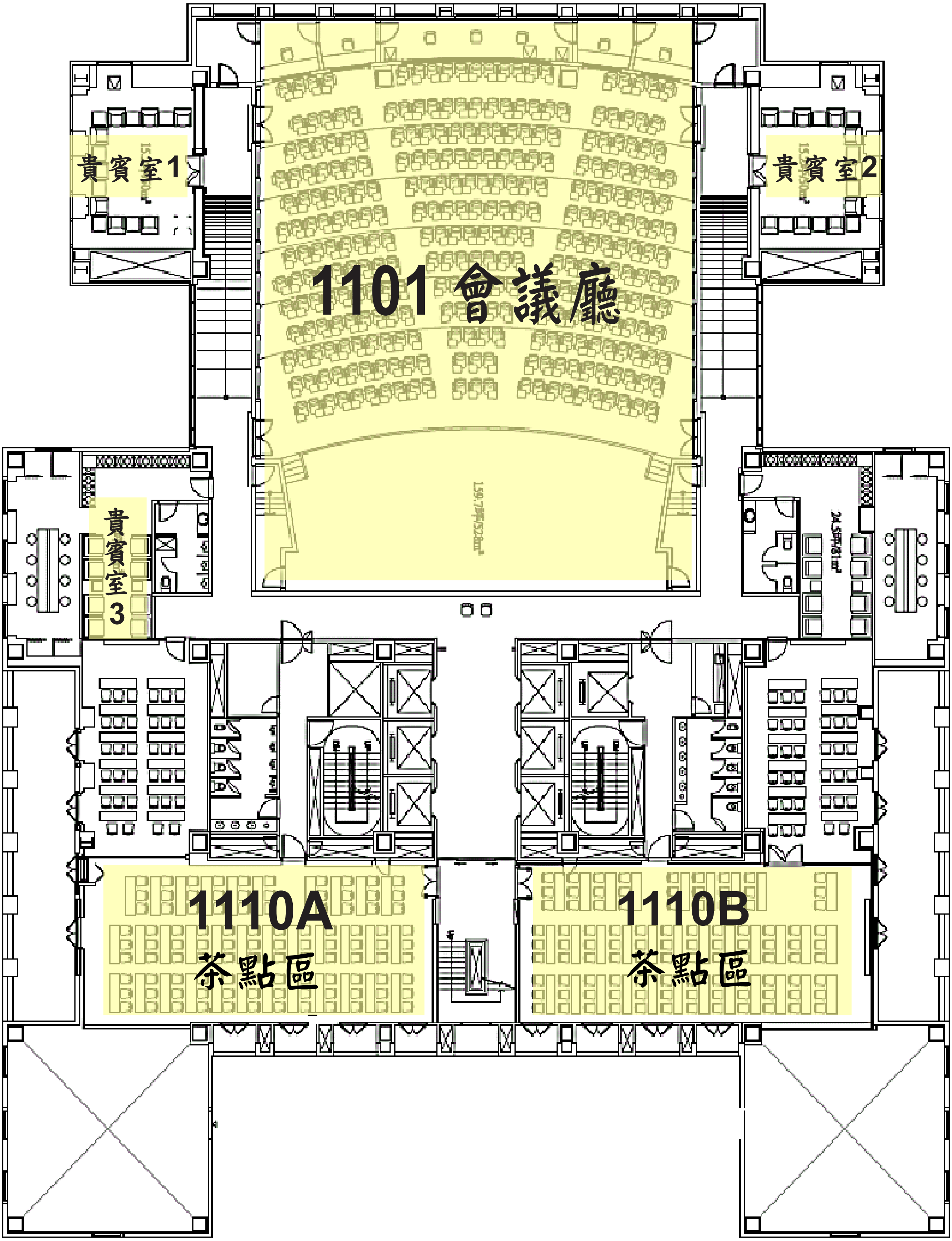
時　　間	2018年6月26-27日
地　　點	張榮發基金會國際會議中心11樓
會議網址	http://www.tbi.org.tw/big-data-conf-2018/wp/
主辦單位	國家衛生研究院 衛生福利部 科技部生技醫藥核心設施平台 衛福部衛生福利資料科學中心國衛院分中心 ICSA-Taiwan Chapter

BIG DATA in Health Sciences

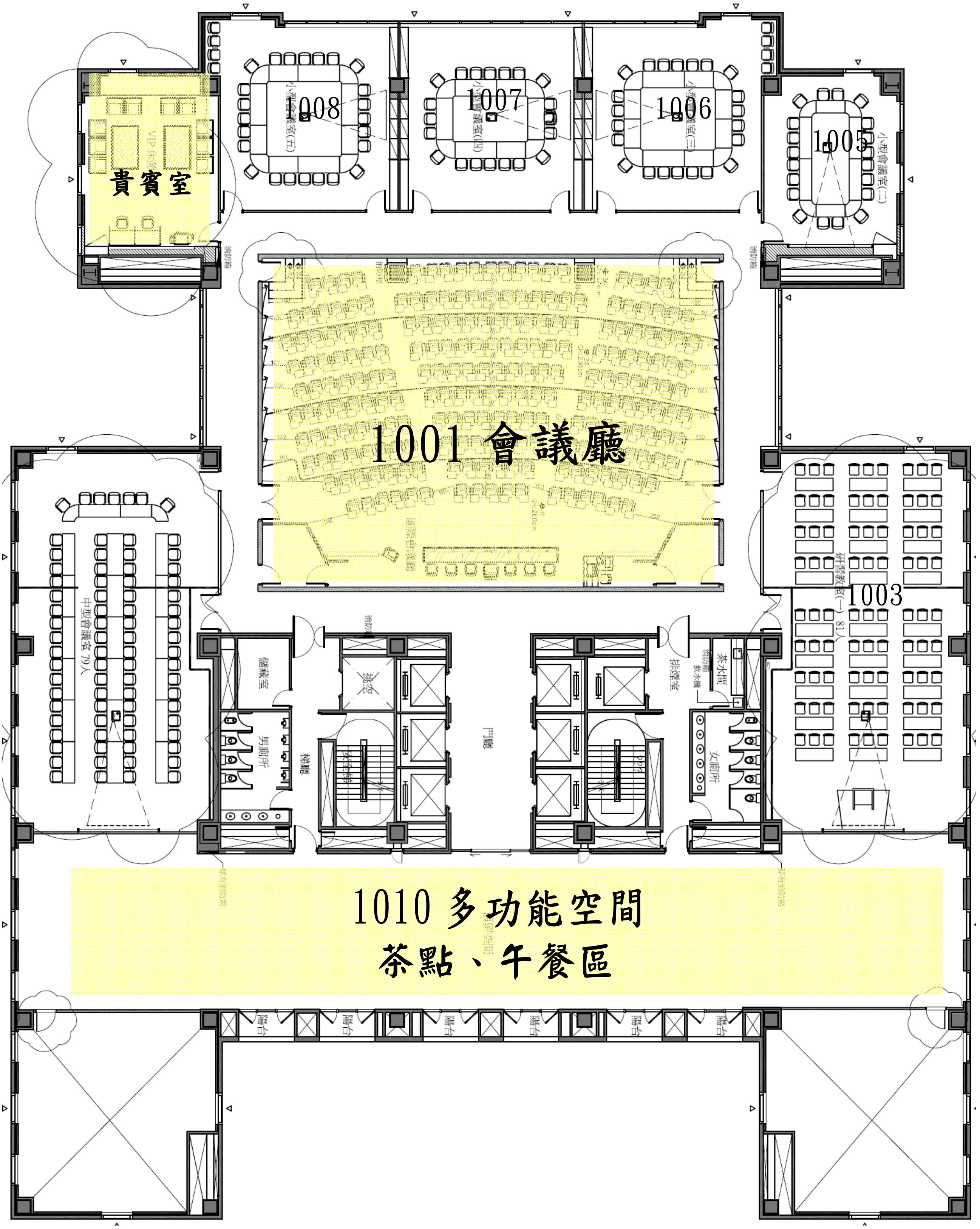
Innovations for health care, medical product development and regulatory science

Agenda

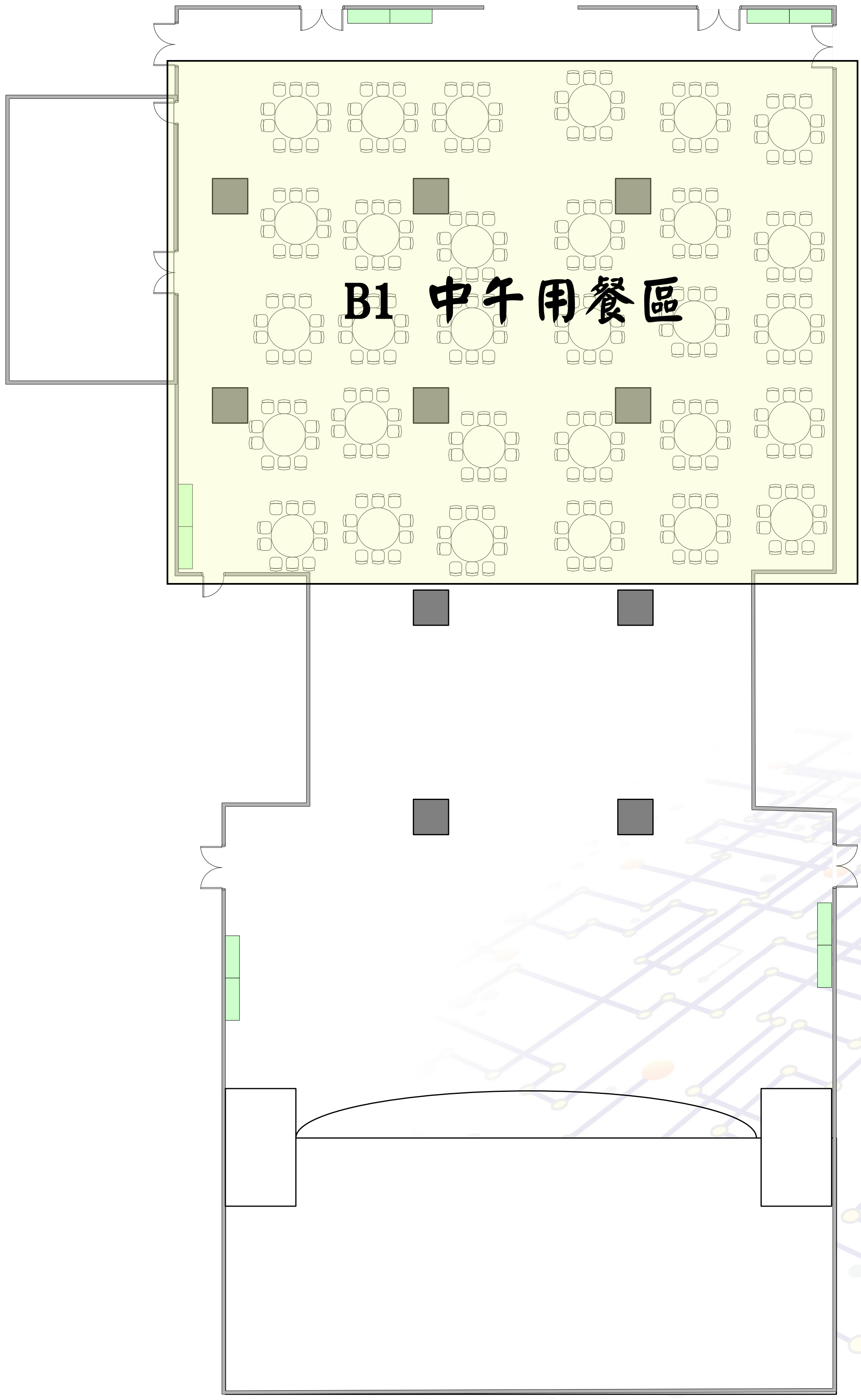
財團法人張榮發基金會國際會議中心 11 樓平面圖



財團法人張榮發基金會國際會議中心 10 樓平面圖



財團法人張榮發基金會國際會議中心 B1 平面圖



Wi Fi

CHANG YUNG FA

問　卷

http://www.tbi.org.tw/data_feedback

登錄線上問卷所需之隨機碼請見名牌下方

Day 1 - 6/26（二）

時間	**主持人 / 主講人**	**會議室 1101（會議室 1001 同步視訊）**		
8:20-8:50	報到			
8:50-9:00	梁賡義院長 / 國家衛生研究院	**院長致詞**		
	主持人：司徒惠康副院長 / 國家衛生研究院	**Session 1 : Precision Medicine and Clinical Trial**		
9:00-9:35	黎子良院士 / Department of Statistics, Biomedical Data Science,and Computational & Mathematical Engineering,Stanford University, USA	Adaptive Design of Affordable Clinical Trials Using Master Protocols in the Era of Precision Medicine		
9:35-10:00	熊昭所長 / 國家衛生研究院群體健康科學研究所	Lung Cancer Pharmacogenomics – An Integrative Analysis of Patient Survival, Genetic Variants, and Gene Expression		
10:00-10:25	徐麗娟副執行長 / 財團法人醫藥品查驗中心	Real World Evidence in Drug Review		
10:25-10:40	Coffee Break (11F, 10F 皆備有茶點)			
10:40	主持人 : 熊昭所長 / 國家衛生研究院群體健康科學研究所	**Session 2 : Big Data and AI in Health Industry**		
10:45-11:10	瞿志豪創新長 / 科技部生醫創新執行中心	Artificial Intelligence in Healthcare: Opportunities and Challenges		
11:10-11:35	郭彤博士 /IQVIA 大中華區商務發展副總裁	Big Data and Artificial Intelligence in Site Identification and Patient Recruitment		
11:35-12:00	Dr. Kang Liu/ 台灣雲檢股份有限公司 CSO	Multi-Omics and AI on Translational Medicine Research and Application		
12:00-13:00	午餐 (10F 及 B1)			
	會議室 1101		**會議室 1001**	
13:00	**Session 3A : Big Data Analytics in Bioinformatics**		**Session 3B : Analytic Methods for Infectious Diseases**	
	主持人 : 楊欣洲研究員 / 中央研究院統計科學研究所		主持人 : 廖經倫所長 / 國家衛生研究院感染症與疫苗研究所	
13:05-13:30	孫孝芳教授 / 國立成功大學醫學院分子醫學研究所所長	Application of NGS-based Test in the Preimplantation Genetic Screening	林培生研究員 / 國家衛生研究院群體健康科學研究所	An Integrated Surveillance System for Dengue Control
13:30-13:55	鍾仁華副研究員 / 國家衛生研究院群體健康科學研究所	A Large-scale Genetic Association Study for Fasting Glucose from Multiple Cohorts	詹大千副研究員 / 中央研究院人文社會科學研究中心	從個人到群體的流感傳播
13:55-14:20	杜憶萍研究員 (副所長)/ 中央研究院統計科學研究所	Statistical Analysis for Cryo-electron Microscopy Images	謝英恆教授 / 中國醫藥大學公共衛生學系	Modeling Infectious Diseases in the Big Data Era: Challenges and Promises

Day 1 - 6/26（二）

	會議室 1101		會議室 1001	
14:20	Session 4A : Smart Device Developments		Session 4B : Environmental Health	
	主持人 : 林峯輝所長 / 國家衛生研究院生醫工程與奈米醫學研究所		主持人 : 郭育良所長 / 國家衛生研究院國家環境醫學研究所	
14:25-14:50	詹寶珠司長 / 教育部資訊及科技教育司	When AI Meets Digital Pathology	王玉純教授 / 中原大學環境工程學系	整合環境及健康巨量數據系統性探索氣候變異健康風險關聯性
14:50-15:15	王振興特聘教授 / 國立成功大學電機工程系	Applications of Wearable and AI Technology in Sleep Centers	陳主智研究員 / 國家衛生研究院群體健康科學研究所	Short- and Long-term Prediction of Extremely Hot Days due to Climate Change and Related Attributable Mortality
15:15-15:40	孫永年特聘教授 / 國立成功大學資訊工程學系	Deep Learning for Medical Image Analysis	王淑麗研究員 / 國家衛生研究院國家環境醫學研究所	Environmental, Epigenetic, and Genetic Interactions and Human Health Protection
15:40-16:00	Coffee Break（11F, 10F 皆備有茶點）			
16:00	Session 5A : Regulatory Science & Government Policy		Session 5B : New Developments in NGS Data Analysis and Visualization	
	主持人 : 鄭守夏教授 / 國立台灣大學健康政策與管理研究所		主持人 : 陳豐奇研究員 / 國家衛生研究院群體健康科學研究所	
16:05-16:30	吳俊穎主任 / 台北榮民總醫院轉譯研究科	大數據與 AI 宣言：解放數據、重塑法律、追求至善	許聞廉所長 / 中央研究院資訊科學研究所	High Throughput NGS Data Analysis
16:30-16:55	蔡淑鈴副署長 / 衛生福利部中央健康保險署	NHI MediCloud System 之應用與結果	黃憲達講座教授 / 國立交通大學生物科技學系（所）	Short and Long Read Sequencing Technologies and Their Applications in Biomedical Research
16:55-17:20	龐一鳴處長 / 衛生福利部資訊處	Policies for e-Health	陳君厚所長 / 中央研究院統計科學研究所	Matrix Visualization for (Big) Health Science Data

Day 2 - 6/27 (三)

時間	主持人 / 主講人	會議室 1101（會議室 1001 同步視訊）
8:30-9:00	報到	
09:00	主持人：王英偉署長 / 衛生福利部國民健康署	**Session 6 : Using Big Data in Primary Prevention**
9:05-9:30	袁啟亞營運總監 / 工研院服務系統科技中心	大數據與智慧健康照護服務系統
9:30-9:55	陳立昇教授 / 台北醫學大學口腔衛生學系主任	Big Data in Non-communicable Disease Prevention
9:55-10:20	張新儀研究員 / 國家衛生研究院群體健康科學研究所	An Example of Using Big Data in Primary Prevention of Cardiovascular Disease 大型資料庫在心血管疾病初級預防上的應用實例
10:20-10:40	Coffee Break	
10:40	主持人 : 吳秀英主任秘書 / 國家衛生研究院	**Session 7 : Big Data Analysis in Health Care**
10:45-11:10	張憶壽名譽研究員 / 國家衛生研究院癌症研究所	Improvements of Net Cancer Survival in Taiwan – A Study Based on Cancer Registry, Cause of Death and Health Insurance Database
11:10-11:35	許志成副所長 / 國家衛生研究院群體健康科學研究所	Big Data Analysis and Application in Healthcare Research 巨量資料分析應用於醫療照護研究
11:35-12:00	邱燕楓研究員 / 國家衛生研究院群體健康科學研究所	Health Benefits of Plant-based Diets: Evidence from Big Data Analysis
12:00-13:00	午餐	
	主持人：許元春教授 / 國立交通大學應用數學系	**Session 8 : Mathematical Approaches to Healthcare Research**
13:00-13:20	吳浩榧副教授 / Department of Mathematics, Duke University	How does Geometry Help Physician's Diagnosis?
13:20-13:40	劉聚仁助理教授 / 國立成功大學數學系	Diffuse to Fuse EEG Spectra - Intrinsic Geometry of Sleep Dynamics for Classification
13:40-14:00	何弘棋醫師 / 中國醫藥大學附設醫院心臟內科	Estimation and Model Checking for General Semiparametric Recurrent Event Models with Informative Censoring
14:00-14:20	林祐霆醫師 / 臺北榮民總醫院麻醉部	Smart Medicine in Sedation, Anesthesia and Patient Monitoring

Day 2 - 6/27 （三）

	主持人：邱弘毅教授 / 台北醫學大學公共衛生學系	**Session 9 : Disease Screening and Surveillance**
14:20-14:40	陳秀熙教授 / 臺灣大學公共衛生學院	Stochastic Process for Disease Screening and Surveillance
14:40-15:00	嚴明芳副教授 / 臺北醫學大學口腔衛生學系	Stochastic Model for Overdiagnosis in Disease Screening and Surveillance
15:00-15:20	許辰陽助理教授 / 國立臺北護理健康大學	Efficient Sampling-design in Multistate Disease Process for Screening and Surveillance
15:20-15:40	賴昭智主任 / 台北市立聯合醫院緊急醫療部	Stochastic Differential Equation Model for Disease Surveillance
15:40-16:00	Coffee Break	
16:00	主持人：陳華鍵執行長 / 行動基因生技股份有限公司	**Session 10 : Medical Product Developments and Related Topics**
16:05-16:30	楊進木教授 / 國立交通大學生物科技學系（所）	Molecular Interaction Family for Systems Biology and Drug Design
16:30-16:55	郭立威助研究員 / 國衛院生醫工程與奈米醫學研究所	Exploring Human Brain Networks with Advanced MR Neuroimaging Technology
16:55-17:20	盧鴻興教務長（教授）/ 國立交通大學（統計學研究所）	On AI for Medical Images

開場致詞　梁賡義院長

Name

Keng-Yee Liang 梁賡義

Position Title / Affiliations

President / National Health Research Institutes

Education and Degrees

1982	Ph.D., Biomathematics – Biostatistics, University of Washington, Seattle, Washington, USA
1979	M.S., Statistics, University of South Carolina, Columbia, South Carolina, USA
1973	B.A., Mathematics, National Tsing Hua University, Hsin Chu, Taiwan, R.O.C.

Professional Experience

2010/08-2017/11	President, National Yang-Ming University, Taiwan, R.O.C.
2003/08-2006/08	Vice President (Acting President, January 1 to June 30, 2006), National Health Research Institutes, Taiwan, R.O.C.
1982-2010	Professor, Department of Biostatistics, Bloomberg School of Public Health, The Johns Hopkins University

Honor and Award

1990	American Public Health Association's Spiegelman Award for outstanding accomplishments in the field of health statistics.
2002	Elected Academician, Academia Sinica, Taiwan, R.O.C.
2010	American Public Health Association’s Rema Lapouse Award for significant contributions to the scientific understanding of the epidemiology and control of mental disorders.
2012	Elected Member, the Academy of Sciences for the Developing World (TWAS)
2015	International Statistical Institute’s Karl Pearson Prize for contemporary research contribution that has had profound influence on statistical theory, methodology, practice, and/or applications
2015	Elected Member, the National Academy of Medicine (NAM)
2016	Heritage Award, Johns Hopkins University
2016	Elected Member, Society of Scholars, Johns Hopkins University

Research Interest

Biostatistics, Psychiatric and Genetic Epidemiology

Session 1 : Precision Medicine and Clinical Trial

主持人　司徒惠康副院長

Name

Huey-Kang Sytwu 司徒惠康

Position Title / Affiliations

國家衛生研究院 副院長

Education and Degrees

1997	博士 , 美國史丹福大學微生物及免疫學研究所
1987	醫學士 , 國防醫學院醫學系

Professional Experience

2018- 迄今	副院長 , 國家衛生研究院
2018- 迄今	特聘研究員 , 國家衛生研究院感染症及疫苗研究所
2004- 迄今	講座教授 , 國防醫學院梁序穆暨許織雲基金會
2013-2018	校長 , 國防醫學院
2013-2018	所長 , 國防醫學院與中央研究院及國家衛生研究院合辦生命科學研究所
2004- 迄今	教授 , 國防醫學院微生物暨免疫學研究所

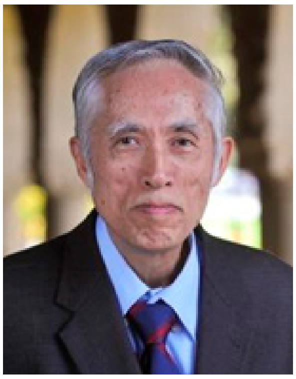
Research Interest

免疫學

自體免疫疾病

基因操控

醫學教育



Name

Tze Leung Lai

Position Title / Affiliations

Ray Lyman Wilbur Professor of Statistics / Department of Statistics, Biomedical Data Science, and Computational & Mathematical Engineering, Stanford University, USA

Education and Degrees

1967	University of Hong Kong, B.A. with First Class Honors
1970	Columbia University, M.A.
1971	Columbia University, Ph.D.

Professional Experience

1996-2006	Advisory Committee Member, National Health Research Institute, Taipei
1992-present	1992-present Advisory Committee Member, Institute of Statistical Science, Academia Sinica
1991-present	External Assessor, Chinese University of Hong Kong
1999-2014	Steering Committee Member, Interdisciplinary Program in Financial Mathematics, Stanford
2001-2004	Chair, Department of Statistics, Stanford
2005-2008	External Examiner, Risk Management Science Program, Chinese University of Hong Kong
2005-2008	Steering Committee Member, Methods of Analysis Program in the Social Sciences, Stanford
2005-2014	Director, Interdisciplinary Program in Financial Mathematics, Stanford
2005-present	Co-director, Biostatistics Core, Stanford Cancer Institute
2007-present	Professor, by courtesy, of Health Research and Policy, Stanford School of Medicine
2009-present	Professor, by courtesy, of the Institute of Computational and Mathematical Engineering, Stanford School of Engineering
2009-present	Co-director, Center for Innovative Study Design, Stanford School of Medicine
2010-present	International Advisory Committee Member, Center for Statistical Sciences, Peking University
2011-present	Advisory Board Member, Department of Statistics and Actuarial Sciences, University of Hong Kong
2011-present	Advisory Committee Member, Institute of Mathematical Research, University of Hong Kong
2011-present	Chair, Pao-Lu Hsu Distinguished Lecture Series in Statistics and Probability, Center for Mathematical Sciences, Tsinghua University, Beijing
2012-present	International Advisory Committee Member, Mathematical Sciences Center, Tsinghua University
2012-present	Director, Financial and Risk Modeling Institute, Stanford University
2014-present	Co-chair, Steering Committee, Mathematical and Computational Finance Program, Stanford

Research Interest

My present research areas include sequential experimentation, adaptive design and control, stochastic optimization, time series analysis and forecasting, change-point detection, hidden Markov models and particle filters, empirical Bayes modeling, multivariate survival analysis, probability theory and stochastic processes, biostatistics, econometrics, quantitative finance and risk management. My methodological research in these areas has been motivated by and is closely related to my applied interests in engineering, finance, and the biomedical sciences. As director of the Financial Mathematics Program, co-director of the Biostatistics Core of the Stanford Cancer Institute, and co-director of the Center for Innovative Study Design in the Stanford School of Medicine, I am involved in multiple research projects in these fields.

Adaptive Design of Affordable Clinical Trials Using Master Protocols in the Era of Precision Medicine

Prof. Tze Leung Lai

Department of Statistics, Biomedical Data Science, and Computational & Mathematical Engineering, Stanford University, USA

Advances in pan-omic technologies and systems biology have led to novel therapies in the era of precision medicine. After describing the challenges in designing randomized controlled trials to evaluate these new treatments, such as recruiting patients with rare genetic subtypes of a disease and the eventual unaffordability of the treatment, we give a brief review of recent developments in master protocols for umbrella, basket, and platform trials to address these challenges. We then introduce innovative adaptive designs of basket trials, which we illustrate with a master protocol of a clinical trial to evaluate the effect of a CK2 inhibitor on four baskets of cancers involved in the hedgehog pathway for pediatric patients.

Name

Chao Agnes Hsiung

Position Title / Affiliations

Distinguished Investigator and Director /
Institute of Population Health Sciences,
National Health Research Institutes, Taiwan

Education and Degrees

1972	B.S., Mathematics, National Tsing-Hua University, Taiwan
1973	M.A., Statistics, Columbia University, U.S.A.
1975	Ph.D., Statistics, Columbia University, U.S.A.

Professional Experience

2010-present	Distinguished Investigator and Director, Institute of Population Health Sciences, National Health Research Institutes, Taiwan
2008-2010	Distinguished Investigator and Acting Director, Institute of Population Health Sciences, National Health Research Institutes, Taiwan
2005-present	Adjunct Professor, Institute of Statistics and Department of Life Science, National Tsing-Hua University, Taiwan
2002-2014	Distinguished Investigator and Director, Division of Biostatistics and Bioinformatics, National Health Research Institutes, Taiwan
1985-1997	Research Fellow, Institute of Statistical Science, Academia Sinica, Taiwan

Research Interest

Dr. Hsiung's current research interests include genetic epidemiology and genomics research. Her research team has established the Healthy Aging Longitudinal Study in Taiwan(HALST). Many aspects of aging including nutrition, life style, biomarkers etc. have been studied through this cohort study. Her research team has also participated in the international genetic study – Stanford-Asian Pacific Program in Hypertension and Insulin Resistance (SAPPHIRe), and later extended to TAICHI study on Metabochip, THRV study on rare variants in hypertension among Chinese. Collaborating with several medical centers in Taiwan, rich clinical, environmental and genetic data were collected and analyzed. The research team has also established the Genetic Epidemiological Study of Lung Adenocarcinoma (GELAC) with six hospitals in Taiwan. Recently they have collaborated with NCI of NIH-US on non-smoking female lung cancer and other topics. The research team has published a series papers on genetic determinants of lung cancer, including the recent papers published in Nature Genetics, PLoS Genetics, Human Molecular Genetics etc. They have also worked on pharmacogenomics topics for lung cancer, some of the work was published in AJRCCM.

Lung Cancer Pharmacogenomics - An Integrative Analysis of Patient Survival, Genetic Variants, and Gene Expression

Chao A. Hsiung
Institute of Population Health Sciences, National Health Research Institutes

This work resulted from integrative analyses of several association studies based on different high-throughput genome-wide data. Patients with non–small cell lung cancer (NSCLC) with mutated epidermal growth factor receptor (EGFR) are relatively sensitive to EGFR–tyrosine kinase inhibitor (TKI) treatment and have longer progression-free survival (PFS) when treated with EGFR-TKI compared with platinum-based chemotherapy. However, many patients with advanced NSCLC who have mutated ***EGFR*** do not respond to first-line EGFR-TKI treatment and still have short PFS. The aim of this study was to identify genetic variants associated with PFS among never-smoking lung adenocarcinoma patients treated with first-line EGFR-TKIs.

A genome-wide association study on PFS was performed in never-smoking female lung adenocarcinoma treated with first-line EGFR-TKIs. Significant single-nucleotide polymorphisms (SNPs) were selected for follow-up association analysis and for replication assay in another independent cohort.

We identified SNPs at 4q12 associated with PFS at genome-wide significance ($P<10^{-8}$) and with an estimated hazard ratio of more than 4. This association was also replicated in a larger but similar cohort and in an independent NSCLC cohort. Follow-up functional analyses based on gene expression array data showed that these SNPs were associated with the expression of ***EGFR***, which encodes the TKI target, and with a nearby gene neuromedin-U, which encodes a G protein–coupled receptor ligand known to be involved in the progression of NSCLC. Considering these genetic variants in 4q12 as possible prognostic biomarkers for the treatment of patients with late-stage lung cancer, they merit further investigation to assess their potential as pharmacogenomic predictors for patients treated with TKI therapy. The result served as an example for precision medicine in late-stage lung adenocarcinoma.

Name

徐麗娟

Position Title / Affiliations

副執行長 / 財團法人醫藥品查驗中心

Education and Degrees

中國醫學大學 醫學系

Professional Experience

ICH E17 MRCT 台灣專家代表
台大醫院家庭醫學部兼任主治醫師
國立台灣大學醫學院藥學系暨臨床藥學研究所臨床藥學指導教師
財團法人醫藥品查驗中心 臨床組審查員
財團法人醫藥品查驗中心 臨床組小組長
財團法人醫藥品查驗中心 新藥科技組組長

Research Interest

藥品法規科學、家庭醫學

論文及著述

1. 降血壓藥物之臨床審查注意事項——新藥開發與臨床試驗，第 277-284 頁
2. 降血壓複方藥物——新藥開發與臨床試驗，第 284-288 頁
3. 靜脈營養製劑之臨床考量——新醫藥品法規科學論文集，第 193-188 頁
4. 新成分新藥查驗登記療效及安全性之考量重點——食品藥物管理署 2012 年公告
5. 固定複方藥物與法規科學考量—— page 1-7, RegMed 2012 Vol.15
6. 萊克多巴胺與人體癌症之相關性評估報告—— page 6-11,RegMed 2013 Vol.36

Real World Evidence in Drug Review

徐麗娟副執行長
財團法人醫藥品查驗中心

傳統藥品研發者常以典型的隨機分派、雙盲、安慰劑或活性對照之試驗提供藥品主要療效及安全性證據以支持藥品上市，這樣的試驗設計無疑提供新成分新藥最堅實的療效證據，其缺點在這樣嚴格控管的試驗環境與將來上市後多樣的臨床使用情境差異很大，例如併用藥物及共病狀態在臨床使用時要相較臨床試驗執行時複雜許多，也間接影響臨床試驗情境所產生之療效及安全性資訊外推至有此適應症之所有病人。

另一方面在臨床治療時會紀錄病歷資料，申請保險給付時會使有健保資料，甚至因不同目的而登錄的疾病資料都是隨手可得的真實世界數據， 這些資料相較臨床試驗可能更真實地反映病患治療的成效。法規單位過往已經接受真實世界數據 / 資料可佐證藥品的部份安全性資料，如上市後安全性通報，然而若欲支持療效，其資料之品質及分析方式至為重要，否則可能產生偏差而得到錯誤的結論。

國外已有法規單位公告如何收集品質良好的真實世界數據 / 資料支持醫材的查驗登記，查驗中心亦將研擬「真實世界數據 / 證據」相關研發策略指導原則供業界參考，希冀減少藥物研發成本，促使有效藥物早日上市，嘉惠病患。

Session 2 :
Big Data and AI in Health Industry

主持人 熊昭所長

Name

Chao Agnes Hsiung

Position Title / Affiliations

Distinguished Investigator and Director /
Institute of Population Health Sciences,
National Health Research Institutes, Taiwan

Education and Degrees

1972	B.S., Mathematics, National Tsing-Hua University, Taiwan
1973	M.A., Statistics, Columbia University, U.S.A.
1975	Ph.D., Statistics, Columbia University, U.S.A.

Professional Experience

2010-present	Distinguished Investigator and Director, Institute of Population Health Sciences, National Health Research Institutes, Taiwan
2008-2010	Distinguished Investigator and Acting Director, Institute of Population Health Sciences, National Health Research Institutes, Taiwan
2005-present	Adjunct Professor, Institute of Statistics and Department of Life Science, National Tsing-Hua University, Taiwan
2002-2014	Distinguished Investigator and Director, Division of Biostatistics and Bioinformatics, National Health Research Institutes, Taiwan
1985-1997	Research Fellow, Institute of Statistical Science, Academia Sinica, Taiwan

Research Interest

Dr. Hsiung's current research interests include genetic epidemiology and genomics research. Her research team has established the Healthy Aging Longitudinal Study in Taiwan(HALST). Many aspects of aging including nutrition, life style, biomarkers etc. have been studied through this cohort study. Her research team has also participated in the international genetic study – Stanford-Asian Pacific Program in Hypertension and Insulin Resistance (SAPPHIRe), and later extended to TAICHI study on Metabochip, THRV study on rare variants in hypertension among Chinese. Collaborating with several medical centers in Taiwan, rich clinical, environmental and genetic data were collected and analyzed. The research team has also established the Genetic Epidemiological Study of Lung Adenocarcinoma (GELAC) with six hospitals in Taiwan. Recently they have collaborated with NCI of NIH-US on non-smoking female lung cancer and other topics. The research team has published a series papers on genetic determinants of lung cancer, including the recent papers published in Nature Genetics, PLoS Genetics, Human Molecular Genetics etc. They have also worked on pharmacogenomics topics for lung cancer, some of the work was published in AJRCCM.

Name

Michel Chu　瞿志豪

Position Title / Affiliations

General Partner / Acorn Campus Taiwan
Chief Innovation Officer / Biomedical Development Board Taiwan
Chairman / VSense Limited
合夥人 / 橡子園創投
創新長 / 生醫創新方案執行中心
董事長 / 永加利醫學科技股份有限公司

Education and Degrees

PhD candidate, Institute of International Business, National Taiwan University
MBA, Executive MBA program, School of Management, National Taiwan University
PhD candidate, Electrical Engineering, National Taiwan University
M.S., Electrical Engineering, National Taiwan University
B.S., Electrical Engineering, National Taiwan University

Professional Experience

Michel Chu is a serial entrepreneur and currently a General Partner at Acorn Campus Taiwan, a leading early-stage venture capital. Michel co-founded GigaMedia (NASDAQ: GIGM), the only NASDAQ-listed Internet company in Taiwan, and led the company through a US$4B IPO in 2000. From 2004, Michel also served as the Executive Vice President of GigaMedia in charge of strategic planning, M&A and corporate management. Michel also founded and currently serves as the Chairman of VSense, a diagnostics company developing semiconductor-based biosensors. In addition, Michel is facilitating innovation in Taiwan's healthcare sector in his capacity as the Chief Innovation Officer of Taiwan's Biomedical Development Board.

Michel has extensive domain expertise in diverse fields including medical devices, cloud computing and mobile Internet. He has been an active angel investor with 15+ years of experiences of coaching, building, inspiring and accelerating entrepreneurial teams. Michel is currently an adjunct faculty of National Taiwan University, giving courses on Multi-sided Platforms, Biodesign for Medical Devices, Entrepreneurship, Group Dynamics and Leadership.

Artificial Intelligence in Healthcare: Opportunities and Challenges

瞿志豪創新長
科技部生醫創新執行中心

The application of artificial intelligence in healthcare has been widely anticipated. AI technology has already been used in multiple areas to improve patient medical records, care delivery, diagnostic accuracy, and drug development. However, the healthcare system is also widely known for its ultra-conservatism, and every application of AI in healthcare is regulated by that fundamental philosophy. We those in mind, we will talk about areas of opportunities where medical AI may perform best, as well as their respective risks and challenges.

Name

郭彤

Position Title / Affiliations

大中华区商务发展副总裁，IQVIA（原昆泰艾美仕）

Education and Degrees

加拿大麦吉尔大学，生物统计学博士
加拿大麦吉尔大学，生物统计学硕士

Professional Experience

2016.4 至今	IQVIA 亚太及非洲生物统计 执行总监
2015.4 至今	拜耳医药保健有限公司北京国际研发中心数据科学与分析 亚太总监
2013.1 至今	上海康德保瑞医学临床研究有限公司临床信息及 FSP 业务部门 公司副总裁，及临床信息及 FSP 业务部门负责人
2012.8-2013.1	高知特信息技术 (上海) 有限公司生物统计及生命科学 BPS 部门 部门主管

Research Interest

郭彤博士具有近二十年的国际大制药公司新药研发经验。曾任拜耳医药保健有限公司北京国际研发中心，数据科学与分析亚太总监；上海康德保瑞医学临床研究有限公司副总裁，临床信息及 FSP 业务部门负责人；高知特信息技术 (上海) 有限公司生物统计及生命科学 BPS 部门主管；美国百时美施贵宝主任生物统计师及美国强生研发总部生物统计师；并在加拿大麦科马思特大学心血管项目中心及兰州生物制品研究所从事过研究工作。主持过多个全球多中心临床试验的统计设计及分析。特别是对生物统计及大数据分析在生命科学及新药研发上的应用方面颇具建树。

Big Data and Artificial Intelligence in Site Identification and Patient Recruitment

郭彤博士
IQVIA 大中華區商務發展副總裁

In the recent years, we have observed rapid development for the use of Artificial Intelligence, machine learning and advanced analytics to improve the performance clinical research. AI-powered applications can help better manage the operational health of a trial by improving site identification and patient enrollment, site performance and feasibility. This session focuses on how to effectively implement big data analytics and AI in clinical research, by merging “big data” access, artificial intelligence and cognitive computing with the therapeutic expertise and clinical trial operational capabilities. This session will share real examples of how the cutting-edge platform and AI can be used to improve clinical research for faster and higher quality outcomes.

Name

Kang Liu

Position Title / Affiliations

CSO/ 台灣雲檢股份有限公司

Education and Degrees

1986	Beijing Medical College, Dept. of Medicine
1996	The University of Lowa, PhD
1997	Institute of Computational Biomedicine, UI NIH Postdoc

Professional Experience

2017–Present	CSO, mProbe TaiWan Inc.
2011–2016	Director of ClinGen, Stanford University, CA USA
2008–2010	R&D Director, HBI Solutions, Palo Alto CA USA
2001–2007	Sr. Research Scientist, Dept. of Genetics, Stanford University
1997–2000	Research Scientist, Dept. of Genetics, UI

Research Interest

- 利用多組學大數據和人工智慧建立慢性病的數字模型
- 高通量質樸靶在蛋白體和小分子代謝體的靶向（Targeted）和非靶向（Untargeted）定性和定量研究
- 高通量質樸的 QC 和 Normalization

Multi-Omics and AI on Translational Medicine Research and Application

Dr. Kang Liu
台灣雲檢股份有限公司

多組學（Multi-omics）研究統籌測量和分析基因、蛋白、多肽、小分子代謝物、腸道菌群、環境致病物等多類人體內外物質的信息，單次檢測就可以形成百萬級別的數據量，傳統的生物統計方法很難有效處理，而人工智慧（AI）在此即可發揮重大作用。

台灣雲檢公司利用 AI 深度學習（Deep Learning）分析多組學檢測、臨床電子病歷（EMR）、病史資料、個人信息（Demographic）等多種數據，開發出 100 餘種疾病的數字模型，可進一步應用於發病風險評估、早期診斷、個人化治療、預後評估等多方面。

在此，我們將在方法學、基本流程、核心要素等幾個方面概要介紹多組學檢測、AI 分析和疾病模型的開發和應用。

Session 3A :
Big Data Analytics in Bioinformatics

主持人 楊欣洲研究員

Name

Hsin-Chou Yang 楊欣洲

Position Title / Affiliations

Research Fellow / Institute of Statistical Science, Academia Sinica (研究員 / 中研院統計所)

Education and Degrees

1990.09 – 1994.06	B.B., Department of Statistics, National Cheng Kung University
1994.09 – 1996.06	M.B., Graduate Institute of Statistics, National Cheng Kung University
1996.09 – 2002.07	Ph.D., Institute of Statistics, National Tsing Hua University

Professional Experience

2018.01 – Present	Research Fellow. Institute of Statistical Science, Academia Sinica
2017.12 – Present	Joint Associate Professor. Institute of Public Health, National Yang-Ming University
2016.12 – Present	Core Faculty. Data Science Program, Degree Program, Academia Sinica & National Taiwan University
2016.02–Present	Adjunct Associate Professor. Institute of Statistics, National Tsing Hua University
2015.02–Present	Joint Associate Professor. Institute of Statistics, National Cheng-Kung University
2012.09–Present	Adjunct Associate Professor. School of Public Health, National Defense
2011.02–Present	Core Faculty. Translational Medicine Program, Degree Program, Academia Sinica
2008.02–Present	Core Faculty. Bioinformatics Program, Taiwan International Graduate Program, Academia Sinica
2014.09 – 2017.12	Adjunct Associate Professor. Institute of Public Health, National Yang Ming University
2011.03 – 2018.01	Associate Research Fellow. Institute of Statistical Science, Academia Sinica
2006.07 – 2011.03	Assistant Research Fellow. Institute of Statistical Science, Academia Sinica
2004.07 – 2006.06	Postdoctoral Fellow of Academia Sinica (in Institute of Biomedical Sciences, Academia Sinica) [In military service]
2002.10 – 2004.06	Postdoctoral Fellow of National Science Council (in Institute of Biomedical Sciences, Academia Sinica) [In military service]

Research Interest

Statistical genomics, Bioinformatics

Name

H. Sunny Sun

Position Title / Affiliations

Professor and Director, Institute of Molecular Medicine, National Cheng Kung University

Education and Degrees

1991/09-1996/03	Ph.D, Department of Animal Sciences/Genetics University of Wisconsin-Madison, USA.
1989/10-1991/05	MS, Department of Animal Sciences, University of California-Davis, USA

Professional Experience

2016/8 ~	Director, Institute of Molecular Medicine, National Cheng Kung University
2011/8 ~	Director, Center for Genomic Medicine, National Cheng Kung University
2007/8 ~	Professor, Institute of Molecular Medicine, National Cheng Kung University
2003/08 ~ 2007/7	Associate Professor, Institute of Molecular Medicine, National Cheng Kung University
1998/08 ~2003/07	Assistant Professor, Institute of Molecular Medicine, National Cheng Kung University
1996/03 ~1998/02	Postdoctoral fellow, Department of Animal Sciences, Iowa State University, USA

Research Interest

1.Genomic medicine
2.Bioinformatics
3.Molecular genetics
4.Comparative genomics

Application of NGS-based Test in the Preimplantation Genetic Screening

孫孝芳教授 / 所長
國立成功大學醫學院分子醫學研究所

The rapid development of genomic technology has made the twenty-first century the most prominent century for the scientific research in genomic medicine. Technical advances by means of next generation sequencing (NGS) technologies improve the capacity to detect and quantify genetic variants, including germline and somatic mutations and polymorphisms, across the genome. The growing number of publications and patents indicate that application of NGS-based molecular testing to assist accurate diagnosis of disease incidence, the degree of prognosis or the most appropriate treatment for individual disease is inevitable in the future trend. And it is the main spirit of “Precision Medicine”. A number of NGS applications with established values are already available in the market such as diagnosis of cancers and personal genomics. The commercial availability points out the NGS application is in its transition from bench to the bed-site and directs toward a value for clinical routines. For the foreseeable future, NGS-based molecular testing will be as common as the current biochemical tests or general physical examination. The application of genomics in preventive medicine, especially in prenatal care, is particularly important. The development of NGS-based prenatal testing through the use of as little as 1-10 cells from a single embryo to detect whether the embryo has chromosomal abnormalities provides several advantages over the traditional approaches. As NGS-based preimplantation genetic screening has shown greatly improved the chance of pregnancy and the birth of a healthy baby, it becomes increasingly indispensable and a trend leader in the treatment of infertile patients. This presentation will introduce the development of NGS technology and its application in personalized precision prenatal medicine.

Name

Ren-Hua Chung 鍾仁華

Position Title / Affiliations

Associate Investigator / National Health Research Institutes

Education and Degrees

North Carolina State University, PhD in Bioinformatics
University of California at Davis, MS in Computer Science
National Chiao-Tung University, BS in Computer Science

Professional Experience

2012/2 ~ Now	Associate Investigator, National Health Research Institutes
2008/4 ~ 2011/12	Assistant Professor, University of Miami Miller School of Medicine
2007/1~2008/3	Postdoctoral Fellow, Duke University

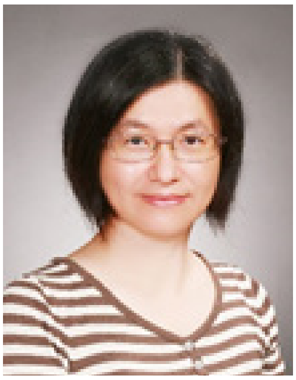
Research Interest

Multi-omics data simulation and analysis, big data analysis, statistical genomics, bioinformatics

A Large-scale Genetic Association Study for Fasting Glucose from Multiple Cohorts

鍾仁華副研究員
國家衛生研究院群體健康科學研究所

Complex traits, such as blood pressure, fasting glucose, and type 2 diabetes are caused by multiple factors such as environment, genetics, and epigenetics. Genome-wide association studies (GWAS), which aim to identify common genetic variants associated with the complex traits, have been widely adopted for genetic studies. Furthermore, with the advancement of next-generation sequencing (NGS), whole-exome or whole-genome sequencing has also become possible. In this study, we took advantages of three GWAS cohorts and an NGS cohort to investigate the genetic roles in fasting glucose in terms of copy number variations (CNVs), common SNPs, gene-gene interactions, and rare variants. We developed a family-based CNV association test and identified deletions in the SFMBT1 gene that significantly lowered the fasting glucose level in a family cohort. The results were validated by PCR-based amplification and replicated in another population-based cohort. We also performed genotype imputations and meta-analysis for the GWAS cohorts and identified some novel candidate SNPs for fasting glucose. These SNPs explain approximately 5% of phenotype variation in fasting glucose, and genetic risk scores constructed based on these SNPs show prediction ability for diabetes development. We also developed a powerful gene-gene interaction test, which can incorporate protein-protein interactions, for quantitative trait. The test was applied to a GWAS cohort and some promising gene-gene interactions were identified. Finally, we performed gene-based association tests using the NGS cohorts and some promising genes with rare variants were identified for fasting glucose.



Name

I-Ping Tu 杜憶萍

Position Title / Affiliations

研究員兼副所長 / 中研院統計所

Education and Degrees

9/92--6/97	Ph.D. in Statistics, Stanford University
9/89--6/91	M.S. in Physics, National Taiwan University
9/85--6/89	B.S. in Physics, National Taiwan University

Professional Experience

May. 2013 ~ present	Research Fellow, The Institute of Statistical Sciences, Academia Sinica
Aug. 2003 ~ May. 2013	Associate Research Fellow, The Institute of Statistical Sciences, Academia Sinica

Research Interest

My research has mainly focused on developing statistical methods to analyze cryo-electron microscopy (cryo-EM) image data. In recent years, technical breakthrough has transformed cryo-EM to become a main tool for determination of molecular structure to atomic resolution without crystals or in solution. However, the process of structural determination from single-particle cryo-EM images is still very challenging because it involves processing extremely noisy images of unknown orientation. We have developed dimension reduction and clustering algorithms for highly noise image data. We will continue exploring statistical machine learning methods to improve the image analysis.

Statistical Analysis for cryo-Electron Microscopy Images

杜憶萍研究員兼副所長
中央研究院統計科學研究所

In the field of structural biology, X-ray crystallography and NMR spectroscopy have been two major high-resolution techniques. The former requires crystallization of macromolecules while the latter is a solution method but would meet limit when the macromolecule is large. Very recently, breakthrough in the camera together with microscopy automation, advancement of algorithm and GPU-accelerated computations has transformed cryo-EM to become a standard technique to solve structures of macro- molecules at near atomic resolution. In contrast to X-ray crystallography, single particle cryo-EM does not need crystalline sample because it focuses the transmitted electrons to directly provide electron density information of a macromolecule. As a result, single particle cryo-EM has been highlighted as the method of 2015 by Nature Method and awarded Nobel Prize in chemistry in 2017. Because biological molecules are extremely vulnerable, very low doses of electrons are used by cryo-EM, leading to very noisy images. In this talk, we will present our experiences in data analysis for cryo-EM images.

Session 3B : Analytic Methods for Infectious Diseases

主持人 廖經倫所長

Name

Ching-Len Liao

Position Title / Affiliations

Investigator and Director/National Institute of Infectious and Vaccinology

Education and Degrees

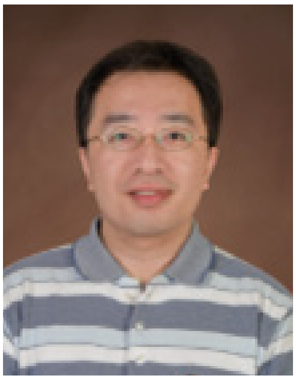
1973-1977	BS, School of Pharmacy, National Defense Medical Center (NDMC).
1983-1985	MS, Graduate Institute of Microbiology and Immunology, NDMC.
1990-1994	PhD, Department of Microbiology and Immunology, School of Medicine, University of Southern California.

Professional Experience

2000-2008	Professor and Chairperson, Department of Microbiology and Immunology, NDMC.
2009-present	Professor, Department of Microbiology and Immunology, NDMC.
2014-present	Director, National Institute of Infectious Diseases and Vaccinology, NHRI.
2015-present	Director, National Mosquito-Borne Diseases Control Research Center, NHRI.

Research Interest

Molecular Virology; Vaccinology for Influenza, JEV, and Dengue Viruses; Viral Pathogenesis



Name

林培生 Pei-Sheng Lin, PhD

Position Title / Affiliations

研究員 / 國家衛生研究院群體健康科學研究所

Education and Degrees

美國威斯康辛大學統計系 博士

Professional Experience

國家衛生研究院群體健康科學研究所 副研究員
國家衛生研究院群體健康科學研究所 助研究員

Research Interest

空間統計、時間空間隨機模型、環境統計、流行疾病監測資料分析

主要成就：

林培生博士於美國威斯康辛大學統計系獲得統計博士學位後，主要的研究領域在於發展統計方法去分析具有時間和空間相關性的資料。除了發展數理統計模型之外，林博士也同時應用這些統計方法於不同的科學領域，包括發表研究論文於疾病監測模型、生態與環境研究、基因表現關聯性和功能性核磁共振等領域上。近年來，林博士也參與在國家蚊媒傳染病防治的研究計畫中，以大數據資料方法建立風險預測模型。

An Integrated Surveillance System for Dengue Control

林培生研究員
國家衛生研究院群體健康科學研究所

由於全球暖化和氣候變遷等影響，過去主要盛行於熱帶蚊媒傳染病，如茲卡和登革熱，也開始受到整個國際的關注。而台灣在 2014 年和 2015 年的南部登革熱大爆發後，中央政府在多位專家學者的建議下成立了病媒蚊防治中心。由於目前並沒有有效的登革熱疫苗，因此建立整合性的疾病監測系統以作為清除孳生源和化學防治的依據就成為一項重要的課題。在此計畫中，我們利用大數據資料的原則，建立一個多重性的整合系統以進行數位化資料收集、雲端儲存、多變向的整合整合庫、數據分析和疫情變化的視覺化呈現。我們發展擴散模型以捕捉疫情的區域性變化。同時，我們根據地方政府的需求建立數理統計模型以探索登革熱風險因子 (如四米窄巷、老舊房屋型態、降雨、蚊媒密度等因子) 是否與登革熱疫情有關。而為了能提供科學性的證據來協助地方政府之防疫工作，對於所蒐集到的資料需要先進行資料品質評估，以減少資料的錯誤率和增加資料的完整性與正確性。

Name

Ta-Chien Chan 詹大千

Position Title / Affiliations

Associate Research Fellow / Research Center for Humanities and Social Sciences, Academia Sinica

Education and Degrees

June 2010	Ph.D., Institute of Epidemiology, National Taiwan University, Taipei, Taiwan
June 2006	M.S., Institute of Health Informatics & Decision Making, National Yang Ming University, Taipei, Taiwan
January 2004	B.A., Division of Public Administration, Department of Political Science, National Taiwan University, Taipei, Taiwan
January 2004	B.S., Department of Public Health, National Taiwan University, Taipei, Taiwan

Professional Experience

2016/5-present	Associate Research Fellow, Center for Geographic Information Science, Research Center for Humanities and Social Sciences, Academia Sinica, Taiwan
2012/8-2016/5	Assistant Research Fellow, Research Center for Humanities and Social Sciences, Academia Sinica, Nankang, Taipei, Taiwan

Research Interest

Spatial epidemiology; Infectious disease epidemiology; Health informatics on disease surveillance; Spatio-temporal statistics and data visualization; Health disparity of chronic disease; Spatial accessibility of health resources and long-term care; Social network and health behaviors

從個人到群體的流感傳播
Influenza transmission from individuals to groups

詹大千副研究員
中央研究院人文社會科學研究中心

流行性感冒的流行每年在全球造成極大的疾病負擔與經濟的損失，各國政府除了疫苗政策、抗病毒藥物等藥物方面的提供外，個人的自我防護、停課政策、疫情的早期監測、非傳統的疾病監測方式 (庶民監測) 等策略也都是降低流感傳播風險與早期預警的重要資訊，台灣擁有健康保險資料、急診症候群監測系統、肺炎與流感死亡率監測系統、法定傳染病通報系統、學童傳染病通報系統等跨不同時空解析度的大數據，群體的資料若能善用進行即時的監測與預警，將能爭取時間進行疫情的防治，本次演講中，將自全民健保資料的鄉鎮市區尺度出發，接著降尺度到醫院急診室與學校症候群監測系統，最後將以線上個人長期追蹤的點日記 (ClickDiary) 資料，反映個體層級流感傳播的可能危險因子，期望透過本次分享，讓聽眾了解在不同的大數據底下，如何觀察流感的傳播動態。

參考文獻 :

1. Ta-Chien Chan, Tsuey-Hwa Hu, Jing-Shiang Hwang*, 2018, “Estimating the Risk of Influenza-Like Illness Transmission Through Social Contacts: A Web-Based Participatory Cohort Study”, JMIR Public Health and Surveillance, 4(2):e40, 1-11.
2. Ting-Chia Weng, Ta-Chien Chan, Hsien-Tang Lin, Chia-Kun Jasper Chang, Wen-Wen Wang, Zheng-Rong Tiger Li, Hao-Yuan Cheng, Yu-Roo Chu, Allen Wen-Hsiang Chiu, Muh-Yong Yen*, Chwan-Chuen King*, 2015, “Early Detection for Cases of Enterovirus- and Influenza-like Illness through a Newly Established School-based Syndromic Surveillance System in Taipei, January 2010 ~ August 2011”, PLoS One, 10(4): e0122865.
3. Ta-Chien Chan, Yung-Chu Teng, Jing-Shiang Hwang* , 2015, “Detection of influenza-like illness aberrations by directly monitoring Pearson residuals of fitted negative binomial regression models”, BMC PUBLIC HEALTH, 15:168.
4. Kao CL, Chan TC, Tsai CH, Chu KY, Chuang SF, Lee CC, Li ZR, Wu KW, Chang LY, Shen YH, Huang LM, Lee PI, Yang C, Compans R, Rouse BT, King CC, 2012, “Emerged HA and NA mutants of the pandemic influenza H1N1 viruses with increasing epidemiological significance in Taipei and Kaohsiung, Taiwan, 2009-10.”, PLoS one, 7(2), e31162.
5. Chan TC, King CC, Yen MY, Chiang PH, Huang CS, Hsiao CK, 2010, “Probabilistic daily ILI syndromic surveillance with a spatio-temporal Bayesian hierarchical model.”, PLoS one, 5(7), e11626.

Name

Ying-Hen Hsieh 謝英恆

Position Title / Affiliations

Professor / Department of Public Health, China Medical University, Taichung, Taiwan

Education and Degrees

Carnegie-Mellon University, Ph.D. in Applied Mathematics

Professional Experience

2007-present	Professor, Department of Public Health, China Medical University
1987-2007	Professor, Department of Applied Mathematics, National Chung Hsing University

Research Interest

Mathematical and statistical modeling of infectious diseases
Analysis of infectious disease epidemiology relating to public health policies
Mathematical Biology
Population Dynamics
Mathematical Ecology

Modeling Infectious Diseases in the Big Data Era: Challenges and Promises

謝英恆教授
中國醫藥大學公共衛生學系

Although the term “Big Data” has only become popular in the past two decades, the idea of Big Data and the challenge that it begets had already been in existence for several decades. I will outline the challenges that I had encountered personally dealing with big data in infectious disease modeling research for more than two decades, the directions to explore its implications, and the future promises that Big Data has in store for us going forward.

Session 4A :
Smart Device Developments

主持人　林峯輝所長

Name

Feng Huei Lin 林峯輝

Position Title / Affiliations

1. Director, Institute of Biomed Eng & Nanomed., National Health Research Institutes (NHRI), Taiwan
2. Tenure Distinguished Prof., Inst. of Biomed.Eng., National Taiwan University (NTU)

Education and Degrees

1985/09~1989/11	Dept. Mater. Sci., National Cheng-Kung University, Taiwan. Ph.D., Institute of Materials Sciences, Biomaterials
1983/09~1985/06	Dept. Mater. Sci., National Cheng-Kung University, Taiwan. Master, Institute of Materials, Biomaterials
1976/10~1980/06	Dept. Earth Sci., National Cheng-Kung University, Taiwan. Bachelor, Dept Earth Science

Professional Experience

2014/08-	Director, Institute of Biomed Eng & Nanomed., National Health Research Institutes (NHRI), Taiwan
2012/08-	Tenure Distinguished Prof., Inst. of Biomed.Eng., National Taiwan University (NTU)
2017/08-	Executive Yuan Member, Science & Technology Program Executive Review Board, Adjunct Research Fellow office of Ministry Science and Technology, Executive Yuan.
2016/08-2017/07	Lecture Professor, Institute of Technology National United University

Award(s) and honor(s)

1. 2000, 2003, 2009, 2010, 2011 Excellent Teaching Award, National Taiwan University
2. 2004, 2012, 2015 Outstanding Teaching Award, National Taiwan University
3. 2004, 2010, 2015 Outstanding Research Award, Ministry of Science and Technology
4. 2005, 2011, 2016 Outstanding Research Award, National Taiwan University
5. 2008 Taiwan Medicine Society, Dr. Cong-Ming Tu Outstanding Research Award
6. 2012 International Fellow, International College of Biomaterials Science and Engineering
7. 2012 Chau-Jean Lee Research Scholar Award, Society of Biomaterials & Control Release
8. 2013 Far Eastern Y.Z Hsu Science and Technology Memorial Foundation of Lecture Professor Award
9. 2014 International Fellow, World Federation of Preventive & Regenerative Medicine
10. 2016 International Fellow, International Society of Blood Biomaterials (ISBB)
11. 2018 International Fellow, American Institute for Medical and Biological Engineering

Name

詹寶珠

Position Title / Affiliations

司長 / 教育部資訊及科技教育司

Education and Degrees

Ph.D., Department of Electrical Engineering, Texas Tech University, USA
MS, Department of Electrical Engineering, National Cheng Kung University, Taiwan
BS, Department of Electrical Engineering, National Cheng Kung University, Taiwan

Professional Experience

Director General	Department of Information and Technology Education, Ministry of Education, Taiwan
Distinguished Professor	Department of Electrical Engineering, National Cheng Kung University, Taiwan
Vice President	IEEE Computational Intelligence Society (CIS)
President	Chinese Image Processing and Pattern Recognition Society

Research Interest

Dr. Chung's research interests include computational intelligence, medical image analysis, video image analysis, and pattern recognition. She applies most of her research results to healthcare and medical applications. She has been working on medical image analysis using computational intelligence techniques, such as combining probabilistic neural network with fractal dimension on CT images for liver disease analysis, abdominal organ identification using contextual neural network, microcalcification detection and classification from mammograms with shape cognitron neural networks and probabilistic neural networks, spatiotemporal neural networks for detecting recurrent nasal papilloma detection. She also worked on activity pattern analysis for the elderly and have applied it on Alzheimer patient balance and walking pattern analysis, using a designed wearable device. Currently she is working on AI based digital pathology analysis with deep learning neural networks.

When AI Meets Digital Pathology

詹寶珠司長
教育部資訊及科技教育司

While filmless has been widely adopted in radiology and implemented in PACS systems, digital pathology is one potential follower. Advantages of realizing digital pathology are multifold in clinic particularly the easy for tele-consultation, emergency diagnosis, and education. However, there are still concerns and debates about the readiness of broadly adoption of digital pathology. The current trend of AI power is one key momentum pushing pathology going to digitization and the trend is becoming clearer and optimistic. On the other hand, the diagnostic pathology involves both micro cell level features and macro level structure patterns. As such, when AI is applied on digital pathology, considerations to meet such diagnosis necessity have to be taken.

Currently deep convolutional neural networks (DNN) play as the main role in AI for image analysis. The tasks in the context of DP analysis include the detection and counting, segmentation (e.g. of nuclei), and tissue classification (e.g. cancerous vs non-cancerous). One common challenge with DNN training is the requirement of large amount of database. Another problem which will be faced is the variety of the resolution levels, and the decision of the resolution level image for analysis. In this talk we will present the results of our works in terms of the above mentioned task targets using DNN in the analysis of liver digital pathology. The analysis will cover the tasks on micro level analysis and on macro level observations based on the liver pathology characteristics. In this talk issues in the implementation of AI based digital pathology will also be presented, and solutions to address these issues will also be discussed.

Name

Jeen-Shing Wang 王振興

Position Title / Affiliations

Distinguished Professor / Department of Electrical Engineering, NCKU

Education and Degrees

2001 Purdue University Electrical and Computer Engineering PhD
1997 University of Missouri-Columbia Electrical Engineering MSEE
1996 University of Missouri-Columbia Electrical Engineering BSEE

Current Position

1. Distinguished Professor, Department of Electrical Engineering, NCKU
2. Director of Heart Science & Medical Devices Research Center, NCKU
3. Director & CEO of AI Service and Data Center, NCKU

Research Interest

1. Artificial Intelligence
2. Intelligent Control
3. Embedded System and Its Applications
4. Optimization Theory
5. Sensing and Wearable Technology

Applications of Wearable and AI Technology in Sleep Centers

王振興特聘教授
國立成功大學電機工程系

Recent researches have proven that AI-enabled technology has the ability to enhance the capabilities of today's wearable devices and analytics. In this talk, I will first describe the recent effort of my interdisciplinary research team in developing a smart healthcare wearable device and cloud-based services platform. This research project was sponsored by the Ministry of Science and Technology, Taiwan for a three-year term and has developed core technologies and proactive clinical applications implemented at the sleep center of National Cheng Kung University Hospital. Then, I will describe the performance evaluation of the wearable device designed to analyze physiological parameters including activities, pulse rate variability, and SpO2 as well as ideas to integrate AI technology to design a more efficient hospital scheduling and EEG autoscoring methods for the sleep center. Finally, concluding remarks and future research directions are given.

Name

Yung-Nien Sun

Position Title / Affiliations

Principal Investigator
/MOST AI Biomedical Research Center in NCKU

Education and Degrees

1978	B.S. Department of Control Engineering, National Chiao Tung University, Taiwan
1983	M.S. Department of Electrical Engineering, University of Pittsburgh, USA
1987	Ph.D. Department of Electrical Engineering, University of Pittsburgh, USA

Professional Experience

2018/01-present	Principal Investigator, MOST AI Biomedical Research Center in NCKU, Tainan, Taiwan, ROC
2017/02-2017/07	Director, Medical Device Innovation Center, Tainan, Taiwan, ROC
2009/08-2010/07	Vice President, National Pingtung Institute of Commerce, Pingtung, Taiwan, ROC
2007/05-2009/07	Vice Dean, National Cheng Kung University, Tainan, Taiwan, ROC
2002/08-present	Distinguished Professor, National Cheng Kung University, Tainan, Taiwan, ROC
1993/08-present	Professor, National Cheng Kung University, Tainan, Taiwan, ROC
1996-1999	Chairman, Department of Computer Science & Information Engineering, National Cheng Kung University, Tainan, Taiwan, ROC
1989-1993	Associate Professor, National Cheng Kung University, Tainan, Taiwan
1991-1996	Group Leader, Computer & Communication Center, National Cheng Kung University, Taiwan
1987-1989	Assistant Scientist, Brookhaven National Laboratory, Long Island, NY, USA

Research Interest

Image Processing, Deep Learning, Medical Imaging, Industrial Vision, Visual Technology

Deep Learning and Medical Image Analysis

Prof. Yung-Nien Sun
National Cheng Kung University

In recent years, artificial intelligence and deep learning have made major breakthroughs not only in theory but in practical applications. The use of Convolutional Neural Network (CNN) for image processing has especially made great progress. In this presentation, I will illustrate some of the possible applications of deep learning in image analysis and share some recent research on biomedical image analysis at NCKU with you. Three research projects have been investigated in our laboratory. First is to develop the growth parameter assessment and midsagittal plane (MSP) detection for 3D fetal ultrasound image. The second is to develop a training system for trigger finger surgery. And the last is to design and implement an automatic identification systems of Mycobacterium tuberculosis. With the developed CNN systems, image preprocessing is much simplified and the testing results usually have much higher accuracy. It greatly improves the shortcomings of traditional methods. Therefore, we would expect that the deep learning methods will have better applicability and play more important roles in medical image analysis.

Session 4B : Environmental Health

主持人　郭育良所長

Name

Yue-Liang Leon Guo, MD, MPH, PHD

Position Title / Affiliations

Distinguished Investigator and Director
National Institute of Environmental Health Sciences
National Health Research Institutes

Education and Degrees

1982	M.D., National Taiwan University, School of Medicine. Taipei, Taiwan, R. O. C.
1983	M.P.H., Harvard University, School of Public Health. Boston, Massachusetts
1987	Ph.D., Johns Hopkins University, School of Hygiene and Public Health. Department of Environmental Health Sciences, Division of Occupational Medicine Baltimore, Maryland

Professional Experience

2006-2012	Professor and Director, Department of Environmental and Occupational Medicine, National Taiwan University College of Medicine,
2006-present	Distinguished Professor, Department of Environmental and Occupational Medicine, National Taiwan University College of Medicine
2006-present	Clinical Staff, Department of Environmental and Occupational Medicine, National Taiwan University Hospital
2006-present	Clinical Staff, Department of Internal Medicine, National Taiwan University Hospital
2000-2006	Professor and Director, Environmental and Occupational Medicine, National Cheng Kung University Medical College
1990-1995	Associate Professor, Department of Environmental and Occupational Health,National Cheng Kung University Medical College
1995-2006	Professor, Department of Environmental and Occupational Health, National Cheng Kung University Medical College
1990-1996	Director, Department of Environmental and Occupational Health, National Cheng Kung University Medical College
1995	Founder, Graduate Institute for Environmental Health, National Cheng Kung University Medical College
1995-present	Professor, Graduate Institute for Environmental Health, National Cheng Kung University Medical College
1995-1996	Director, Graduate Institute for Environmental Health, National Cheng Kung University Medical College
2000- 2005	Adjunct Professor, Graduate Institute for Clinical Medicine, National Cheng Kung University Medical College
1990-2006	Clinical Staff, Department of Internal Medicine, National Cheng-Kung University Hospital
1999-2006	Chief, Division of Occupational Medicine, National Cheng-Kung University Hospital
2005-2006	Clinical Staff and Director, Department of Environmental and Occupational Medicine, National Cheng-Kung University Hospital
1995-2006	Director, Research Laboratory for Human Health Effects from Exposure to PCBs/PCDFs, National Cheng Kung University
1998-1999	Visiting Scientist, Department of Environmental Health Sciences, Harvard School of Public Health
2001-2003	Department of Occupational Health, Co-supervisor of PHD student Derek Smith, with Professor Atkins, University of South Queensland Project: Skin Conditions in Health Care Workers in Taiwan and in Australia, University of South Queensland
2000-2004	Department of Maternal and Child Health, Co-supervisor of PHD student Iliana del Rio-Gomez, with Professor Tom Marshall, London School of Hygiene and Tropical Medicine Project: Human Reproductive Effects from Exposure to Polychlorinated Biphenyls and Polychlorinated Dibenzofurans

Name

Wang, Yu-Chun 王玉純

Position Title / Affiliations

Professor & Chairman / Dept. of Environmental Engineering,
Chung Yuan Christian University
教授兼系主任 / 中原大學環境工程系

Education and Degrees

2002/08-2007/01	NationalTaiwan University, Taiwan Ph.D., Department of Environmental Health
2000/08-2002/06	National Taiwan University, Taiwan MS, Department of Environmental Health

Professional Experience

2017/08-present	Chung Yuan Christian University, Taiwan Professor and Chairman, Department of Environmental Engineering
2013/08-2017/08	Chung Yuan Christian University, Taiwan Associate Professor, Department of Environmental Engineering

Research Interest

- Environmental health risk assessment / Environmental epidemiology
- Air pollution modeling / Climate change and human health
- Infectious diseases prediction and control

整合環境及健康巨量數據系統性探索氣候變異健康風險關聯性

王玉純教授
中原大學環境工程學系

氣候變遷對全體人類健康的影響是近年世界衛生組織關注焦點，國內多篇研究證實臺灣大氣條件的不同對人體健康風險具有顯著的衝擊與影響，但過往研究多探討特定都會區，目前台灣沒有全面性整體評估氣候變遷對各地區的健康影響程度有多大。在未來氣候變遷趨勢下，已經確定極端溫度及其連續事件，如 : 熱浪，發生的強度將越強，延續時間越長，頻率越高。世界各國預測極端高溫的影響會顯著衝擊世界人群健康。再加上人口老化趨勢，老年人口向來是極端溫度的高風險族群，易受到極端溫度的影響，預測未來氣候變遷的極端溫度健康問題將日益嚴重。本研究整合 1995 年至 2014 年之全台灣大氣環境資料，包含中央氣象局局屬測站每日溫度、降雨量、相對濕度、風速等測值，60 個環保署一般空氣品質監測站每小時懸浮微粒、細懸浮微粒、臭氧及氮氧化物等濃度資訊，以及衛生福利部全台灣死亡統計資料、2300 萬人口健保就醫資訊，利用廣義非線性模型分析地區別每日溫度與氣溫敏感疾病死亡及急診就醫關聯性，並以整合分析估算全台灣疾病別健康損失 (死亡與就醫) 與大氣溫度風險相關性。本研究成果將有助於了解本土溫度敏感疾病之高風險區位及關鍵閾值，可作為本國因應氣候變遷規劃健康調適之基礎資訊。

Name

Chu-Chih Chen 陳主智

Position Title / Affiliations

Investigator/Institute of Population Health Sciences, National Health Research Institutes

Education and Degrees

1988/12- 1993/12	Ph. D., Biostatistics, University of North Carolina-Chapel Hill, USA
1986/08- 1988/12	M. S., Mathematical Statistics, University of North Carolina-Chapel Hill, USA
1979/09- 1983/06	B. S., Applied Mathematics, National Tsing-Hua University, Taiwan

Professional Experience

2014/07-present	Investigator, Division of Biostatistics and Bioinformatics, Institute of Population Health Sciences, National Health Research Institutes, Taiwan
2010/09-present	Adjunct Associate Professor, Institute of Occupational Medicine and Industrial Hygiene, College of Public Health, National Taiwan University
2006/08-2014/06	Associate Investigator, Division of Biostatistics and Bioinformatics, National Health Research Institutes, Taiwan
2008/09-2010/08	Joint Associate Professor, Institute of Occupational Medicine and Industrial Hygiene, College of Public Health, National Taiwan University, Taiwan
2002/08- 2006/07	Professor, Department of Mathematics, Tamkang University, Taiwan
1993/09- 2002/07	Associate Professor, Department of Mathematics, Tamkang University, Taiwan

Research Interest

Dr. Chen's research interests mainly focused on statistical methodologies and applications in the broad area of environmental exposure assessment and related health risk assessment, including benchmark dose modeling, phthalates exposure and risk assessment, food safety, air pollutants and other toxic chemicals. He is also recently interested in statistical modeling on climate change.

Short- and Long-term Prediction of Extremely Hot Days due to Climate Change and Related Attributable Mortality

Chu-Chih Chen

Institute of Population Health Sciences, National Health Research Institutes

Summer days with extremely hot temperature in Taiwan is observed to have been increasing for the past few decades, which is known to worsen heat-related mortality. To reduce corresponding health impact, in this study we developed a statistical state-space model to predict the number of extremely hot days in June-September. Based on historical data of 1951-2017, we estimated the climate change trend after adjusting for nonlinear lagged effect of Nino3.4 index. A state-space model was then built using these two primary influential factors and residual autocorrelations for the prediction. Validation study showed that almost 70% of the predicted hot days for 24 meteorological stations across Taiwan had an average difference within 2 days compared to the observed 3-year average days in 2015-2017. We adopted a comparative risk assessment (CRA) approach using the predicted outcomes to project heat-related attributable mortality (AM) in 2018-2020 relative to the reference period 2001-2010. The results showed that Taipei metropolitan in northern Taiwan is most affected with AMs up to several thousands, followed by Kaohsiung in the south. Statistical downscaling for projections in 2021-2040 and 2041-2060 were also performed based on 8 CMIPS climate models from IPCC.

Name

Shu-Li (Julie) Wang

Position Title / Affiliations

Investigator / Division of Environmental Health and Occupational Medicine, National Health Research Institutes

Education and Degrees

1990/10- 1995/02	Ph.D., Epidemiology and Public Health, University of London, UK
1986/09- 1990/06	B.S, Public Health, National Taiwan University, Taiwan

Professional Experience

2015-present	Adjunct Professor, Center for Environmental Medicine, Kaohsiung Medical University, Taiwan
2013- present	Adjunct Professor, Department of Public Health, National Defense Medical Center, Taiwan
2012-2013	Visiting Scholar, National Institute of Environmental Health Sciences, National Institute of Health (NIEHS/NIH), U.S.A.
2010- present	Professor, Department of Public Health, China Medical University, Taiwan
2009- present	Investigator, Division of Environmental Health and Occupational Medicine, National Health Research Institutes, Taiwan
2004- 2008	Associate Professor, Graduate Institute of Occupational Safety and Health, Kaohsiung Medical University, Taiwan
2004- 2008	Associate Investigator, Division of Environmental Health and Occupational Medicine, National Health Research Institutes, Taiwan
2001- 2002	Adjunct Assistant Professor, Graduate Institute of Public Health, National Cheng Kung University, Taiwan
2000- 2004	Assistant Principal Investigator, Division of Environmental Health and Occupational Medicine, National Health Research Institutes, Taiwan
2000- 2003	Assistant Investigator, Division of Environmental Health and Occupational Medicine, National Health Research Institutes, Taiwan
1997- 2000	Assistant / Associate Professor, Department of Public Health, Chung-Shan Medical University, Taiwan
1996- 1997	Post-doctoral researcher, Division of Epidemiology & Public Health, Institutes of Biomedical Sciences, Academia Sinica, Taiwan
1995- 1996	Post-doctoral researcher, Department of Gerontology, University of Cambridge, U.K

Research Interest

Wang's research interests are mainly on Environmental Children Health with regards to pollutant form air, water, food, climate change, and life styles, and its effects on endocrine system, neuron-cognitive function, immunity (i.e. obesity, behavioral problem, allergic diseases). The approach is primarily from pre-birth cohort, which is the follow-up of children from in utero till adolescents. The studied causation agents include endocrine disruptors (i.e. phthalates, dioxins), metals (lead, arsenic, cadmium), and pathogen (virus). Professor Wang is also interested in searching for environmental factors contributing to the pathogenesis of cardiovascular disease and cancer. The interaction between the environment and genes is investigated to understand how the environment may affect gene expression, and how genetic factors might modify the effect of pollutants.

The research interests might also include environmental and occupational health with regards to electroplating industry, semi-conductor, and epidemiological investigations for residents living with high background exposure level to toxic metals (Changhua) and dioxins (i.e. An-Nan area). It is hoped that the research may help managing the environmental pollutions, preventing the related health effects, and improve health and welfare particularly among maternal and children population.

Environmental, Epigenetic, and Genetic Interactions and Human Health Protection

Shu-Li Julie Wang[1], Chung-Hsing Chen[2], Shih-Sheng Jiang[2], I-Shou Chang, Yuliang Leon Guo[1]

National Institute of Environmental Health Sciences[1],

National Institute of Cancer Research[2],

National Health Research Institutes, Zhunan, Taiwan (slwang@nhri.org.tw)

Human diseases may result from un-favored environmental factors interacted with genetic characteristics. The pathophysiology may associate with altered gene expressions. DNA methylation may serve as relatively stable control for gene expression, as compared to histone modification and micro RNA levels. Recently the fast-improved technique of genome-wide DNA methylation has provided the opportunity to examine the association between altered DNA methylation patterns with environmental pollutants' exposure.

Our 15-year follow-up birth cohort study in Taiwan demonstrated that, prenatal exposure to phthalate plasticizer, was associated with postnatal health effects, including decreased sex hormone levels, reduced reproductive organ growth, increased behavioral problems, decreased intelligent quotients, and allergic symptoms in children. We retrieved archived cord blood DNA samples from 64 mother-children pairs. DNA methylation levels at more than 450,000 CpG sites were measured using Illumina Infinium HumanMethylation450 BeadChips.

We identified 25 CpG sites whose methylation levels in cord blood were significantly correlated with prenatal DEHP exposure. There was significant enrichment of genes involved in the androgen response, estrogen response, and spermatogenesis within those genes showing DNA methylation changes in response to exposure. Specifically, PA2G4, HMGCR, and XRCC6 genes were involved in genes in response to androgen. Another panel of significant altered DNA methylation sites is related to immune function. We recently also reported the example concerning prenatal arsenic exposure, the associated DNA methylations at birth, and thereby increased low-density lipoprotein lipids (LDL) at adolescence.

Taking together, early-life environmental factors may have long-term health effects through altered DNA methylations. This deserve big data analysis input for pathway analyses and parallel studies. Future perspectives are directed to the application of precision medicine, and to form the Asian consortium on cord blood DNA methylation panel.

Session 5A : Regulatory Science & Government Policy

主持人 鄭守夏教授

Name

Shou-Hsia Cheng 鄭守夏

Position Title / Affiliations

Professor and associate dean, Institute of Health Policy and Management, College of Public Health, National Taiwan University

Education and Degrees

1993	Department of Epidemiology and Public Health, School of Medicine, Yale University, United States, PhD.
1987	Institute of Public Health, College of Medicine, National Taiwan University, Taiwan, Master
1983	Department of Public Health, College of Medicine, National Taiwan University, Taiwan, Bachelor

Professional Experience

2004/08-present	Professor, Institute of Health Policy and Management, College of Public Health, National Taiwan University, Taiwan.
2016/08-2017/01	Fulbright Scholar and Takemi Fellow, Harvard Chan School of Public Health, Boston, MA, USA.
2010/08-2016/07	Professor and director, Institute of Health Policy and Management, College of Public Health, National Taiwan University,Taiwan.
2013/01-2015/12	Chairman, National Health Insurance Committee, Ministry of Health and Welfare, Executive Yuan, Taiwan.
2009/09-2010/08	Director General, Bureau of National Health Insurance, Department of Health, Executive Yuan, Taiwan.
2008/05-2009/09	Deputy Minister, Department of Health, Executive Yuan, Taiwan.
2005/03-2008/05	Chairman, National Health Insurance Medical Expenditure Negotiation Committee, Department of Health, Executive Yuan, Taiwan.
1998/07-2008/05	Member, National Health Insurance Research Database working team, National Health Research Institutes (NHRI), Taiwan.
2004/01-2007/12	Associate Editor, Taiwan Journal Public Health, Taiwan.
1998/08-2004/07	Associate Professor, Institute of Health Policy and Management, College of Public Health, National Taiwan University, Taiwan.
1995/08-1998/07	Associate Professor, Institute of Public Health, College of Medicine, National Taiwan University, Taiwan.
1994/08-1995/07	Lecturer, Institute of Public Health, College of Medicine, National Taiwan University, Taiwan.

Research Interest

Health insurance payment reform and evaluation
Continuity of primary care and health outcome
Patient experience of health care services
Medication management among chronic patients

Name

Chun-Ying Wu 吳俊穎

Position Title / Affiliations

台北榮民總醫院 轉譯研究科 主任
Chief, Division of Translational Research, Taipei Veterans General Hospital

Education and Degrees

台灣大學醫學士、醫學博士
美國哈佛大學法學碩士、公衛碩士
東海大學法學士

Professional Experience

國家衛生研究院 癌症研究所 合聘研究員
陽明大學醫學系暨臨床醫學研究所 教授
台灣醫事法律學會理事長
台灣微菌聯盟理事長
台灣實證醫學學會常務監事
衛生福利部醫事審議委員會委
東海大學法律系暨法律研究所 合聘教授

Research Interest

大數據與 AI 研究
消化系癌症研究
醫事法律實證研究
生物科技法規研究
微菌叢研究

大數據與 AI 宣言：解放數據、重塑法律、追求至善

吳俊穎主任
台北榮民總醫院轉譯研究科

大數據與人工智慧的時代已經全面來臨，Google, Facebook, Amazon, 各國政府、各個研究機構，紛紛把大數據的研究與人工智慧的發展，視為本世紀最重要的競爭領域之一，從而涉及許多資料的取得、分析、分享、等等，許多倫理及法律的議題。

本演講將以近年來最熱門的許多新聞事件談起，繼而介紹大數據所可能產生的利益，包括商業利益以及公共利益，繼而探討相關大數據研究對於個人隱私以及資訊自主權所可能衍伸的傷害。隨後，將討論大數據知情同意的法律規範，特別是剛剛生效的歐盟一般資料保護法(GDPR)，將探討其對於個人資料的同意要件以及可以行使的權利。

本演講最後將發表相關宣言：「解放資訊、重塑法律、追求至善」，希望藉由合理的法律規範，讓資訊的利用符合個人權利的期待，也能追求社會的最大公益。

Name

蔡淑鈴

Position Title / Affiliations

副署長 / 衛生福利部中央健康保險署

Education and Degrees

國立陽明大學公共衛生研究所公共衛生博士
台灣大學公共衛生研究所碩士

Professional Experience

衛生福利部中央健康保險署主任秘書
中央健康保險局醫務管理處、台北分局、中區分局、企劃處經理

Research Interest

醫療制度、健康保險

NHI Medi-Cloud System 之應用與結果

蔡淑鈴副署長
衛生福利部中央健康保險署

臺灣自 1995 年實施全民健康保險，讓全民享有自由就醫便利性，免除民眾就醫的經濟障礙並保障其醫療權益，民眾僅需繳納掛號費及少許部分負擔即可就醫，健保滿意度在 2017 年來到歷史新高，有 8 成 5 的民眾對健保感到滿意，臺灣的健保已成為國家最珍貴的資產，也廣受世界各國贊譽。

隨著人口老化及國人平均壽命延長，多重慢性病越來越普遍，且國人就醫自由、方便，目前平均門診量已突破每天 100 萬人次，2017 年平均每人門診就醫次數為 15.18 次；又因醫療科技日益進步、新藥不斷開發，醫療給付範圍持續擴大，支出亦相對增加，這些都使得我們的醫療費用持續增加，根據健保署 2017 年的統計資料顯示，全年門住診醫療支出為 6,934 億點，其中 26% 是藥費，透過健保資料分析發現門住診藥費申報，從 2013 年的 1,540 億點增加到 2017 年的 1,834 億點，而民眾使用特定昂貴醫療儀器檢查也逐年明顯增加，從電腦斷層攝影、磁振造影到正子斷層掃描都有這種情形，以 2016 年健保檢查項目點數前 20 排名，健保支出費用達 688 億點。

由於許多民眾就醫習慣會依不同症狀尋求不同的醫院或醫師看診，個人的就醫與用藥資料就分散在不同的醫療院所內，因醫師沒有病患完整的就醫史，較容易發生重複開藥或重複檢查 (驗)，而重複開立的藥品易產生藥物交互作用，很可能因為劑量過多，影響病人用藥安全；另過多的檢查 (驗)，除造成不必要的醫療資源浪費外，亦有可能造成健康傷害。

為提升病人就醫及用藥安全，避免低效益醫療，同時使健保資源更有效率的使用，以提升醫療服務品質，健保署運用雲端科技，於 2013 年 7 月建置健保雲端藥歷系統，2016 年再升級為「健保醫療資訊雲端查詢系統」(NHI Medi-Cloud system)，利用資訊科技將病人就醫資料歸戶，提供全國特約院所透過雲端系統平台查詢病人跨院的就醫紀錄，作為醫師處方及藥師調劑之參考，以避免重複用藥、檢驗 (查)，提升病人安全及避免浪費。雲端系統除作為上述資訊共享平台外，健保署更進一步藉由資訊分享機制推動分級醫療，鼓勵大小院所間發展垂直整合，促使病人在一個固定醫療院所中接受醫療照護，如近期林口長庚紀念醫院響應健保署北區業務組「雁行專案 - 社區醫療合作推動計畫」，跨縣市結合雙北、桃竹苗縣市各級醫療機構及照護單位共 278 家，合作成立北台灣規模最大「長庚雁行醫療照護團隊」，透過醫院、診所各司其職、分工合作，使民眾能獲得最好的醫療照護，最終不僅可提升醫療照護品質，也解決「看病多」、「拿藥多」及「檢驗多」之三多問題。

NHI Medi-Cloud system 提供醫師及藥事人員更全方位資訊，協助整合病人跨院就醫處方及診斷，保障民眾就醫用藥安全，共創醫病雙贏環境，為國際上有使用醫療資訊交換系統的國家中，少數具備全國普及並完整健保就醫用藥資訊的國家。在 2014 年至 2016 年健保滿意度調查指出，83.0%-85.8% 民眾贊成醫療院所配合健保雲端資料庫即時查詢病人過去就醫與用藥紀錄，且有 97.6% - 99.2% 民眾願意多花 1-2 分鐘等待醫師確認就醫與用藥紀錄。

另統計 2017 年全年共有 24,478 家院所、62,796 位醫事人員查詢使用本系統，病人數查詢比率已成長至 82.4%。2018 年 1-4 月份共有 23,552 家院所、56,742 位醫事人員查詢使用本系統，總查詢病人次約計 2.4 億人次。據統計，在每天 100 萬健保就醫人次中，約有 82.4% 的病人在就醫或領藥時，均有透過醫事人員查詢本系統，其中最容易重複開藥的降血壓、降血脂、降血糖、思覺失調、抗憂鬱症及安眠鎮靜等六類慢性病藥品用藥日數重疊率於 2014 年至 2016 年降低超過一半，約節省 3 億元藥費支出。在檢查檢驗資料分析則發現，2017 年 7 月至 12 月電腦斷層 (CT)、磁振造影 (MRI)、血液檢查等 20 類 274 項檢查檢驗醫令，合計執行次數較 2016 年同期共減少 479.33 萬次，約節省 12 億點檢查檢驗費用支出。

除持續精進現有雲端醫療查詢系統外，目前健保署已開始規劃建置醫療影像資料倉儲及人工智慧應用雛型，未來將運用已收載大量的醫療資料與影像匿名化後，在符合相關法律規範下，逐步開放外界進行加值應用，讓醫療科技等相關產業能夠利用健保大數據發展更好的健康照護與醫療模式。

Name

I-Ming Parng 龐一鳴

Position Title / Affiliations

Director-General of Information Management / MOHW

Education and Degrees

MPH, National Taiwan University

Professional Experience

Director of Medical Affairs Division, NHIA

Director of Southern Division, NHIA

Research Interest

Epidemiology
Health Administration
Health Insurance

Policies for e-Health

龐一鳴處長
衛生福利部資訊處

E-health is one of the important policies of WHO documented in the resolutions and decisions of 58th World Health Assembly. Although Taiwan is not one of the member countries of the Organization, we should adopt the principles of the decision encouraging. No matter big data or AI for health care, cannot escaped from the scope of e-health WHO issues. The EU published a report for e-Health interoperability in 2010. The CMS also designed a roadmap for e-health for the United States. In Taiwan, the EMR project has built a fundament for health records exchange, the NHS has set a benchmark for the world in the field of health information technology and the 8th medical network project is going to make the intelligent medicine come true. In the blossom period for big data, AI and health information innovation we should always remind ourselves the technologies should service for health or better life, not for utilization only. In the world of Internet we cannot forget the threaten from cyberattack even for one second.

Session 5B :
New Developments in NGS Data Analysis and Visualization

主持人 陳豐奇研究員

Name

陳豐奇

Position Title / Affiliations

研究員 / 國家衛生研究院 群體健康科學研究所

Education and Degrees

清華大學生命科學系博士

Professional Experience

台灣演化與計算生物學會理事、監事
交通大學生命科學系合聘教授
交通大學科技法律研究所兼任副教授
國家衛生研究院資訊中心主任

Research Interest

生物資訊
分子演化
轉錄體與疾病之關連
智慧財產權
美國專利多方複審制度

Name

Wen-Lian Hsu 許聞廉

Position Title / Affiliations

Distinguished Investigator and Director / Institute of Information Science, Academia Sinica

Education and Degrees

1980	Ph.D., Cornell University, (Operations Research) (Advisor- George L. Nemhauser)
1978	M.S., Cornell University, (Operations Research)
1973	B.S., National Taiwan University, (mathematics)

Professional Experience

2012-present	Director of Institute of Information Science. Academia Sinica
2008-present	Distinguished Research Fellow, Institute of Information Science, Academia Sinica.

Research Interest

Dr. Hsu’s main interests are in designing efficient algorithms for various problems in graphs, bioinformatics (e.g. NGS mapping and variant calling), and natural language. In 1993, he developed a Chinese input software, 自然輸入法 , which has since revolutionized Chinese input in Taiwan. Dr. Hsu is an active researcher in AI. He has been involved in designing systems that can understand natural language, such as question answering, dialogue, biological literature mining, and elementary school Mathematical Word Problem. He has also been working on protein structure prediction, proteomic data analysis.

High Throughput NGS Data Analysis

許聞廉所長
中央研究院資訊科學研究所

Next-generation sequencing (NGS) provides a great opportunity to investigate genome-wide variation at nucleotide resolution. Due to the huge amount of data, NGS applications require very fast and accurate alignment algorithms. Most existing algorithms for read mapping basically adopt seed-and-extend strategy, which is sequential in nature. We developed a sequence partitioning algorithm, called Kart, which can process long reads as fast as short reads by dividing a read into small fragments that can be aligned independently. Our experiment result indicates that the average size of fragments requiring gapped alignment is around 22bp regardless of the original read length. Furthermore, it can tolerate much higher error rates. The experiments show that Kart spends much less time on longer reads than other aligners and still produce reliable alignments even when the error rate is as high as 15%.

Our sequence partitioning algorithm can also be applied to the RNA-Seq problem. Various de novo spliced RNA aligners have been developed in recent years. Though these aligners can handle spliced alignment and detect splice junctions, some challenges still remain to be solved. We proposed a novel RNA-seq de novo mapping algorithm, called Dart to handle spliced alignment with a divide-and-conquer strategy. Dart can handle both short and long RNA-seq reads. The experiment results on synthetic datasets and real NGS datasets show that Dart is a highly efficient aligner that yields the highest or comparable sensitivity and accuracy. More importantly, it spends the least amount of time among the selected aligners.

Our divide-and-conquer idea has also been applied to whole human genome comparison and yielded an ultra-efficient algorithm, GSAlign, which is about 400 times faster than the second best algorithm.

Name

Hsien-Da Huang

Position Title / Affiliations

Chair Professor and Vice Dean
Institute of Bioinformatics and Systems Biology, Department of Biological Science and Technology, National Chiao Tung University

Education and Degrees

Ph.D., Institute of Computer Science and Information Engineering, National Central University, Taiwan

Professional Experience

2004-2007	Assistant Professor, Department of Biological Science and Technology, Institute of Bioinformatics, National Chiao Tung University, Taiwan
2007-2010	Associate Professor, Department of Biological Science and Technology, Institute of Bioinformatics and Systems Biology, National Chiao Tung University, Taiwan
2009-2016	Chairman, Department of Biological Science and Technology, National Chiao Tung University, Taiwan
2010-2016	Professor, Department of Biological Science and Technology, Institute of Bioinformatics and Systems Biology, National Chiao Tung University, Taiwan
2013~	Vice Dean, College of Biological Science and Technology, National Chiao Tung University, Taiwan
2016~2017	Distinguished Professor, Department of Biological Science and Technology, Institute of Bioinformatics and Systems Biology, National Chiao Tung University, Taiwan
2017~	Chair Professor, Department of Biological Science and Technology, Institute of Bioinformatics and Systems Biology, National Chiao Tung University, Taiwan

Research Interest

Bioinformatics, Systems Biology, Comparative genomics, Regulatory RNA

Short and Long Read Sequencing Technologies and Their Applications in Biomedical Research

黃憲達講座教授
國立交通大學生物科技學系（所）

近十年來，高通量定序技術（High-throughput Sequencing）的進步，造就了許多生物醫學研究上的突破。其中，定序過程中所產生的序列片段長短（Read Length），是一個關鍵實驗參數（Key parameter）。我們將以短序列讀長（Short reads）與長序列讀長（Long reads）為觀點，闡述定序技術在各項生物醫學研究與應用之內涵。再者，生物資訊分析（Bioinformatics）對於高通量定序技術在生物醫學研究上的應用，亦相當重要，本演講將以 MicroRNA 研究、Metagenomics、人類基因體學、藥物基因體學為面向，舉例說明。

Name

Chun-houh Chen 陳君厚

Position Title / Affiliations

研究員 / 中央研究院

Education and Degrees

1987- 1992	Ph.D., Department of Mathematics, UCLA, USA
1987- 1990	M.S., Department of Mathematics, UCLA, USA
1980- 1984	B.S. Department of Statistics, National Chung-Hsing Univ., Taiwan

Professional Experience

2017- present	Director, Institute of Statistical Science, Academia Sinica (AS)
2011- present	Research Fellow, Institute of Statistical Science, AS
2016- 2017	Director, Department of Academic Affairs and Instrument Service, AS
2012- 2016	Deputy Director, Institute of Statistical Science, AS
2002- 2011	Associate Research Fellow, Institute of Statistical Science, AS
1993- 2002	Assistant Research Fellow, Institute of Statistical Science, AS
1992- 1993	Assistant Professor, Department of Statistics/Computer and. Information Systems, George Washington University, Washington, D.C., U.S.A.

Research Interest

Bioinformatics, Data/Information Visualization, Dimension Reduction, Matrix Visualization, Multivariate Statistical Methods, Pattern Recognition

Matrix Visualization for (Big) Health Science Data

Chiun-How Kao[1,2], Chuan-kai Yang[2], Chun-houh Chen[1,*]
1. Academia Sinica
2. National Taiwan University of Science and Technology

Keywords: Exploratory Data Analysis (EDA), Generalized Association Plots (GAP), Hadoop, Health Science, Symbolic Data Analysis (SDA)

"It is important to understand what you CAN DO before you learn to measure how WELL you seem to have DONE it" (Exploratory Data Analysis: John Tukey, 1977). Data analysts and statistics practitioners nowadays are facing difficulties in understanding higher and higher dimensional data with more and more complex nature while conventional graphics/visualization tools do not answer the needs. It is more difficult a challenge for understanding overall structure in big data sets so good and appropriate Exploratory Data Analysis (EDA) practices are going to play more important roles in understand what one can do in the big data era.

Matrix Visualization (MV) has been shown to be more efficient than conventional EDA tools such as Boxplot, Scatterplot (with dimension reduction techniques), and Parallel Coordinate Plot for extracting information embedded in moderate to large data sets of binary, continuous, ordinal, and nominal nature. In this study we plan to investigate feasibility and potential difficulties for applying related MV techniques for visualizing and exploring structure from big data: 1). Memory/computation (permutation with clustering) of proximity matrices for variables and subject; 2). Display of data and proximity matrices for variables and subject. We shall integrate techniques from Hadoop computing environment, Image scaling, and Symbolic Data Analysis into the framework of GAP (Generalized Association Plots) in coming up with an appropriate package for conducting Big Data EDA with visualization. Several international data (HCAHPS 2013 Data, MS-DRG 2011 Data) and local data (National Health Insurance Data) will be used to demonstrate the bigGAP environment.

References

Tukey, John W (1977). Exploratory Data Analysis. Addison-Wesley.

Session 6 :
Using Big Data in Primary Prevention

主持人 王英偉署長

Name

Ying-Wei Wang

Position Title / Affiliations

Director-General / Health Promotion Administration, Ministry of Health and Welfare, Taiwan

Education and Degrees

- Dr.P.H., School of Public Health & Tropical Medicine, Tulane University, U.S.A.
- M.P.H., School of Public Health & Tropical Medicine, Tulane University, U.S.A.
- M.D., School of Medicine, National Taiwan University, Taiwan

Current Position & Professional Experience

- Director-General, Health Promotion Administration, Ministry of Health and Welfare, Taiwan
- Associate Professor, School of Medicine, Tzu Chi University, Taiwan
- Deputy Director, School of Medicine, Tzu Chi University
- Director, Department of Medical Humanities, School of Medicine, Tzu Chi University
- Director, Heart Lotus Care Ward, Buddhist Tzu Chi General Hospital
- Secretary-general, Taiwan Society of Health Promotion Hospitals
- Director, Asia Pacific Hospice Palliative Care Network
- Director, Department of Family Medicine, Buddhist Tzu Chi General Hospital
- Director, Center for Faculty Development and Instructional Resources, Tzu Chi University
- Deputy Director General, Bureau of Health Promotion, Department of Health, Taiwan
- Attending Physician, Department of Family Medicine, Buddhist Tzu Chi General Hospital
- Attending Physician, Department of Geriatrics, Taipei Hospital
- Resident, Department of Family Medicine, National Taiwan University Hospital

Research Interest

Dr. Ying-Wei Wang received his doctorate in School of Public Health & Tropical Medicine, Tulane University, U.S.A. His recent publications include "Development of Mandarin Multidimensional Health Literacy Questionnaire (MMHLQ)(Taiwan J Public Health, 2017)","An anthropological approach to teach and evaluate cultural competence in medical students the application of mini-ethnography in medical history taking(Med Educ Online,2016)","Barriers to and facilitators of the implementation of health promoting hospitals in Taiwan: a top-down movement in need of ground support(Int J Health Plann Mgmt,2012)","The Application of Microteaching to Improve Teaching Skill in Medical School(J Med Education,2012)" and "Application of signs of dying identified in traditional Chinese, Tibetan, and modern Western medicine in terminal care(Tzu Chi Medical Journal, 2012)". His current research interests include Family Medicine, Palliative Care, Community Health, Health Promotion, Medical Education

Name

袁啓亞

Position Title / Affiliations

營運總監 / 工研院服務系統科技中心

Education and Degrees

國立成功大學 機械工程 碩士

Professional Experience

工研院服務系統科技中心 營運總監

工研院服務系統科技中心 健康照護服務組 組長

工研院服務系統科技中心 企劃推廣組 組長

工研院服務系統科技中心 智慧安全服務組 組長

重要成果：

1. 參與國內第一台臥式綜合加工機 MC-15H 之開發工作。
2. 協助國內工具機業者提升產品至 FMS 系統層次。
3. 榮獲 85 年度機械學會傑出工程師獎。
4. 以健康風險評估結合 ICT 裝置協助保險業者發展健康促進外溢保單。
5. 與糖尿病診所共同發展第 2 型糖尿病人餐後運動血糖改變量預測模式。

Research Interest

健康照護服務 / 智慧生活服務系統 / 自動化生產系統 / 流程分析整合

大數據與智慧健康照護服務系統

袁啟亞營運總監
工研院服務系統科技中心

依據內政部統計資料，107 年 3 月台灣已正式進入高齡社會 (老年人口 >14%)，預計 115 年進入超高齡社會 (老年人口 >20.0%)。又依據國健局資料，台灣銀髮族 88.7%至少罹患 1 種慢性病，71.7%罹患 2 種，51.3%罹患 3 種。而慢性病已逐漸成為各國健康支出的要項，以美國為例，慢性病照護已達健康支出的 86%，故慢性病健康照護或預防已成為我們必須重視的議題。

在健康照護方面，透過數位轉型科技，WEF(世界經濟論壇) 預期會有兩個極大的破壞式轉型，包括 (1) 健康照護地點從醫院轉移到居家及 (2) 健康照護模式從診斷和治療轉移到預防和管理方面。又從經濟發展角度來看，WEF 認為數位轉型科技應用在病患大規模參與 (Patient engagement at scale)，以改善病患健康行為 (如透過雲與端的整合，運用 AI 結合大數據，早期識別健康退化跡象，並預防再次入院等不良事件) 的效益最大。

工研院服務系統科技中心 (簡稱服科中心) 從健康照護數位轉型服務缺口及服務設計切入，發展一系列的健康照護服務系統解決方案，從醫檢設備之整合，進而發展出智慧診間服務雛型，並運用國內外相關之健康大數據結合 AI 技術，發展出慢性病進程之早篩技術。

本次研討會，服科中心將針對慢性病中的糖尿病照護服務，說明工研院在數位轉型及大數據應用解決方案的進展。

Name

Li-Sheng Chen

Position Title / Affiliations

Professor, Director / School of Oral Hygiene, Taiwan Medical University

Education and Degrees

PhD. National Yang Ming University

Professional Experience

2017~present	Professor, School of Oral Hygiene, College of Oral Medicine, Taipei Medical University, Taiwan 2014~Chair, School of Oral Hygiene, College of Oral Medicine, Taipei Medical University, Taiwan
2013~present	Associate Professor, School of Oral Hygiene, College of Oral Medicine, Taipei Medical University, Taiwan
2010-2013	Assistant Professor, School of Oral Hygiene, College of Oral Medicine, Taipei Medical University, Taiwan
2007-2010	Vice Chair, Research Department, Changhua Christian Hospital, Taiwan

Research Interest

My research interest is non-communicable disease prevention, with the emphasis on the outcomes research

Big Data in Non-communicable Disease Prevention
非傳染病預防之大數據科學

陳立昇教授
台北醫學大學口腔衛生學系

As informatics are likely to have a significant impact on the efficiency and quality of hospital medicine, ambulatory medicine, telemedicine, and public health. A telemedicine system can support multiple tasks in diabetes care including surveillance, on-line health education, risk assessment, and self-care. At the crossroads of medical informatics and public health, Cybermedicine is proposed to support self-care, consumer empowerment, and prevention. Cybermedicine deals with global exchange of open and non-clinical information, mostly from patient-to-patient, sometimes from patient-to-physician and from physician-to-physician using information technology. The revolution of digital health is now moving forward to big data movement across systems and services.

Big data characterized the following 7 Vs including volume, velocity, variety, variability, veracity, visualization, and value. Targeting data on clinical medical data and community health data in non-communicable diseases, big data is to process data storage and management, analysis and processing with various kinds of state-of-the-art technique, and the translation of their results into health decision-making.

To develop consumer-based informatics, the “BlockChain” model can be used. The blockchain technology is designed to streamline the sharing of health records in a secure way and give data owners more control over their information. Based on this Blockchain model, the enterprise model for sharing health data to supporting the prevention studies with EBM and to developing the applications of digital health becomes feasible in the near future.

These aid the feasibility of reaching the goals of P4 medicine. P4 medicine, raised by Leroy Hood, is comprised of predictive, personalized, preventive, and participatory aspects. P4 medicine proposes a systematic approach to apply biologic data including omics, metabolic data, therapy monitoring, and clinical information on the influence of an individual’s biological systems to better define health or wellness for each person. P4 medicine itself is basically referring to individual health, however, P4 medicine should be considered through a renewed partnership between medicine and public health. Population is the key of this approach, a systematic framework aimed at preventing the progression of disease in healthy persons, which linked to the natural history of the disease. The corresponding preventing strategies could be concluded from primary prevention, secondary prevention to tertiary prevention. The 3S (successive successful surveillance) models with evidence-based medicine (EBM) is needed to perform simultaneously for the most benefit of diseases control. This framework is a continuous improvement in prevention and treatment by combining scientific and technology with active participation. It also integrates determinants of health at multiple levels, assessing micro- and macro-level factors as determinants of health and disease across the life span with big data can improve our ability to reduce the risk of diseases, to predict the occurrence of disease, to avoid the recurrence/ death of diseases, and to devise better interventions; not only for treatment and may include life style modification and screening by randomized control trials or simulating models.

Breast cancer is one of examples that demonstrates the useful of genome analysis, by producing numerous tests based on complex biomarkers, that can be able to improve disease diagnosis, prognosis, and prediction of response to therapy. As the results, stratifying breast cancer into subtypes based on biomarkers can lead to the development of targeted therapeutics. Although, the best design for the evaluation was randomized controlled trial (RCT) in alignment with the principle of evidence-based medicine. However, it is not always feasible to conduct RCT. For example, how to develop an individual-tailored prevention approach with the incorporation of information on life-style and biochemical factors under the principle of EBM is unclear. Thus, an examples of personalized hypertension prevention is illustrated in my speech.

Name

Hsing-Yi Chang（張新儀）, Dr. PH

Position Title / Affiliations

Investigator / Institute of Population Health Sciences, National Health Research Institutes

Education and Degrees

- Dr. PH in in Biostatistics, University of North Carolina at Chapel Hill, U.S.A.
- M.P.H. in Biostatistics, University of North Carolina at Chapel Hill, U.S.A.
- B.S. in Forestry, National Chung-Hsing University, Taiwan

Professional Experience

2013.7-present	Institute of Population Health Sciences, National Health Research Institutes, Taiwan, Investigator

Research Interest

Dr. Chang's research interest is on the time trend and development of health/risk behaviors. To achieve this, she has conducted the National Health Interview Survey (NHIS) since 2001 and the Child and Adolescent Behaviors in Long-term Evolution (CABLE) since 2006. She is also a co-pi in the Nutrition and Health Survey in Taiwan. She is able to apply her training in biostatistics to integrate the survey outcomes for her research interests. She has worked on risk prediction models providing prediction formula to the Industrial Research Institutes for health screening. Given her training in biostatistics, she is able to apply or modify statistical methods in dealing with complicated epidemiological data.

An Example of Using Big Data in Primary Prevention of Cardiovascular Disease

張新儀研究員
國家衛生研究院群體健康科學研究所

Background

The WHO Global NCD Action Plan 2013-2020 stressed that to achieve the goal of reducing NCD requires cooperation from different health sectors. Death due to cardiovascular diseases is still rising in 2016 in Taiwan. Heart disease increased 8.4% and cerebrovascular diseases increased 6.1%. Thus, we apply the modern technology in primary prevention of cardiovascular diseases.

Objectives

There are two parts of this talk. One is on the development/validation of risk prediction model, another is the establishment of a platform for disease prevention.

Method

We use the data from Nutrition and Health Survey in Taiwan (NAHSIT) linked with the data from the National Health Insurance (NHI), and the national registry of mortality to establish the risk prediction model for the probability of having coronary heart disease (CHD), diabetes (DM), chronic kidney disease (CKD) etc. We, then, use the data from the Taiwan Survey of Hypertension, Hyperglycemia, and Hyperlipidemia (TwSHHH) to validate the models. The calculation engine is applying the models for risk prediction in health check-ups. Health education material are sent to patients with high risk.

Results

Our models show reasonable validity in predicting 10-year risks of diseases. We also develop platforms for risk prediction in hospital/community care and web page for self-evaluation. We will demonstrate our models and the platforms.

Session 7 :
Big Data Analysis in Health Care

主持人 吳秀英主任秘書

Name

Shiow-Ing Wu, Ph.D.

Position Title / Affiliations

Associate Investigator and Secretary-General / Institute of Population Health Sciences, National Health Research Institutes, Taiwan

Education and Degrees

1982	D.D.S. in Dentistry, Taipei Medical College, Taiwan
1998	M.P.H. in Public Health (Biostatistics & Epidemiology), National Yang-Ming University, Taiwan
2005	Ph.D. in Public Health (Metabolic Syndrome Epidemiology), National Yang-Ming University, Taiwan

Professional Experience

2013/7-2018/1	Food and Drug Administration, Ministry of Health and Welfare, Taiwan Deputy Director General
2010/10-2013/7	Food and Drug Administration, Department of Health, Taiwan. Deputy Director General
2005/10-2010/10	Bureau of Health Promotion, Department of Health, Taiwan Deputy Director General
2003/8-2005/10	Department of Health, Taipei City Government Chief Secretary
2000/7-2003/7	Taipei City STD Control Center, Department of Health, Taipei City Government Superintendent

Research Interest

HIV/AIDS, drug abuse, chronic disease prevention, translational research

Name

I-Shou Chang 張憶壽

Position Title / Affiliations

Emeritus Investigator / National Institute of Cancer Research, National Health Research Institutes

Education and Degrees

1976	Ph.D., Mathematics, Columbia University, USA
1972	M.A., Mathematics, Wayne State University, USA
1969	B.S., Mathematics, National Tsing-Hua University, Taiwan

Professional Experience

2016/05-2017/08	國家衛生研究院學術發展處處長
2011/03-2017/08	國家衛生研究院生醫資源中心召集人
2007/05-2011/02	國家衛生研究院生醫資源中心主任
2000/09-2007/04	國家衛生研究院研究資源處處長
1983/08-1985/07	國立中央大學數學系及研究所系主任 / 所長
2006/01-2017/08	國家衛生研究院生物統計與生物資訊研究組合聘研究員
2006/01-2017/08	國家衛生研究院癌症研究所研究員
2000/09-2005/12	國家衛生研究院院長實驗室研究員
1989/09-1990/05	美國哥倫比亞大學統計系訪問教授
1982/08-2002/02	國立中央大學數學系及研究所教授

Research Interest

Genomic epidemiology
Risk prediction model
Cancer surveillance research
Survival analysis

Improvements of Net Cancer Survival in Taiwan - A Study Based on Cancer Registry, Cause of Death and Health Insurance Database

張憶壽名譽研究員
國家衛生研究院癌症研究所

In high-income countries, advances in early diagnosis and treatment have improved net cancer survival. However, socioeconomic inequalities in net survival have persisted or increased for some adult cancers. Using Taiwan Cancer Registry, Cause of Death Database, and National health Insurance Research database jointly, we assessed net survival for the 20 most common adult cancers in Taiwan. They were stratified into six age groups and three socioeconomic groups. Out of 120 cancer site and age group combinations, 49 showed improvements in 5-year net survival from 2000–2004 to 2005–2010. Only cervix uteri cancer in the 35–49-year age group showed a deterioration. During 2000–2010, 13 of the 20 cancer cases experienced socioeconomic inequalities for all age groups combined, and the deprivation gaps varied with cancer site and age at diagnosis. For the five most common cancers –liver, colon and rectum, lung, breast, and oral – there were socioeconomic inequalities, and 5-year net survival improved for most or all of the six age groups from 2000–2004 to 2005–2010. Reducing socioeconomic inequality in survival may lead to improvements in survival overall. We should focus on the age groups with large deprivation gaps. Our results are useful for prioritizing cancer sites and age groups for in-depth socioeconomic disparity studies and for proposing interventions for health disparity reductions and net cancer survival improvements. (Based on work jointly done by Li-Hsin Chien, Tzu-Jui Tseng, Fang-Yu Tsai, Jie-Huei Wang, Chao A. Hsiung, Tsang-Wu Liu)

Name

Chih-Cheng Hsu

Position Title / Affiliations

Deputy Director
Institute of Population Health Sciences

Education and Degrees

1996-2000	DrPH, major in community health sciences, Tulane School of Public Health and Tropical Medicine, USA
1990-1992	MPH, major in preventive medicine, College of Public Health, National Taiwan University, Taiwan
1979-1986	MD, School of Medicine, National Yang-Ming University, Taiwan

Professional Experience

2014-present	Investigator and Deputy Director, Institute of Population Health Sciences, National Health Research Institutes, Taiwan
2006-2014	Associate Investigator, Institute of Population Health Sciences, National Health Research Institutes, Taiwan
2001-2006	Assistant Investigator, Division of Health Policy Research, National Health Research Institutes, Taiwan

Research Interest

1. Risk factors and prevention of diabetic nephropathy
2. Chronic kidney diseases in the elderly
3. Geriatric syndrome and sarcopenia
4. Tobacco control

Big Data Analysis and Application in Healthcare Research
巨量資料分析應用於醫療照護研究

許志成副所長
國家衛生研究院群體健康科學研究所

台灣的糖尿病發生率過去十年來增加 11%，盛行率增加了近五成，歷年來台灣透析的發生率與盛行率也都名列世界前茅。近十年糖尿病與慢性腎臟病防治工作最重要的項目，首推整合照護方案，包含：糖尿病共同照護網，糖尿病醫療給付改善方案，初期慢性腎臟病醫療給付改善方案 (early-CKD 計畫)，末期腎臟病前期之病人照護與衛教計畫 (pre-ESRD 計畫) 等。對糖尿病及慢性腎臟病患病人而言，加入整合照護方案可以獲得減少醫療花費、降低死亡率，以及降低或延緩透析的發生率等的正向效益，但從文獻上也發現，病情較為嚴重、年齡較大及經濟較為弱勢者，常常會被排除在整合照護方案之外，且目前這些整合照護方案的收案人數也有待加強。這一類全國性之衛生政策實務與其他臨床監測與應用必須依賴大數據分析，才能確實掌握全貌與趨勢變化。本次演講，我將說明如何以健保資料庫來做臨床暨醫療政策之轉譯研究並藉此促進跨領域的合作。

Name

Yen-Feng Chiu 邱燕楓

Position Title / Affiliations

Investigator 研究員 / 國衛院 群健所
Institute of Population Health Sciences
National Health Research Institutes, Taiwan

Education and Degrees

Ph.D. in Biostatistics, Johns Hopkins University, Baltimore, Maryland, USA

Professional Experience

2012/01-Present	Investigator, Institute of Population Health Sciences, National Health Research Institutes, Miaoli, Taiwan
2013/09-Present	Joint Professor, Graduate Institute of Biostatistics, China Medical University, Taichung, Taiwan
2013/09-2017/07	Joint Professor, Graduate Institute of Statistics, National Chiao Tung University, Hsinchu, Taiwan
2006/11-2011/12	Associate Investigator, Division of Biostatistics and Bioinformatics, National Health Research Institutes, Miaoli, Taiwan
2002/11-2006/10	Assistant Investigator, Division of Biostatistics and Bioinformatics, National Health Research Institutes, Taipei, Taiwan
2000/08-2002/10	Research Assistant Professor, Department of Biostatistics, Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, USA
1999/11-2000/07	Post-doctoral fellow in Biostatistics, Johns Hopkins University, Baltimore, Maryland, USA

Research Interest

Dr. Chiu's research interests and expertise lies in statistical genetics, genetic epidemiology and statistical applications to a wide range of medical, biomedical and public health researches. She has developed machine learning and statistical methods to identify common and rare variants, gene-gene and gene-environment interactions associated with complex disease, for population- and family-based studies. Currently, she is developing statistical framework and computing tools to combine multiple genetic epidemiological studies with different designs. In addition, for disease prevention and control, she has been devoting to a variety of observational and clinical studies such as the Healthy Aging Longitudinal Study in Taiwan, the Stanford Asia-Pacific Program for Hypertension and Insulin Resistance Family Study and its extension projects, the longitudinal health check-up study, etc., to investigate how lifestyle, environmental and genetic factors influence human health.

Health Benefits of Plant-based Diets: Evidence from Big Data Analysis

邱燕楓研究員
國家衛生研究院群體健康科學研究所

In recent years, plant-based diets are growing in popularity among youth for the concerns of environment, ethical issues about animal care, the threat of animal-borne diseases, the use of antibiotics and growth stimulants for the production of animals, and the health advantages. Previous studies have suggested beneficial associations between a vegetarian diet and health. However, Western and Taiwanese vegetarian diets differ substantially, it is unknown whether the beneficial effect of vegetarian diets observed in Western populations is reproducible in Taiwanese vegetarians. Although several small cross-sectional studies have compared body mass index (BMI), blood pressure (BP), fasting blood glucose (FBG), triglycerides (TG), total cholesterol (TC), low-density lipoprotein (LDL) cholesterol levels between Taiwanese vegetarians and nonvegetarians, examinations of the longitudinal effect of different types of vegetarian diets (e.g., vegan, lacto-ovo, and lacto) on metabolic health remain scarce.

We examined the effects of different types of vegetarian and nonvegetarian diets on metabolic traits in a large Taiwanese cohort. We also investigated the possible association between a plant-based diet and hypertension incidence in the cohort of Taiwanese adult nonsmokers, and studied whether this association was mediated through metabolic traits. Further, we compared the subjects reported food intake from food frequency questionnaires (FFQs) to provide information for speculation on the potential impact of these diets on health outcomes.

(This talk includes the joint works with Drs. Chih-Cheng Hsu, Chao A. Hsiung, Shao-Yuan Chuang, Su-Chun Chuang, and Tina H. T. Chiu.)

Session 8 : Mathematical Approaches to Healthcare Research

主持人 許元春教授

Name

Yuan-Chung Sheu

Position Title / Affiliations

Professor, Department of Applied Mathematics, National Chiao Tung University

Education and Degrees

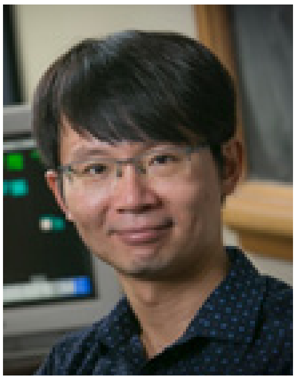
1981	B.S. in Mathematics, National Central University
1993	Ph.D. in Mathematics, Cornell University

Current Position & Professional Experience

1993-1998	Associate Professor of Mathematics, NCTU
1999-present	Professor of Mathematics, NCTU
1997-1998	General Member, MSRI at Berkeley
2001-2003	Chair, Mathematics Department, NCTU
2004-2015	Associate Editor of Taiwanese Journal of Mathematics
2006-2007	Visiting Scholar, University of Washington, Seattle, USA
2005-2006, 2007-2008	Associate Dean, College of Science, NCTU
2012-2013	Vice President, Taiwanese Mathematical Society

Research Interest

Probability Theory & Applications.



Name

Hau-tieng Wu

Position Title / Affiliations

Duke University, Mathematics and Statistical Science

Education and Degrees

2006-2011	Ph.D., Mathematics, Princeton University, Advisor: Ingrid Daubechies
1996-2003	M.D., National Yang-Ming University

Education and Degrees

2017/01-	Duke University, Mathematics Department and Department of Statistical Science, Associate Professor
2014-2017	University of Toronto, Mathematics, Assistant Professor
2013-2014	Stanford University, Mathematics, Postdoctoral Research Associate
2012-2013	UC Berkeley, Statistics, Postdoctoral Research Associate
2011-2012	Princeton University, PACM, Postdoctoral Research Associate

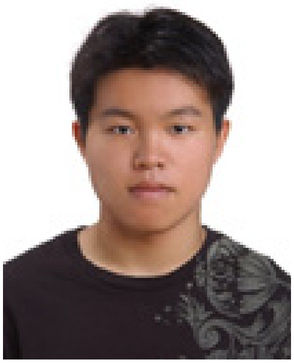
Research Interest

Signal processing, applied harmonic analysis, time-frequency analysis, machine learning, manifold learning, high-dimensional statistics, etc. The main application is medical data. I have interest in various kinds of medical datasets, mainly continuous physiological waveform signals, like ECG, EEG, PPG, BP, Resp, fMRI, or anything that has time as the main component (medical signal analysis). The target is extracting nonstationary dynamical information from (multimodal) time series that complements static information commonly used in clinics.

How does Geometry Help Physician's Diagnosis?

Hau-Tieng Wu
Department of Mathematics, Duke University

Compared with the snapshot health information, long term physiological signal provides complementary information. To extract relevant features and convert them into clinically useful information, we encounter new challenges; for example, limited channels with limited signal quality. I will discuss recent progress in solving this kind of problem by taking differential geometry into account with some clinical applications.



Name

Gi-Ren Liu 劉聚仁

Position Title / Affiliations

助理教授 / 國立成功大學 / 數學系

Education and Degrees

2008.9-2013.6	Ph. D. in Mathematics, National Taiwan University. Thesis Title: Partial Differential Equations with Random Initial Data (Advisor: Dr. Narn-Rueih Shieh, Co-advisor: Jenn-Nan Wang)
2011.6-2012.5	Military service in Taiwan
2004.9-2007.6	B.S. in Mathematics, National Taiwan University

Professional Experience

2016.8-present	Assistant Professor at the Department of Mathematics, National Cheng Kung University, Tainan.
2015.8-2016.7	Assistant Professor at the Department of Mathematics, National Tsing Hua University, Hsinchu.
2014.8-2015.7	Postdoctoral fellow in Department of Mathematics, University of California, Davis, USA.
2013.8-2014.7	Postdoctoral fellow in Department of Computer Science, National Chiao Tung University, Taiwan.

Research Interest

2013-present:
Random processes and their applications on mobile communication networks
2008-2012:
- Nonlinear functions of Gaussian random fields and their applications
- Some connections between probability and partial differential equations
- Central limit theorems of the trajectories of passive tracers in random media

2013:
- Mathematical modeling for smart grids and green routers
- Performance evaluation of wireless communication systems

2014-2015:
- Phase retrieval
- Mathematical modeling for wireless communication systems

2016-2018:
- Diffusion map and its application in the sleep assessment

Diffuse to Fuse EEG Spectra - Intrinsic Geometry of Sleep Dynamics for Classification

劉聚仁助理教授
國立成功大學數學系

Background

Based on the clinical needs, we introduce a novel sleep stage visualization and prediction algorithm based on two electroencephalogram signals. New Method: The nonlinear-type time-frequency analysis and diffusion geometry are combined to extract and visualize intrinsic sleep dynamics features. The hidden Markov model is trained to predict the sleep stage. Results: The extracted features reconstruct the nonlinear geometric structure of the sleep dynamics. The prediction algorithm is validated on a publicly available benchmark database, Physionet Sleep-EDF SC* and ST*, and a private database of sleep apnea subjects with the leave-one-subject-out cross validation. The overall accuracy and macro F1 achieve 82.66% and 74.95% in Sleep-EDF SC*, 76.7% and 71.7% in Sleep-EDF ST*, and 63.2% and 49.7% in the private database. Comparison with Existing Methods: The performance is compatible or slightly better than the state-of-the-art results. Conclusion: In addition to visualizing the geometric structure of different sleep stages, the prediction result suggests its potential in practical applications. This is a joint work with Hautieng Wu (Duke University), Yuan-Chung Sheu (National Chiao Tung University) and Yu-Lun Lo (Chang Gung Memorial Hospital, Chang Gung University).

Name

Ho, Hung-Chi 何弘棋

Position Title / Affiliations

Attending physician / Division of Cardiology, China Medical University Hospital, Taichung, Taiwan

Education and Degrees

- MD, National Taiwan University Department of Medicine
- MS, Mathematics, National Taiwan University Department of Mathematics
- PhD, Mathematical Statistics, National Taiwan University Institute of Applied Mathematical Sciences (Advisor: Prof. Chin-Tsang Chiang 江金倉)

Professional Experience

- Residency, Internal Medicine, National Taiwan University Hospital
- Fellowship, Cardiology, National Taiwan University Hospital
- Current: Attending Physician, Division of Cardiology, China Medical University Hospital, Taichung, Taiwan

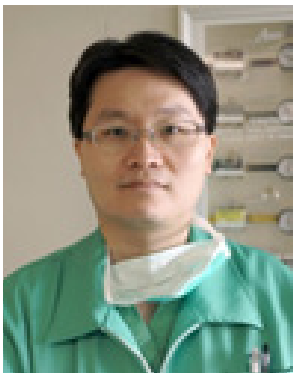
Research Interest

- Survival and Recurrent event analysis
- Empirical process; Semiparametric regression; Kernel smoothing; Dimension reduction
- General cardiology

Estimation and Model Checking for General Semiparametric Recurrent Event Models with Informative Censoring

何弘棋醫師
中國醫藥大學附設醫院心臟內科

This research aims to explore a recurrent event process with informative censoring through a general semiparametric latent intensity regression model. When the distributions of a subject-specific latent variable and a censoring time are left unspecified, the distinct distribution features of the recurrent event times are shown to be linked to the shape parameter and should be taken into account when constructing the estimation and testing procedures. In light of this finding, different approaches are developed to estimate shape-dependent and-independent occurrence rate regression models. Especially, our novel estimation criteria are also useful for building test rules to check between competing occurrence rate regression models without specifying a significance level. Meanwhile, large-sample properties of the estimators and model selection consistency of the test statistics are established under very mild conditions. A finite-sample performance of the proposed estimators and testing procedures is further assessed through comprehensive simulations. Moreover, the applicability of the proposed methodology is demonstrated on recurrent event samples of intravenous drug users needing inpatient care and patients with chronic granulomatous disease.



Name

Yu-Ting Lin 林祐霆

Position Title / Affiliations

Attending physician / Taipei Veteran General Hospital, Anesthesiology Department

Education and Degrees

1996-2003 M.D., National Yang Ming University

2010-2015 Ph.D., Electrical Engineering and Computer Science, National Taiwan University

Professional Experience

- Attending physician, Taipei Veteran General Hospital
- Attending physician, Shin Kong Wu Ho-Su Memorial Hospital
- Resident physician, Taipei Veteran General Hospital

Research Interest

My research interests are physiological signal processing in clinical medicine, including electrocardiogram analysis, pulse wave analysis, breathing analysis, and their application to clinical anesthesia. My specialty in engineering is time-frequency analysis and physiological signal analysis. Time-frequency analysis is used to resolve multiple time-varying oscillatory components in the data. Physiological signal analysis contains multiple components, which are non-stationary due to biological nature. My specialty in medicine is clinical anesthesiology. Anesthesia is vital for every patient undergoing surgery. My current research is regarding the joint of these two fields.

Smart Medicine in Sedation, Anesthesia and Patient Monitoring

林祐霆醫師
臺北榮民總醫院麻醉部

In clinical medicine, sometimes the condition of human body needs to be watched with real-time continuous monitoring. Monitoring instruments in emergency room, operating room and critical care unit acquire large amount of physiological signal data. Though indispensable to people undergoing anesthesia and sedation, these physiological signals contain information currently being neglected. In this talk, I will present the merit of modern data analysis techniques in retrieving features in the data overlooked by human eyes. The output of modern time-frequency analysis, manifold learning, and modeling might smartly support the physician to make diagnosis and decision in the future.

Session 9 :
Disease Screening and Surveillance

主持人 邱弘毅講座教授

Name

邱弘毅

Position Title / Affiliations

特聘教授 / 臺北醫學大學公共衛生學系講座教授

Education and Degrees

1991-1996	國立臺灣大學公衛所流行病學組 博士
1987-1989	國立臺灣大學公衛所公共衛生組 碩士
1981-1985	國立臺灣大學公共衛生學系 學士

Current Position & Professional Experience

	臺北醫學大學 講座教授
2017- 迄今	臺北醫學大學公共衛生學系 特聘教授
2017- 迄今	臺北醫學大學應用分子流行病學學程 主任
2013- 迄今	臺北醫學大學健康暨臨床研究資料加值中心 主任
1999- 迄今	臺北醫學大學公共衛生學系 教授
2017- 迄今	亞太公共衛生學術聯盟 (APACPH) 副理事長
2017- 迄今	台灣長照及高齡健康管理發展協會 理事長
2016- 迄今	亞太癌症預防學會 (APOCP) 台灣區召集人
2013- 迄今	台北市政府衛生局公共衛生學門 學門長
2012-2017	臺北醫學大學 副校長
2009-2013	臺北醫學大學公共衛生暨營養學院 院長
2005-2009	臺北醫學大學公共衛生學系 主任
2000-2002	台灣國際健康功能與身心障礙分類系統 (ICF) 研究學會 理事長
2000-2003	台灣公共衛生學會 理事長
1997-2000	台灣流行病學學會創會 理事長

Research Interest

公共衛生
心血管／癌症分子流行病學
大型資料庫加值應用分析

Name

Hsiu-Hsi Chen

Position Title / Affiliations

Professor and Associate Dean / College of Public Health, National Taiwan University, Taipei, Taiwan

Education and Degrees

Ph.D. in Biostatistics, Biostatistics Unit of Medical Research Council (MRC), Institute of Public Health, Cambridge University, UK

Professional Experience

Chairman, Department of Public Health, CPH, NTU

Research Interest

Stochastic Process, Preventive Medicine

Stochastic Process for Disease Screening and Surveillance

Hsiu-Hsi Chen, Chen-Yang Hsu

Stochastic process used for elucidating the dynamics of multi-state outcomes have gained popularity. In health care science, it can be used to answer several common questions in relation to time dimensions particularly involved in a multi-state process, such as (a) How many bouts of health promotion or education, frequencies of health check-ups, round of screens, and rounds of adjuvant therapies, are required to achieve the targeted multi-state outcome (early stage cases)? (b) What is the exact time required to achieve the targeted outcome and also what is the exact dwelling time (sojourn time) between states if there are multi-state outcomes involved in the entire event process? (c) How many bouts (visits) required to reach the threshold value of an interval-scaled biomarker that is used for monitoring the flux of this biomarker (such as FIT) to reflect the disease (colorectal cancer)? (d) What is the exact time required to reach the threshold value of an interval-scaled biomarker that is used for monitoring the instantaneous change of this biomarker (such as blood pressure and heart rate in patients staying in intensive unit or during an operation) in instantaneous potential to reflect deterioration (recrudescence) or improvement (recovery)? More importantly, when it comes to personalized health care, all the questions (a)-(d) are related to whether the estimate of such a quantity related to time dimension varies with individual characteristics (including genetic predisposition, demographics (age, gender, and socio-economic status), relevant biomarkers, and disease attributes).

In this speech, I will propose a generalized stochastic regression framework by unifying different types of stochastic process which links different types of stochastic models in order to facilitate the systematic personalized health care.

Name

Amy Ming-Fang Yen

Position Title / Affiliations

Associate Professor / School of Oral Hygiene, Taipei Medical University

Education and Degrees

PhD in Biostatistics, University College London, London, UK

Professional Experience

2015.02-present	Associate Professor, School of Oral Hygiene, College or Oral Medicine, Taipei Medical University
2010.07-2015.01	Assistant Professor, School of Oral Hygiene, College or Oral Medicine, Taipei Medical University

Research Interest

Markov model, Disease Screening

Stochastic Model for Overdiagnosis in Disease Screening and Surveillance

Amy Ming-Fang Yen

Estimating over-diagnosed screen-identified cancers is a thorny issue in population-based service screening data. The Markov process with a variant Coxian phase-type distribution making allowance for these non-progressive (over-detected) cancers is therefore proposed to quantify the proportion of over-diagnosis in various types of population-based screening by combining the concept of the cure model. The two applications show a small fraction of over-detected breast cancer (3%) from mammography and a substantial proportion of over-detected prostate cancer (60%) from prostate specific antigen test. The proposed Coxian phase-type variant Markov process with separate non-progressive state can be further applied to economic decision analysis to deal with the harm caused by over- diagnosis.

Name

ChenYang Hsu 許辰陽

Position Title / Affiliations

Assistant Professor / National Taipei University of Nursing and Health Sciences

Education and Degrees

PhD and MSc Graduate Institute of Epidemiology and Preventive Medicine, College of Public Health, National Taiwan University, Taipei, Taiwan

MD Kaohsiung Medical University, Kaohsiung, Taiwan

Professional Experience

Post-Doctoral Research Fellow, Graduate Institute of Epidemiology and Preventive Medicine, College of Public Health, National Taiwan University, Taipei, Taiwan

Doctor, Dachung Hospital

Emergency Physician, Taipei City Hospital

Research Interest

Cancer Screening
Multistate model
Stochastic process
Epidemiology
Biostatistics
Medicine

Efficient Sampling-design in Multistate Disease Process for Screening and Surveillance

Chen-Yang Hsu, Weng-Fong Hsu

While the advancement in omics research render the realization of personalized prevention strategies possible, the information needed for stratifying target population into a spectrum of risk levels often relies on the results derived from longitudinal follow-up data for the entire cohort. The requirement for such a big data and the need for collecting information on novel biomarkers of entire population often makes this approach either costly or infeasible. Moreover, the issue of loss to follow-up is always a concern for tracing a cohort. Although case-cohort sampling design is an efficient method to assess the effect of factors on the occurrence of disease under the context of big cohort study, the application and the statistical characteristics have been barely addressed for multistate outcome. Chen et al. (2004) applied the case-cohort design to multi-state disease progression to quantify the effect of risk factors at each state of disease using prevalent screening data only, which render the estimated results vulnerable to length bias.

In this study, we extend the Chen's method and propose a multistate model with two-stage sampling design for the derivation of the state-specific effects of covariates and the baseline disease progression rates with the consideration of measurement error. The method was first applied to data on population-based colorectal cancer screening program to elucidate age- and sex- specific disease progression based on a three-state Markov model. We then validated the method by using simulated data on three-state breast cancer progression for the estimation of BRCA effect under the context of mass screening. The statistical performance of the proposed method was explored by using different sampling schemes. We further demonstrated the minimum sampling probability required to optimize the trade-off between efficiency and consistency.

Keywords: Markov model, cancer screening, case-cohort design

Name

Chao-Chih Lai

Position Title / Affiliations

Chief, Division of Emergency Medicine, Taipei City hospital, Ren-Ai branch, Taiwan

Education and Degrees

2010~2015	PhD in Graduate Institute of Epidemiology and Preventive Medicine, College of Public Health, National Taiwan University, Taiwan
2005~2007	Master in Graduate Institute of Preventive Medicine, College of Public Health, National Taiwan University, Taiwan
2004~2007	Field Epidemiology Training Program (FETP) of CDC, Taiwan

Professional Experience

2016~	Chief, Division of Emergency Medicine, Taipei City hospital, Ren-Ai branch, Taiwan
2000~	Attending physician, Emergency Medicine, Taipei City hospital, Ren-Ai branch, Taiwan

Research Interest

Biostatistics, Epidemiology, Outbreak investigation and infectious disease
Emergency Medicine and Critical Care Medicine, Toxicology
Infectious Disease

Stochastic differential equation model for disease surveillance

賴昭智主任
台北市立聯合醫院緊急醫療部

The definition of infectious disease surveillance is ongoing systematic collection, collation, analysis and interpretation of infectious disease data and the dissemination of information to those who need to know in order that action may be taken. We took hand, foot, and mouth disease (HFMD) for examples to explain how to estimate the value of the basic R0 and evaluate the impact of policies of the isolation strategy with the dynamic model according to the surveillance data. In addition, we provided a brief introduction to solving for the ordinary differential equation of the SIR model with the Markov Chain Monte Carlo method to estimate the basic R0 of MERS (Middle East Respiratory Syndrome) in Korea.

BIG DATA in Health Sciences

Innovations for health care, medical product development and regulatory science

Session 10 : Medical Product Developments and Related Topics

主持人 陳華鍵執行長

Name

Hua-Chien Chen, Ph.D. 陳華鍵 博士

Position Title / Affiliations

Chairman and CEO, Cofounder
ACT Genomics Co., Ltd.
行動基因生技股份有限公司 董事長兼執行長及創辦人之一

Education and Degrees

- Ph.D. in Biochemistry, National Yang-Ming University, Taipei, Taiwan 國立陽明大學生物化學研究所博士
- MS in Life Science, National Tsing Hua University, Hsinchu, Taiwan
- BS in Physics, National Tsing Hua University, Hsinchu, Taiwan 國立清華大學物理系學士及生科所碩士

Current Position & Professional Experience

- Associate Professor, Department of Biomedical Sciences, Chang-Gung University, Taiwan 長庚大學生物醫學系副教授
- Investigator & Molecular Biology Group Leader, TaiGen Biotechnology I 太景生物科技股份有限公司生物處處長
- Principle Investigator, Biotechnology and Pharmaceutical Research Division National Health Research Institutes (NHRI), Taiwan 國家衛生研究院生物技術與藥物研究組助研究員

Research Interest

- Profiling somatic mutations in cancer tissues using Next Generation Sequencing technology
- Developing new technology to detect somatic mutations in liquid biopsy
- Discover circulating microRNAs as biomarkers for tumor diagnosis and prognosis
- Delineating pathological roles of microRNA in human cancers

Name

Jinn-Moon Yang

Position Title / Affiliations

Professor / Institute of Bioinformatics and Systems Biology, NCTU

Education and Degrees

1994/9-2001/1	Ph.D., Computer Science, National Taiwan University, Taiwan
1992/9-1994/6	Master, Computer Science, National Central University, Taiwan

Professional Experience

2007/8-now	Professor of Institute of Bioinformatics and Systems Biology, NCTU
2007/8-2013/7	Director of Institute of Bioinformatics and Systems Biology, NCTU
2004/8-2007/7	Associate Professor of Institute of Bioinformatics and Systems Biology, NCTU
2001/8-2004/7	Assistant Professor of Institute of Bioinformatics and Systems Biology, NCTU

Research Interest

計算藥物設計、計算系統生物、生物資訊

Molecular Interaction Family for Systems Biology and Drug Design

楊進木教授
國立交通大學生物科技學系（所）

The concept of "one-disease, one-target, and one-drug" is the mainstream for drug discovery strategy in the past decades. However, complex diseases (e.g., cancers) are often typically caused by multiple genes and pathways. The drugs derived by the single-target strategy may become ineffective for complex diseases and lead to drug resistance. In this talk, I will introduce the Molecular Interaction Family, such as protein-drug, protein-protein, and protein-DNA families, for exploring molecular interaction/pathway mechanisms with therapeutic targets which are essential for complex diseases. Based on MIF core concept, we have proposed several models (i.e., Homopharma and NetPharmalogs) to discover the inhibitors that inhibit multiple targets in the same pathway or in multiple pathways to increase therapeutic potency and decrease drug resistance for complex diseases. Furthermore, we have built drug-protein-pathway-disease network for the integrations of systems biology and drug design. We have successfully utilized these new computational models to explore the binding and pathway mechanisms for drug design and complex diseases. Additionally, I will also describe several application cases: 1) Discovering new mechanisms and new type inhibitors that are high selectivity and anti-drug resistance for protein kinases; 2) Membrane protein-regulated networks across human cancers; 3) Compound-protein-pathway-disease networks for multiple ingredients of a plant (or herb).

Name

Li-Wei Kuo

Position Title / Affiliations

Assistant Investigator, Institute of Biomedical Engineering and Nanomedicine, National Health Research Institutes, Miaoli, Taiwan

Education and Degrees

2003-2008	Ph.D., Department of Electrical Engineering, National Taiwan University, Taipei, Taiwan
2001-2003	M.S., Department of Electrical Engineering, National Taiwan University, Taipei, Taiwan
1997-2001	B.S., Department of Electrical Engineering, National Taiwan University, Taipei, Taiwan

Professional Experience

2016/8-Present	Adjunct Assistant Professor, Institute of Medical Device and Imaging, National Taiwan University College of Medicine, Taipei, Taiwan
2013/7-Present	Assistant Investigator, Institute of Biomedical Engineering and Nanomedicine, National Health Research Institutes, Miaoli County, Taiwan
2011/9-2013/6	Assistant Investigator, Division of Medical Engineering Research, National Health Research Institutes, Miaoli County, Taiwan
2010/4-2011/8	Visiting Fellow, Advanced MRI Section, Laboratory of Functional and Molecular Imaging, National Institute of Neurological Disorders and Stroke, National Institutes of Health, Bethesda, USA
2009/6-2010/3	Postdoctoral Research Fellow, Advanced Biomedical Lab, Center for Optoelectronic Biomedicine, National Taiwan University College of Medicine, Taipei, Taiwan

Research Interest

Medical Imaging Instrumentations, Magnetic Resonance Imaging, Brain Neuroimaging, Medical Image and Signal Processing

Exploring Human Brain Networks with Advanced MR Neuroimaging Technology

郭立威助研究員
國家衛生研究院生醫工程與奈米醫學研究所

During the past decade, mapping complex structural and functional networks in living human brain using non-invasive neuroimaging technologies has been widely developed and employed on a variety of cognitive and clinical neuroscience researches. Among all modern neuroimaging technologies, magnetic resonance imaging (MRI) has been considered as one of the most reliable and reproducible neuroimaging modalities for exploring the complex brain networks with adequate spatial and temporal resolutions. In this talk, I will introduce how advanced MRI neuroimaging technology can map the brain networks and how the advance of computational technology can accelerate the data acquisition, improve the image reconstruction and enhance the image analysis. Also, the relevance of these technologies to facilitate neuroscience researches and translational applications will be discussed.

Name

Henry Horng-Shing Lu

Position Title / Affiliations

Vice President for Academic Affairs,
National Chiao Tung University,
Taiwan.

Education and Degrees

1994	Ph.D. in Statistics, Cornell University, USA
1990	M.S. in Statistics, Cornell University, USA
1986	B.S. in Electric Engineering, National Taiwan University, Taiwan

Professional Experience

2002/2-present	Professor, Institute of Statistics, College of Science, National Chiao Tung University, Taiwan
2016/1-present	Vice President for Academic Affairs, National Chiao Tung University, Taiwan
2015/7-2018/1	Director, Big Data Research Center, National Chiao Tung University, Taiwan
2011/8-2014/7	Dean, College of Science, National Chiao Tung University, Taiwan
2008/2-2011/7	Chairman, Interdisciplinary Sciences Degree Program, College of Science, National Chiao Tung University, Taiwan
2002/8-2005/7	Director, Institute of Statistics, College of Science, National Chiao Tung University, Taiwan

For more detail : http://www.stat.nctu.edu.tw/misg/eindex.htm

Research Interest

Statistics and Applications

On AI for Medical Images

盧鴻興教務長
國立交通大學

With the thriving of deep learning techniques and high-speed graphics processing units, recent years have witnessed the beginning of a golden era of AI-based medical image analysis and diagnosis. Practicing smart healthcare and using artificial intelligence techniques to classify, segment, and track diseases in medical images, thereby relieving clinicians from the heavy burden of image diagnosis and improving healthcare quality, have evolved into a global trend. In particular, rapidly growing deep learning techniques such as transfer learning, YOLO, and U-Net may be combined with traditional machine learning methods and applied to medical images at varied data volume levels to broaden the spectrum of AI-based diagnostic techniques for medical images. This talk takes practical clinical issues concerning atrial fibrillation, vertebral compression fracture, glaucoma, and intracranial metastasis as examples to explain how important deep/machine learning techniques may be integrated with clinical medical data and professional clinicians' accumulated experience. In the long run, the development of AI-based medical image analysis and diagnosis methods is expected to enhance the establishment of more instant, accurate, and comprehensive clinical diagnoses.

NATIONAL HEALTH RESEARCH INSTITUTES
NHRI

Ministry of Health and Welfare
衛生福利部

NCFB
生技醫藥核心設施平台
National Core Facility for Biopharmaceuticals

ICSA
泛華統計協會

BIG DATA in Health Sciences

Innovations for health care, medical product development and regulatory science