生物資訊暨生物統計核心實驗室

Bioinformatics and Biostatistics Core Laboratory

卓越成員 Remarkable member

Eric Y. Chuang　莊曜宇

Professor教授
臺灣大學生醫電子與資訊學研究所

✚ EDUCATION AND POSITION HELD：

- Sc.D.. (Cancer Biology), 1997, Harvard University, Cambridge, MA
- M.S. (Biology), 1991, Illinois Institute of Technology, Chicago, IL
- B.S. (Biology), 1986, Tunghai University, Taichung, Taiwan
- Professor, 2006-present; Faculty member, 2005-2006, 2002-2004, National Taiwan University, Department of Public Health
- Adjunct Professor, 2006-present; Professor, 2003-2006; Acting Director, Aug.-Dec. 2005; Associate Professor, 1995-2003; ・Instructor, 1994-1995,National Taiwan University, Institute of Epidemiology

✚ HONOR：

- On-the-Spot Award, US Department of Health and Human Services, Public Health Service, 2001
- Travel Award (top 5-ranked winner), 11th International Congress of Radiation Research, Dublin, Ireland, 1999
- Postdoctoral National Research Service Award, US Department of Health and Human Services, 1997
- Student Travel Award, 27th Annual Meeting of the Environmental Mutagen Society, Victoria, British Columbia, Canada, 1996
- Student Travel Award, 43rd Annual Meeting of the Radiation Research Society, San Jose, California, 1995

✚ RESEARCH INTERESTS：

Our major research interests are development and analysis of genomic alteration, bioinformatics algorithm and biostatistical methodology. Current projects include the detection of genetic mutation, concurrent analysis, and hypermethylation detection in esophageal cancer, in non-smoking female lung cancer, and heart failure patients. We also focus on database construction such as DataBase of CpG islands and Analytical Tool (DBCAT), cancer repository system (CRS), first online gene expression analysis platform in Taiwan (NTUMAPs), and algorithm development.

✚ SELECTED PUBLICATION：

- Chen HI, Hsu FH, Jiang Y, Tsai MH, Yang PC, Meltzer PS, Chuang EY, Chen Y. A probe-density-based analysis method for array CGH data: simulation, normalization and centralization. *Bioinformatics* **2008,** 24(16):1749-56.
- Lin YF, Nagasawa H, Peng Y, Chuang EY, Bedford JS. Comparison of several radiation effects in human MCF10A mammary epithelial cells cultured as 2D monolayers or 3D acinar stuctures in matrigel. *Radiat Res.* **2009,** 171:708-15.
- Lu TP, Lai LC, Lin BI, Chen LH, Hsiao TH, Liber HL, Cook JA, Mitchell JB, Tsai MH, and Chuang EY. Distinct signaling pathways after higher or lower doses of radiation in three closely related human lymphoblast cell lines. *Int J Radiat Oncol Biol Phys.* **2010,** 76:212-19.
- Hsiao TH, Lin CH, Lee TT, Cheng JY, Wei PK, Chuang EY, and Peck K. Verifying expressed transcript variants by detecting and assembling stretches of consecutive exons. *Nucleic Acids Res.* **2010,** 38(20):187.
- Lu TP, Tsai MH, Lee JM, Hsu CP, Chen PC, Lin CW, Shih JY, Yang PC, Hsiao CK, Lai LC, and Chuang EY. Identification of a novel biomarker, SEMA5A, for non-small cell lung carcinoma in nonsmoking women. *Cancer Epidemiol Biomarkers Prev.* **2010,** 19:2590-97.

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Chunsing Kate Hsiao　蕭朱杏

Professor 教授
臺大公共衛生學院公共衛生學系流行病學與預防醫學研究所

EDUCATION AND POSITION HELD：

- B.S. (Mathematics), National Tsing Hua University, 1986
- M.S. (Statistics), Carnegie Mellon University, 1989
- Ph.D. (Statistics), Carnegie Mellon University, 1994
- Associate Professor, Graduate Institute of Epidemiology, National Taiwan University, 1995-2003
- Acting Director, Graduate Institute of Epidemiology, National Taiwan University, Oct-Dec, 2005
- Professor, Department of Public Health, National Taiwan University, 2003-Present
- Professor, Graduate Institute of Epidemiology, National Taiwan University, 2003-Present

HONOR：

- Excellent Research Award (National Science Council 1996-1998).
- Excellent Teaching Award, 2001; 2005; 2007; 2009; 2011
- Grant Research Award, (National Science Council) since 2002.
- National Science Council, Department of Health; Bureau of Health, 1995-Present

RESEARCH INTERESTS：

Bayesian statistics, Bioinformatics, Biostatistics, Genetic statistics.

SELECTED PUBLICATION：

- Chen PC, Huang SY, Chen WJ, Hsiao CK. A new regularized least squares support vector regression for gene selection. *BMC Bioinformatics* **2009,** 10:44.
- Wei YC, Wen SH, Chen PC, Wang CH, Hsiao CK. A simple Bayesian mixture model with a hybrid procedure for genome-wide association studies. *European Journal of Human Genetics* **2010,** 942-947.
- Chan TC, King CC, Yen MY, Chiang PH, Huang CS, Hsiao CK. Probabilistic daily ILI syndromic surveillance with a spatio-temporal Bayesian hierarchical model. *PLoS ONE* **2010,** 5(7):e11626.
- Hsiao CK, Chen PC, Kao WH. Bayesian random effects for inter-rater and test-retest reliability with nested clinical observations. *Journal of Clinical Epidemiology* **2011,** 64(7):808-814.
- Lee M, Tzeng JY, Huang SY, Hsiao CK. Combining an evolution-guided clustering algorithm and haplotype-based LRT in family association studies. *BMC Genetics* **2011**, 12:48.
- Huang YH, Lee MH, Chen WJ, Hsiao CK. Using an uncertainty-coding matrix in Bayesian regression models for haplotype-specific risk detection in family association studies. *PLoS ONE* **2011**, 6(7):e21890.

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卓越成員 Remarkable member

Liang-Chuan Lai 賴亮全

Assistant Professor 助理教授
臺大醫學院生理學研究所

EDUCATION AND POSITION HELD：

- B. S. in Physical Therapy, College of Medicine, National Taiwan University, 1988-1992.
- M.S. in Physiology, College of Medicine, National Taiwan University, 1992-1994.
- Teaching assistant, Department of Physiology, College of Medicine, National Taiwan University, 1996-1998.
- M.S. in Physiology, University of Illinois at Urbana-Champaign, USA, 1998-2001.
- Ph.D., University of Illinois at Urbana-Champaign, USA, 1998-2005.
- Post Doc Research Associate, University of Illinois at Urbana-Champaign, USA, 2005-2007.
- Assistant Professor, Department of Physiology, College of Medicine, National Taiwan University, 2007-present.

HONOR：

- Young Investigator Award, 7th Federation of the Asian and Oceanian Physiological Societies Congress, 2011.

RESEARCH INTERESTS：

Our major research interests are using microarray to explore the cancer genomics. Approaches to understand the mechanism of cancer genome by investigating gene expression profiling, copy number variation, single nucleotide polymorphism, epigenetics and microRNA in several cancers, including lung cancer, breast cancer, and esophageal cancer. Recently we identified that several semaphorin gene family members can be used as potential therapeutic targets, and that SEMA5A may be useful as a prognostic biomarker for non-smoking women with non-small cell lung carcinoma.

SELECTED PUBLICATION：

- Lu TP, Tsai MH, Lee JM, Hsu CP, Chen PC, Lin CW, Shih JY, Yang PC, Hsiao CK, Lai LC, Chuang EY. Identification of a Novel Biomarker SEMA5A for Non-Small Cell Lung Carcinoma in Non-Smoking Women. *Cancer Epidem Biomar,* **2010,** 19:2590-97.
- Lu TP, Lai LC, Lin BI, Chen LH, Hsiao TH, Liber HL, J.A. Cook, J.B. Mitchell, Tsai MH, and E. Y. Chuang. *Int J Radiat Oncol Biol Phys,* **2010,** 76:212-19.

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Mong-Hsun Tsai　蔡孟勳

Assistant Professor 助理教授
臺大農學院生物科技研究所

✚ EDUCATION AND POSITION HELD：

· B.S. (Zoology), National Taiwan University, 1993.
· M.S. (Radiation Biology), National Tsing Hua University, 1995.
· Ph.D. (Public Health), National Yang Ming University, 2001.
· Associate Professor, Institute of Biotechnology, National Taiwan University, 2006-Present.

✚ RESEARCH INTERESTS：

· Radiation Biology, Biochip, Cell Biology, Bioinformatics.

✚ SELECTED PUBLICATION：

· Lu TP, Lai LC, Lin BI , Chen LH, Hsiao TH, Howard L. Liber, John A. Cook, James B. Mitchell, Tsai MH and Chuang EY. Distinct signaling pathways after higher or lower doses of radiation in three closely related human lymphoblast cell lines. *Int. J. Radiation Oncology Biol. Phys.* **2010,** 76(1):212-19.

· Lu TP, Tsai MH, Lee JM, Hsu CP, Chen PC, Lin CW, Shih JY, Yang PC, Hsiao CK, Lai LC, and Chuang EY. Identification of a Novel Biomarker, SEMA5A, for Non–Small Cell Lung Carcinoma in Nonsmoking Women. *Cancer Epidemiology, Biomarkers & Prevention* **2010,** 19:2590-97.

· Lin CY, Lin HH, Tsai MH, Lin SP, Chen MH. Zinc Chloride for Odontogenesis of Dental Pulp Stem Cells via Metallothionein Upregulation. *Journal of Endodontics* **2010,** 37(2):211-16.

· Lin CY, Lin HH, Tsai MH, Lin SP, Chen MH. Zinc chloride for odontogenesis of dental pulp stem cells via metallothionein up-regulation. *JEndod* **2011,** 37(2):211-6.

Remarkable result 卓越成績

參與成員：莊曜宇 教授 Eric Y. Chuang、蕭朱杏 教授 Chuhsing Kate Hsiao
蔡孟勳　助理教授 Mong-Hsun Tsai、賴亮全　助理教授 Liang-Chuan Lai

Following the development of advanced technologies in biomedical science, large quantity of basic and clinical data can be generated and obtained effectively through new techniques. For instance, DNA microarray, methylation chips, array comparative genomic hybridization arrays, microRNA arrays, and SNP (Single Nucleotide Polymorphism) arrays provide new platforms for studying genomic medicine. In the post-genomic era, the rapidly increasing number of nucleotide and amino acid sequence data has become a major source of information for biomedical researchers. Knowing how to use appropriate software tools running on powerful computers is a necessity for biologists to identify new genes or targets.

Information about the genetic abnormalities associated with a target disease in human genome can be easily derived and analyzed using both the techniques that confer the vast data of biostatistics and the high performance of computer operation. The establishment of a research service core of Bioinformatics supports the NTU Research Center for Medical Excellence with the issues of genomic information as well as clinical research by utilizing database processing and statistical analysis. This core is devoted to the methodological research of bioinformatics and will provide necessary training courses to researchers and students within the University. In addition, this core is involved in the development, maintenance and management of the center web-site and the file sharing servers. Therefore, the support from biostatistics and bioinformatics is an important issue and becomes an immediate need for medical researchers. Hopefully, with the establishment of this Bioinformatics and Biostatistics Core Facility, the resources in bioinformatics, biostatistics and genomic medicine can be fully integrated in order to extract meaningful INFORMATION from DATA and become valuable KNOWLEDGE.

Figure.1 NTUMAPs. The first online microarray analysis platforms (MAPs) in Taiwan. Users are able to perform the various bioinformatics algorithms and statistical approaches to analyze microarray data. An user-friendly interface is provided to complete in silico analyses.

The primary goal of this Bioinformatics and Biostatistics Core is to provide SERVICES to all biomedical investigators. In addition, we devoted our efforts to conducting the research and development related to biostatistics and bioinformatics.

The specific aims of Bioinformatics and Biostatistics Core are：
1. Microarray data analysis and data mining including gene chips, methylation chips, aCGH chips, miRNA chips, and SNP chips.
2. Microarray data analysis consultation to researchers within/outside NTU.
3. Development of microarray related biostatistical and bioinformatic algorithms.
4. Development of biomedical databases.
5. Association study between disease and genome.
6. To develop analytical systems and tools for genomic research. For instance, the National Taiwan University Microarray Analysis Platform and system (NTUMAPs), an on-line analytical system with powerful function in database management, has been established and maintained by this core facility. This system provides users to proceed with gene analysis, gene match and information search. The database server is the first web-based expert system for DNA microarray analysis in Taiwan; besides managing a large number of chip image files and results, it also can provide results of specific gene analysis to users through statistical and computational methods.
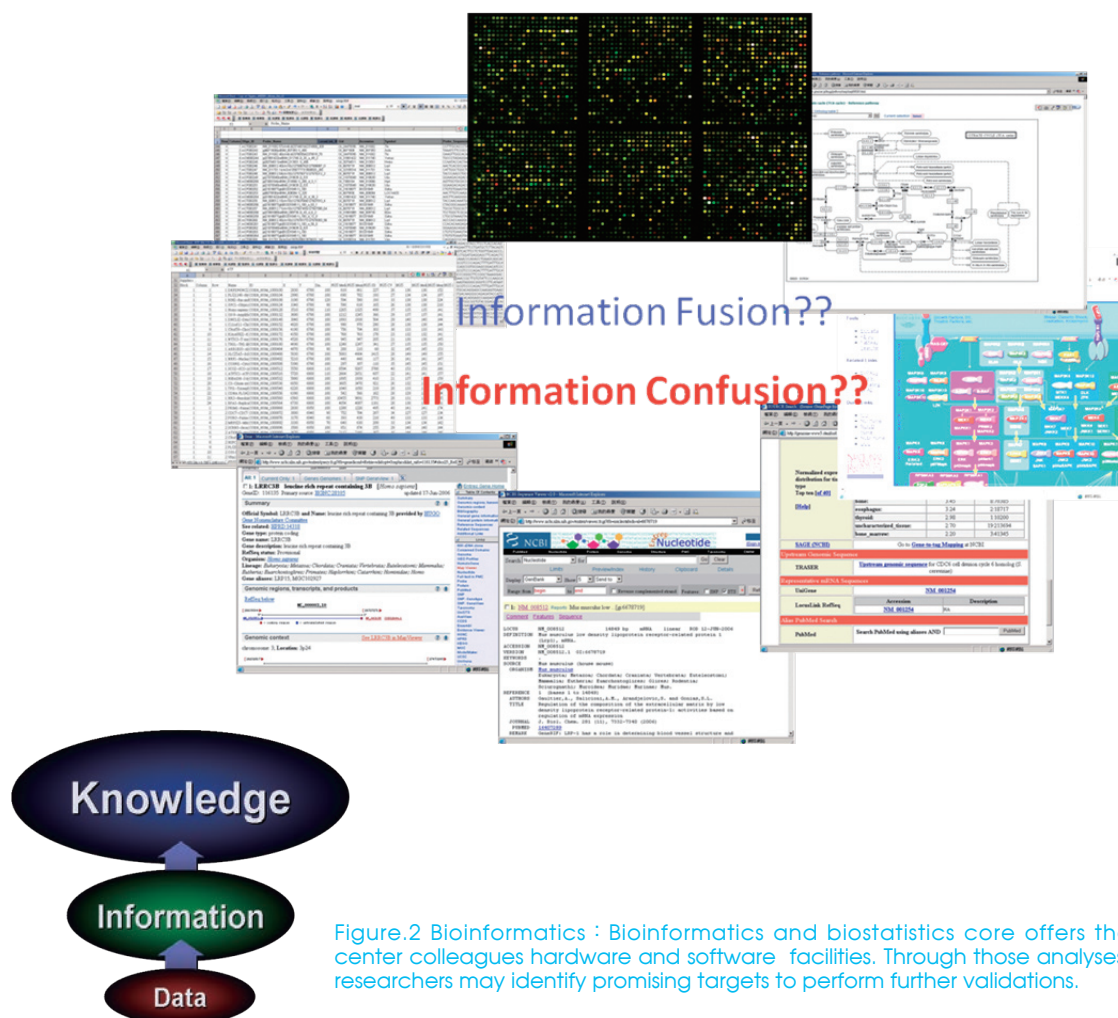

Figure.2 Bioinformatics：Bioinformatics and biostatistics core offers the center colleagues hardware and software facilities. Through those analyses, researchers may identify promising targets to perform further validations.
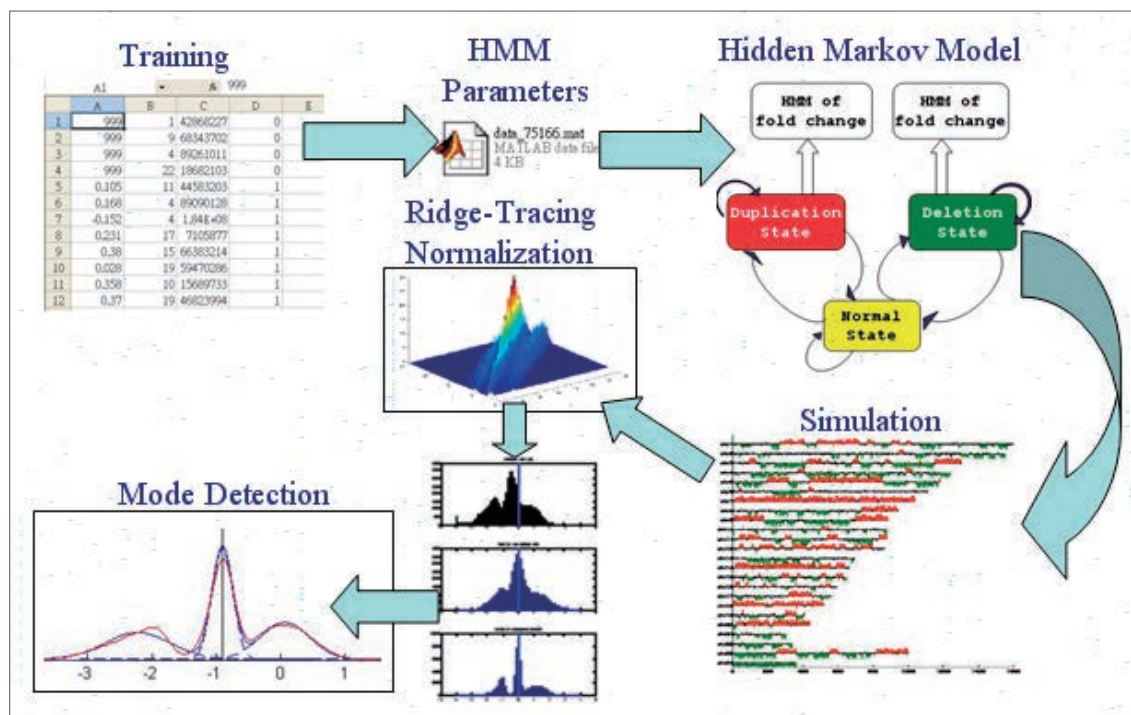
Figure. 3 Array CGH Normalization Flowchart. A probe-density-based analysis method for array CGH data: simulation, normalization, and centralization. *(Chen HI et al, Bioinformatics 2008)*
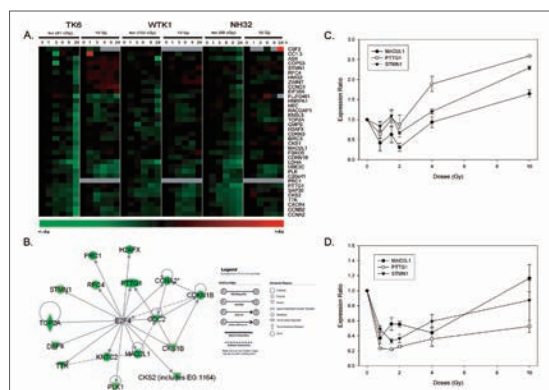

Figure. 4 Expression profiles of differentially expressed genes in lung cancer tissues. Microarray-based analysis of gene expression in 60 pairs of lung cancer patients. *(Lu TP et al, Int J Radiat Oncol Biol Phys 2010)*
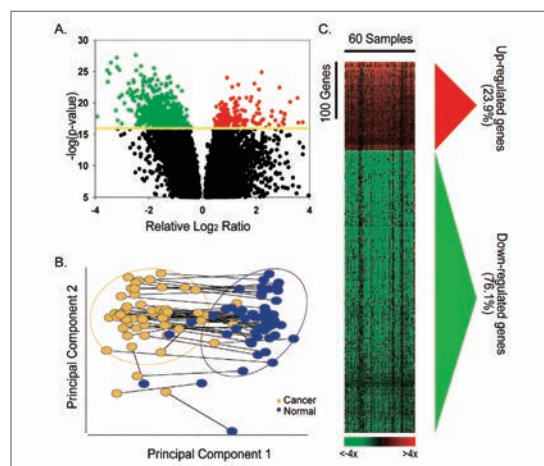

Figure. 5 Data mining Data base searching and analysis tools which can integrate information. *(Lu TP et al, Cancer Epidemiol Biomarkers Prev 2010)*
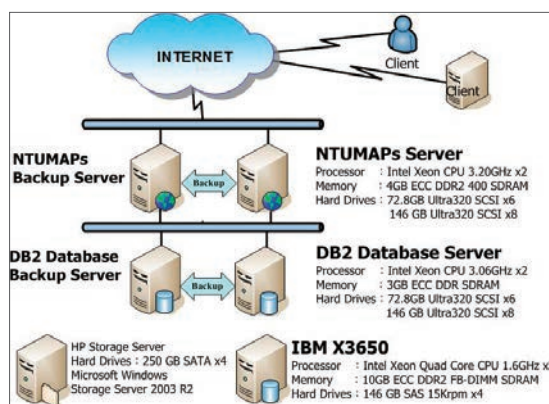

Figure. 6 The hardware of NTUMAPs. After uploading chip data, users are able to use the various algorithms and databases to do analysis.

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申請服務流程

從臺大基因體醫學研究中心首頁中,選擇「生物資訊暨生物統計」分項子計劃進入,再點選左側「申請服務」之選項。

▼

下載服務申請表,並來電預約分析服務諮詢。

▼

繳交服務申請表和待分析之實驗晶片數據,並依據服務申表所填晶片數量和分析方式報價。

▼

依據服務申請表所填之內容和實驗設計,初步檢驗待分析晶片之格式與品質。

→ 晶片內容格式不符或品質不佳,而無法分析即原件退回,等候資料更新。 ←

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進行分析

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分析完成後,以電子郵件回傳分析結果,或是利用儲存媒體現場拷貝

▼

分析結果討論與收費

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