

[Name] Hsin-Chou Yang (楊欣洲)

[Joint appointments]

- 2018.01 – Present Research Fellow. Institute of Statistical Science, Academia Sinica
- 2008.02 – Present Core Faculty. Bioinformatics Program, Taiwan International Graduate Program, Academia Sinica
- 2011.02 – Present Core Faculty. Translational Medicine Program, Degree Program, Academia Sinica
- 2016.02 – Present Adjunct Associate Professor. Institute of Statistics, National Tsing Hua University
- 2016.12 – Present Core Faculty. Data Science Program, Degree Program, Academia Sinica & National Taiwan University
- 2017.12 – Present Joint Associate Professor. Institute of Public Health, National Yang-Ming University
- 2018.09 – Present Joint Professor. Institute of Statistics, National Cheng-Kung University

[Work experience]

- 2002.10 – 2004.06 Postdoctoral Fellow of National Science Council (in Institute of Biomedical Sciences, Academia Sinica) [In military service]
- 2004.07 – 2006.06 Postdoctoral Fellow of Academia Sinica (in Institute of Biomedical Sciences, Academia Sinica) [In military service]
- 2006.07 – 2011.03 Assistant Research Fellow. Institute of Statistical Science, Academia Sinica
- 2011.03 – 2018.01 Associate Research Fellow. Institute of Statistical Science, Academia Sinica
- 2012.09 – 2018.06 Adjunct Associate Professor. School of Public Health, National Defense Medical Center
- 2014.09 – 2017.12 Adjunct Associate Professor. Institute of Public Health, National Yang-Ming University
- 2015.02 – 2018.09 Joint Associate Professor. Institute of Statistics, National Cheng-Kung University

[Review service – Journal editorial board (> 50 papers)]

1. BMC Medical Research Methodology (Associate Editor: 2012/11 – present)
2. Computational Statistics (Associate Editor: 2013/10 – present)
3. Frontiers in Statistical Genetics and Methodology (Review Editor: 2011/09 – present)
4. Journal of Metabolomics and Systems Biology (Review Editor: 2014/05 – present)
5. Journal of the Chinese Statistical Association (Associate Editor: 2018/07 – present)
6. Statistica Sinica (Associate Editor: 2014/08 – 2017/07)
7. Statistica Sinica (Managing Editor: 2014/08 – 2017/07)

[Journal review service (> 80 papers)]

1. American Journal of Hypertension
2. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics
3. Annals of Applied Statistics
4. Australian and New Zealand Journal of Statistics
5. Bioinformatics
6. Biometrics
7. Biometrika
8. BMC Bioinformatics
9. BMC Genetics
10. BMC Medical Research Methodology
11. BMC Research Notes
12. Briefings in Bioinformatics
13. Cancer Informatics
14. Computer Methods and Programs in Biomedicine
15. Computational Statistics
16. Computational Statistics and Data Analysis
17. Diagnostics
18. Expert Opinion on Drug Metabolism and Toxicology
19. Frontiers in Statistical Genetics and Methodology
20. Genetic Epidemiology
21. Genetics
22. ISRN Bioinformatics
23. Journal of Clinical Bioinformatics
24. Journal of Data Science
25. Journal of Medical Genetics
26. Journal of Medical Genetics and Genomics
27. Journal of Probability and Statistics
28. Malaysian Journal of Medical Sciences
29. Molecular Ecology Resources
30. Neuroimmunomodulation
31. Nucleic Acids Research
32. PeerJ
33. PLoS One
34. Scientific Reports
35. Statistica Sinica
36. Statistics in Medicine
37. Test

[Grant review service]

1. Department of Life Sciences, Ministry of Science and Technology
2. Department of Natural Sciences, Ministry of Science and Technology
3. Indonesian Science Fund under the Indonesian Academy of Sciences
4. Ministry of Education
5. National Taiwan University

[Other publication --- Journal paper (Chinese)]

1. Zen, M. M. and [Yang, H.-C.](#) (1996). Estimating the sequential continuity of a semi-Markov process. *Journal of Chinese Statistical Association* (中國統計學報) **34**, 256-274. (In Chinese with English abstract)
2. Chao, A., Lin, S.-P., [Yang, H.-C.](#) and Yip, P. S. F. (2000). The analysis of Hong Kong Big Bird Race data for the year of 2000. *Journal of Chinese Statistical Association* (中國統計學報) **38**, 231-241. (In Chinese with English abstract)
3. [Yang, H.-C.](#) (2007). Disease gene mapping (淺談致病基因定位). *Academia Sinica E-News* (中央研究院電子報) **47**, 3-5. (In Chinese)

[Other publication --- Degree thesis]

1. [Yang, H.-C.](#) (1996). *On Sequential Continuity Based on Semi-Markov Process*. Master thesis, Institute of Statistics, National Cheng Kung University, Tainan, Taiwan. (Under supervision of Prof. Mei-Mei Zen)
2. [Yang, H.-C.](#) (2002). *The Applications of Markov Chain Models and Kernel Smoothing in Capture-Recapture Experiments*. Ph.D. thesis, Institute of Statistics, National Tsing Hua University, Hsin Chu, Taiwan. (Under supervision of Prof. Anne Chao)

[Invited presentation in international conferences or oversea academic institutes]

1. *New adjustment factors and sample size calculation in a DNA-pooling experiment with preferential amplification* (2004/Sep/24). Department of Statistics Latrobe University, Melbourne, Australia. (Invited by Prof. Guoqi Guo)
2. *Disease gene mapping using pooled DNA experiments* (2006/Aug/17). Institute of Mathematics and Statistics, University of Melbourne, Melbourne, Australia. (Invited by Prof. Richard Huggins)
3. *Pooled DNA analysis using oligonucleotide arrays* (2007/Jun/14). The NSF Sponsored International Conference on Bioinformatics, Zhejiang, China. (Invited by Prof. Xiaotong Shen)
4. *KBAT: Kernel-based association test* (2007/Nov/29). Institute of Statistical Mathematics, Tokyo, Japan. (Invited by Institute of Statistical Mathematics).
5. *KBAT: Kernel-based association test* (2007/Dec/29). The International Conference on Multiple Decision Theory, Statistical Inference and Applications, Taipei, Taiwan. (Invited by Prof. Yen-Feng Chiu)
6. *Genomic dissection of preferential amplification/hybridization based on three large-scale genomic projects* (2008/Sep/25). MD Anderson Cancer Center Epidemiology, Texas, USA.

(Invited by Drs. Sanjay Shete and Chih-Chieh Wu)

7. *Applications of individual-level allele frequency in genomic studies* (2010/Jan/22). Indian Statistical Institute (The ISI-ISM-ISSAS Joint Meeting on Statistics & Probability), Kolkata, Indian. (Invited by Indian Statistical Institute)
8. *Homozygosity disequilibrium and its applications* (2011/Sep/28-30). The 9th Symposium of Bioinformatics and Systems Biology in Taiwan. Taipei, Taiwan. (Invited by Profs Chuan-Hsiung Chang and Ueng-Cheng Yang)
9. *Homozygosity disequilibrium and its applications* (2012/Jul/02-04). The 2nd Institute of Mathematical Statistics Asia Pacific Rim Meeting. Tsukuba, Japan. (Invited by Prof. Sungho Won)
10. *Deciphering population genomics and medical genomics through homozygosity disequilibrium using whole-genome single nucleotide polymorphism and next-generation sequencing data* (2013/Aug/21). 2013 International Symposium on Statistical Genetics. Seoul, Korea. (Invited by Prof. Taesung Park)
11. *Genetic dissection of diverse disease prevalence and drug metabolism in human populations using ancestral informative markers* (2013/Aug/22-23). Joint Meeting of the IASC Satellite Conference for the 59th ISI WSC and the 8th Conference of the Asian Regional Section (ARS) of the IASC. Seoul, Korea. (Invited by Dr. Grace Shieh)
12. *Deciphering medical genomics and population genomics using single nucleotide polymorphisms and other types of genetic markers* (2013/Oct/18-20). The 11th Symposium of Bioinformatics and Systems Biology in Taiwan. Taipei, Taiwan. (Invited by Prof. Hsuan-Cheng Huang)
13. *Deciphering medical genomics and population genomics using single nucleotide polymorphisms and other types of genetic markers* (2013/Nov/17-21). The International Workshop on Statistical Genetics. Shanghai, China. (Invited by Prof. Zhiliang Ying)
14. *Applying genome-wide gene-based expression quantitative trait locus mapping to study population ancestry and pharmacogenetics* (2014/Jun/29-Jul/03). The 3rd Institute of Mathematical Statistics Asia Pacific Rim Meeting. Taipei, Taiwan. (Invited by Prof. Ming-Yen Cheng)
15. *Homozygosity disequilibrium and its importance in medical genomics and population genomics* (2014/Dec/06). 2014 Frontiers in Genomic Research. Tainan, Taiwan. (Invited by Prof. Shuen-Lin Cheng)
16. *Homozygosity disequilibrium and its importance in medical genomics and population genomics* (2014/Dec/28-30). IASSL-2014 (Conference at Institute of Applied Statistics at Sri Lanka). Colombo, Sri Lanka. (Invited by Prof. Sanjay Shete)
17. *Genome-wide Association Study Identifies SNP rs17180299 and Multiple Haplotypes on CYP2B6, SPON1 and GSG1L Associated with Plasma Concentrations of the Methadone R- and S-enantiomer in Heroin-dependent Patients under Methadone Maintenance*

- Treatment* (2015/Apr/02-04). The ISI-ISM-ISSAS Joint Conference, Tokyo, Japan. (Invited by Institute of Statistical Mathematics)
18. *Recovering the missing heritability of complex diseases* (2015/Apr/19-20). 2015 Joint Statistical Workshop of the Chinese University of Hong Kong and Academia Sinica. Taipei, Taiwan. (Invited by Dr. Chun-Houh Chen)
 19. *Necessity of statistical data analysis* (2015/Jun/09-11). 2015 GloSYS ASEAN Regional Workshop. Phuket, Thailand. (Invited by Dr. Orakanoke Phanraksa)
 20. *SMART: Statistical Metabolomics Analysis – an R Tool* (2016/Jan/31-Feb/02). The ISI-ISM-ISSAS Joint Conference, Taipei, Taiwan. (Invited by Dr. Tso-Jung Yen)
 21. *GloSYS ASEAN – Quantitative data analysis* (2016/Mar/07-09). GloSYS ASEAN Wrap Up Meeting. Bangkok, Thailand. (Invited by Dr. Orakanoke Phanraksa)
 22. *The Global State of Young Scientists Project GloSYS – ASEAN* (2016/Mar/16-Mar/18). The Asia Meeting of Young Scientist 2016, Tokyo, Japan. (Invited by Dr. Mitsunobu Kano)
 23. *An integrated analysis tool for analyzing hybridization intensities and genotypes using new-generation population-optimized human arrays* (2016/Sep/05-Sep/07). The Japan Joint Statistical Meeting 2016, Kanazawa, Japan. (Invited by Dr. Hideatsu Tsukahara)
 24. *An integrated analysis tool for analyzing hybridization intensities and genotypes using new-generation population-optimized human arrays* (2016/Dec/19-Dec/22). The 10th ICSA International Conference on Global Growth of Modern Statistics in the 21st Century, Shanghai, China. (Invited by Dr. Mei-Ling Ting Lee)
 25. *Statistical analysis tools for biobank genomics data* (2017/Sep/11-Sep/13). VUMC & Academia Sinica Mini-Symposium, Nashville, Tennessee, USA. (Invited by Prof. Yu Shyr)
 26. *Genome-wide analysis of genotypes and hybridization intensities in genomic medicine* (2018/July/01). 30th Anniversary of National Cheng Kung University Hospital – International Symposium of Biomedical Big Data and Precision Medicine in Medical Care, Tainan, Taiwan. (Invited by Deputy Superintendent of NCKUH and Distinguished Prof. Meng-Ru Shen)

[Invited presentation in domestic conferences]

1. *Population size estimation using local sample coverage for open populations* (2003/Jun/26). The 12th Southern Taiwan Statistical Conference. Kaohsiung, Taiwan. (Invited by Prof. Hung Chen)
2. *New adjustment factors and sample size calculation in a DNA-pooling experiment with preferential amplification* (2004/Jun/24). The 13th Southern Taiwan Statistical Conference. Taipei, Taiwan. (Invited by Prof. Hung Chen)
3. *Disease gene mapping using pooled DNA experiments* (2006/Jul/29). The 5th Cross-Strait Conference on Statistics and Probability and Annual Meeting of the Chinese Institute of Probability and Statistics. Miaoli, Taiwan. (Invited by Prof. John Jen Tai)
4. *Genome-wide association study of young-onset hypertension in the Han Chinese*

- population of Taiwan* (2009/Jun/05-06). Workshop on Statistical Methodology of Microarray Data. Taipei, Taiwan. (Invited by Prof. Chun-Houh Chen)
5. *LOHAS: Loss-of-heterozygosity analysis suite* (2010/May/01-02). The 2010 Annual Meeting of the Chinese Institute of Probability and Statistics. Hualien, Taiwan. (Invited by Prof. Shen-Ming Lee)
 6. *Statistics tells you where disease genes are (統計告訴你致病基因在哪裡)* (2010/Sep/02). Statistical Camp, Institute of Statistical Science, Academia Sinica, Taipei, Taiwan. (Invited by Prof. Henghsiu Tsai)
 7. *Dissection of human genome using single nucleotide polymorphism* (2011/Jun/22). Workshop on High-Dimensional Data Modeling. Taipei, Taiwan (Invited by Prof. Hung Chen)
 8. *SAQC: SNP array quality control* (2011/Jun/24-25). The 20th Southern Taiwan Statistical Conference and the 2011 Annual Meeting of the Chinese Institute of Probability and Statistics. Chia-Yi, Taiwan. (Invited by Prof. Yu-Fen Huang)
 9. *Correction for population stratification/admixture in genome-wide methylation association studies* (2012/Mar/31-2012/Apr/01). The 5th France-Taiwan Frontiers of Science – Taiwan FoS. Taipei, Taiwan. (Invited by Department of International Cooperation, National Science Council - Dr. Cheng-Tung Tao)
 10. *Integrative analysis of single nucleotide polymorphisms and gene expression efficiently distinguishes samples from closely related ethnic populations* (2012/Jun/16). The 2012 Annual Meeting of Intelligent Technologies and Applied Statistics. Chiayi, Taiwan. (Invited by Prof. Chih-Hung Yen)
 11. *Homozygosity disequilibrium and its applications* (2012/Jul/24). Workshop on Modeling and Biomedical Data. Taipei, Taiwan (Invited by Prof. Hung Chen)
 12. *DAO gene plays an important role on genetic association and interaction to schizophrenia in the Taiwan Han Chinese population* (2013/Jun/28-29). The 22nd Southern Taiwan Statistical Conference. Kaohsiung, Taiwan (Invited by Prof. Henry Horng-Shing Lu)
 13. *Deciphering medical genomics and population genomics using single nucleotide polymorphisms and other types of genetic markers* (2013/Nov/22). 2013 Promotion Workshop of Medical Statistics (推展醫藥統計研習會). Taipei, Taiwan. (Invited by Dr. Yi-Hau Chen)
 14. *Applying genome-wide gene-based expression quantitative trait locus mapping to study population ancestry and pharmacogenetics* (2014/May/16-18). The 9th Cross-Strait Conference on Statistics and Probability. Taichung, Taiwan. (Invited by Prof. Chuhsing Kate Hsiao)
 15. *Homozygosity disequilibrium and its importance in medical genomics and population genomics* (2014/Dec/06). The Annual Meeting of the Chinese Statistical Association and International Statistical Symposium – CSA-KSS-JSS Special Invited Sessions. Hsin-Chu,

Taiwan. (Invited by Prof. Yen-Feng Chiu)

16. *Genome-wide association study identifies SNP rs17180299 and multiple haplotypes on CYP2B6, SPON1 and GSG1L associated with plasma concentrations of the methadone R- and S-enantiomer in heroin-dependent patients under methadone maintenance treatment* (2015/Jun/27-28). The 24th South Taiwan Statistical Conference, Changhua, Taiwan. (Invited by Prof. Chuhsing Kate Hsiao)
17. *An integrated analysis tool for hybridization intensities and genotypes using new-generation population-optimized human arrays* (2016/Jun/24-25). The 25th South Taiwan Statistical Conference, Kaohsiung, Taiwan. (Invited by Prof. Yu-Feng Huang)
18. *Tools for genomic big-data analytics* (2018/May/29). The Taiwan Biobank Workshop, Taoyuan, Taiwan. (Invited by the Taiwan Biobank)
19. *Statistical gene mapping wars II (統計基因定位大戰二部曲)* (2018/Sep/02). Statistical Science Camp, Institute of Statistical Science, Academia Sinica, Taipei, Taiwan. (Invited by Prof. Yen-Tsung Huang)
20. *Statistics tells you where disease genes are & how to promote precision medicine and healthcare (統計告訴你致病基因在哪裡以及如何促進精準醫療與健康照護)* (2018/Oct/27). Open House, Institute of Statistical Science, Academia Sinica, Taipei, Taiwan. (Invited by Prof. I-Ping Tu)

[Invited speech in domestic academic institutes]

1. *Markov chain models for capture-recapture experiments* (2003/Mar/20). Institute of Statistics, National Cheng Kung University, Tainan, Taiwan. (Invited by Prof. Miin-Jye Wen)
2. *Pooled DNA analysis* (2005/Oct/13). Institute of Mathematics, National Sun Yat-sen University, Kaohsiung, Taiwan. (Invited by Prof. Mong-Na Lo Huang)
3. *A sliding-window weighted linkage disequilibrium test* (2006/March/31). Institute of Statistics, National Tsing Hua University, Hsinchu, Taiwan. (Invited by Prof. Nan-Jung Hsu)
4. *Disease gene mapping using pooled DNA experiments* (2006/May/2). Institute of Mathematics, Tamkang University, Taipei, Taiwan. (Invited by Prof. Steve Yih Huei Huang)
5. *DNA-pooling experiment: An economic method for large-scale disease gene association mapping* (2006/May/11). Institute of Statistics, National Cheng Kung University, Tainan, Taiwan. (Invited by Prof. Yunchan Chi)
6. *A genome-wide scanning and fine mapping study of COGA data* (2006/Nov/29). Institute of Statistics, National University of Kaohsiung, Kaohsiung, Taiwan. (Invited by Prof. Kam-Fai Wong)
7. *Modeling animals' behavioral response by Markov Chain models for capture-recapture experiments* (2006/Dec/04). Institute of Statistics, National Chengchi University, Taipei, Taiwan. (Invited by Prof. Wen-Chi Tsai)
8. *Modeling animals' behavioral response by Markov Chain models for capture-recapture experiments* (2006/Dec/12). Institute of Statistics, National Central University, Taoyuan,

- Taiwan. (Invited by Prof. Wei-Cheng Miao)
9. *MPDA: Microarray pooled DNA analyzer* (2007/Jun/06). Biostatistics Center, China Medical University, Taichung, Taiwan. (Invited by Prof. Honda Wu)
 10. *Pooled DNA analysis using oligonucleotide arrays* (2007/Oct/03). Institute of Medical Research & Education Taipei Veterans General Hospital, Taipei, Taiwan. (Invited by Dr. Shu-Chung Chiang)
 11. *Cost-effective association mapping by analyzing pooled DNA data* (2007/Oct/15). Institute of Medical Research & Education Kaohsiung Veterans General Hospital, Kaohsiung, Taiwan. (Invited by Dr. Luo-Ping Ger)
 12. *Pooled DNA analysis using oligonucleotide arrays* (2008/Mar/13). Taiwan International Graduate Programs, Institute of Information Science, Academia Sinica, Taipei, Taiwan. (Invited by the Program of Bioinformatics)
 13. *A genome-wide study of preferential amplification/hybridization in microarray-based pooled DNA experiments* (2008/May/29). Department of Applied Mathematics, National Chung Hsing University, Taichung, Taiwan. (Invited by Prof. Tsung-Jen Shen)
 14. *Genomic dissection of preferential amplification/hybridization based on three large-scale genomic projects* (2008/June/12). National Health Research Institutes, Miaoli, Taiwan. (Invited by Dr. Chu-Chih Chen)
 15. *Applications of allele frequency in genetic/genomic studies* (2008/Oct/07). Institute of Statistics, National Central University, Taoyuan, Taiwan. (Invited by Prof. Cheng-Der Fuh)
 16. *Applications of allele frequency in genetic/genomic studies* (2008/Oct/28). Department of Mathematics, Tamkang University, Taipei, Taiwan. (Invited by Dr. Chi-Chung Wen)
 17. *Applications of allele frequency in genetic/genomic studies* (2008/Nov/03). College of Pharmacy, China Medical University, Taichung, Taiwan. (Invited by Dr. Chieh-Hsi Wu)
 18. *Loss-of-heterozygosity analysis suite* (2009/Nov/13). Department of Applied Statistics and Information Science, Ming Chuan University, Taoyuan County, Taiwan. (Invited by Prof. Chen-Mao Liao)
 19. *Human genomic studies of individual-level allele frequency* (2010/Mar/26). Master's Program in Biomedical Informatics and Biomedical Engine and Department of Statistics, Feng Chia University, Taichung, Taiwan. (Invited by Prof. Pi-Chiang Li)
 20. *SAQC: SNP array quality control* (2011/Oct/06). Taiwan International Graduate Programs, Institute of Information Science, Academia Sinica, Taipei, Taiwan. (Invited by the Program of Bioinformatics)
 21. *Dissection of the human genome using single nucleotide polymorphisms* (2011/Oct/28). Institute of Public Health and Department of Public Health, National Yang-Ming University, Taipei, Taiwan. (Invited by Prof. Ming-Wei Lin)
 22. *Deciphering population genomics and medical genomics through homozygosity disequilibrium using whole-genome single nucleotide polymorphism and next-generation*

- sequencing data* (2012/Dec/18). Clinical Informatics and Medical Statistics Research Center, Chang Gung University, Taoyuan, Taiwan. (Invited by Prof. Pi-Hua Liu)
23. *Deciphering population genomics and medical genomics through homozygosity disequilibrium using whole-genome single nucleotide polymorphism and next-generation sequencing data* (2013/May/29). Institute of Statistics, National University of Kaohsiung, Kaohsiung, Taiwan. (Invited by Prof. Shu-Hui Yu)
 24. *Deciphering population genomics and medical genomics through homozygosity disequilibrium using whole-genome single nucleotide polymorphism and next-generation sequencing data* (2013/Sep/27). Institute of Statistics, National Tsing Hua University, Hsinchu, Taiwan. (Invited by Prof. Wun-Yi Shu)
 25. *Statistics tells you where disease genes are* (2014/Mar/26). Department of Statistics, National Taipei University, Taipei, Taiwan. (Invited by Prof. Shang-Ying Shiu)
 26. *Deciphering medical genomics and population genomics using single nucleotide polymorphisms and other types of genetic markers* (2014/Mar/27). Department of Environmental and Occupational Health, National Cheng Kung University, Tainan, Taiwan (Invited by Prof. Chih-Chieh Wu)
 27. *Elucidating the relationships between phenotypic traits and single nucleotide polymorphisms, rare variants, copy number variations, gene expressions in the human genome* (2014/Apr/22). Biostatistical Consultation Center, National Yang-Ming University, Taipei, Taiwan. (Invited by Prof. I-Fen Lin)
 28. *Homozygosity disequilibrium and its importance in medical genomics and population genomics* (2014/Dec/25). Taiwan International Graduate Programs, Institute of Information Science, Academia Sinica, Taipei, Taiwan. (Invited by the Program of Bioinformatics)
 29. *Genome-wide pharmacogenomic study on methadone maintenance treatment identifies SNP rs17180299 and multiple haplotypes on CYP2B6, SPON1, and GSG1L associated with plasma concentrations of methadone R- and S-enantiomers in heroin-dependent patients* (2015/Mar/03). Master Program in Statistics, National Taiwan University. (Invited by Prof. Jen-Pei Liu)
 30. *Recovering the missing heritability of complex diseases* (2015/Apr/10). Translational Medicine Ph.D. Program, Institute of Clinical Medicine, National Yang Ming University, Taipei, Taiwan. (Invited by Prof. Mei-Hsuan Lee)
 31. *Statistics tells you where disease genes are* (2015/May/20). General Education Center, National Chung Hsing University, Taichung, Taiwan. (Invited by Prof. Wen-Han Hwang)
 32. *Recovering the missing heritability of complex diseases* (2015/Jun/05). School of Life Sciences, National Yang-Ming University, Taipei, Taiwan. (Invited by Prof. I-Fen Lin)
 33. *Genetics in medicine* (2016/May/06). Department of Environmental and Occupational Health, National Cheng Kung University, Tainan, Taiwan. (Invited by Prof. Chih-Chieh Wu)
 34. *Studying medical genomics and population genomics through big data* (2016/Jun/03).

- Department of Healthcare Administration and Medical Informatics, Kaohsiung Medical University Hospital, Kaohsiung, Taiwan. (Invited by Prof. Shih-Feng Weng)
35. *Analyzing genome-wide genotypes and hybridization intensities data from Affymetrix Axiom SNP arrays for genomic medicine* (2016/Sep/21). Department of Internal Medicine, China Medical University Hospital, Taichung, Taiwan. (Invited by Dr. Che-Yi Chou)
 36. *SMART: Statistical Metabolomics Analysis – an R Tool* (2016/Nov/04). Department of Statistics, Feng Chia University, Taichung, Taiwan. (Invited by Prof. Yu-Chung Wei)
 37. *Analyzing genome-wide genotypes and hybridization intensities data from Affymetrix Axiom SNP arrays for genomic medicine* (2016/Dec/09). Institute of Public Health and Department of Public Health, National Yang-Ming University, Taipei, Taiwan. (Invited by Prof. Chao-Yu Guo and Mr. Reng-Hong Wang)
 38. *OPATs: Omnibus p-value association tests* (2017/Dec/22). School of Life Sciences, National Yang-Ming University, Taipei, Taiwan. (Invited by Prof. Hsuan-Cheng Huang)
 39. *An integrated analysis tool for analyzing hybridization intensities and genotypes using new-generation population-optimized human arrays* (2018/Jan/09). Institute of Population Health Sciences, National Health Research Institutes, Miaoli, Taiwan. (Invited by Dr. Ren-Hua Chung)
 40. *Disease gene mapping and precision medicine* (2018/May/18). Department of Medicine, National Cheng Kung University, Tainan, Taiwan. (Invited by Prof. Chih-Chieh Wu)
 41. *Statistical applications in genetic disorders and precision medicine* (2018/June/11). Department of Statistics, National Cheng Kung University, Tainan, Taiwan. (Invited by Prof. Mi-Chia Ma)
 42. *SMART: Statistical Metabolomics Analysis – an R Tool* (2018/June/13). Institute of Statistics, National University of Kaohsiung, Kaohsiung, Taiwan. (Invited by Prof. Kun-Lin Kuo)

[Contributed presentation in international conferences]

1. [Yang, H.-C.](#), Chen, C.-L. and Fann, C. S. J. (2003/11/04-08). *Estimation of allele frequencies with preferential amplification in a DNA-pooling study*. The 53rd Annual Meeting of American Society of Human Genetics **73**, S2625. (Los Angeles, USA)
2. [Yang, H.-C.](#), Chang, C.-C., Chen, C.-L., Lin C.-Y., Lin, C.-Y., and Fann, C. S. J. (2004/09/07-10). *Identifying alcoholism susceptibility genes via genome-wide linkage/disequilibrium and regression-based haplotype analyses*. Proceeding of Genetic Analysis Workshop 14, 3.31-3.35. (Noordwijkerhout, Holland)
3. [Yang, H.-C.](#), Lin, C.-H. and Fann, C. S. J. (2004/10/26-30). *Cost-benefit and high-throughput method for polymorphism validation*. The 54th Annual Meeting of American Society of Human Genetics, S1678. (Toronto, Canada)
4. Fann, C. S. J. and [Yang, H.-C.](#) (2004/10/26-30). *A haplotype regression model with errors*. The 54th Annual Meeting of American Society of Human Genetics, S1965. (Toronto,

Canada)

5. [Yang, H.-C.](#), Hsu, C.-L., Lin, C.-H. and Fann, C. S. J. (2004/12/15-18). *Population genetics study of Taiwan residents and a comparison with Caucasians*. Proceeding of 2004 Taipei Symposium on Statistical Genomics, S7. (The award of the best poster presentation.) (Taipei, Taiwan)
6. [Yang, H.-C.](#), Hsu, C.-L., Lin, C.-H. and Fann, C. S. J. (2005/04/18-21). *Comparative genetics of the Taiwanese populations*. Proceeding of HGM2005. (Kyoto, Japan)
7. [Yang, H.-C.](#), Lin, C.-Y. and Fann, C. S. J. (2005/10/25-29). *A unified multilocus association test*. The 55th Annual Meeting of American Society of Human Genetics, S2393. (Salt Lake City, USA)
8. [Yang, H.-C.](#), Liang, Y.-J., Huang, M.-C., Hsu, C.-L., Li, L.-H. and Fann, C. S. J. (2006/03/06-10). *On preferential amplification in DNA-pooling studies*. Joint 6th Human Genome Organization (HUGO) Pacific Meeting & 7th Asia-Pacific Human Genetics Conference (HUGO-AP), S186. (Taipei, Taiwan)
9. [Yang, H.-C.](#), Lin, C.-Y. and Fann, C. S. J. (2006/03/06-10). *A sliding-window weighted linkage disequilibrium test*. Joint 6th Human Genome Organization (HUGO) Pacific Meeting & 7th Asia-Pacific Human Genetics Conference (HUGO-AP), S78. (Taipei, Taiwan)
10. [Yang, H.-C.](#), Huang, M.-C., Lin, C.-H., Li, L.-H. and Fann, C. S. J. (2006/08/06-10). *A Microarray-based DNA pooling study based on 100K GeneChip*. The 11th International Congress of Human Genetics, S1286. (Brisbane, Australia)
11. [Yang, H.-C.](#), Chang, C.-C., Mi, H.-C., Chen, P. and Fann, C. S. J. (2006/11/13-15). *Pattern discovery of genomewide transcription levels and linkage/linkage disequilibrium based on microarray and SNP data*. Proceeding of Genetic Analysis Workshop 15, 14.53-14.57. (Florida, USA)
12. [Yang, H.-C.](#), Li, L.-H., Huang, M.-C., Yu, A. L. T., Diccianni, M. B., Lin, C.-H., Wu, J. Y., Chen, Y. T. and Fann, C. S. J. (2007/09/06-08). *Detection of allelic imbalance using accurate allele frequency estimation*. The 9th International Meeting of Human Genome Variation and Complex Genome, S184. (Catalonia, Spain)
13. [Yang, H.-C.](#), Hsieh, H.-Y. and Fann, C. S. J. (2007/10/23-27). *KBAT: Kernel-based association test*. The 57th Annual Meeting of American Society of Human Genetics, S1221. (San Diego, USA)
14. [Yang, H.-C.](#), Liang, Y.-J., Chung, C.-M. and Pan, W.-H. (2008/09/17-20). *Genomewide gene-set analysis of rheumatoid arthritis data*. Proceeding of Genetic Analysis Workshop 16, 16.54-16.58. (St. Louis, USA)
15. [Yang, H.-C.](#), Li, L.-H., Huang, M.-C. and Pan, W.-H. (2008/09/15-16). *Genomic dissection of preferential amplification/hybridization based on three large-scale genome projects*. The 17th Annual Meeting of International Genetic Epidemiology Society, S182. (St. Louis, USA)
16. [Yang, H.-C.](#), Chiang, K.-M., Liang, Y.-J., Chen, J.-W., Chen, Y.-T. and Pan, W.-H.

- (2008/11/11-15). *Disease gene mapping of young-onset hypertension in the Taiwanese population*. The 58th Annual Meeting of American Society of Human Genetics, S1668. (Philadelphia, USA)
17. [Yang, H.-C.](#), Liang, Y.-J., Chiang, K.-M. and Pan, W.-H. (2009/05/23-26) *Hunting young-onset hypertension genes using a genome-wide gene-based association method*. The Annual Meeting of European Society of Human Genetics, P17.28. (Vienna, Austria)
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