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**[Biosketch]**

Dr. Hsin-Chou Yang is a statistician and bioinformatician with expertise in analyzing big data and answering real-world questions. He received his Ph.D. in statistics in 2002 and studied ecological statistics, in which he developed statistical approach to estimating population abundance and related quantities for monitoring the wildlife and human communities. Dr. Yang served as Postdoctoral Research Fellow in the Institute of Biomedical Sciences, Academia Sinica. He changed his research pursuits to statistical genetics and genetic epidemiology, in which he developed statistical/bioinformatics tools for identifying the disease susceptibility genes for complex disorders. Dr. Yang joined the Institute of Statistical Science, Academia Sinica as an Assistant Research Fellow in 2006 and was promoted to Associate Research Fellow in 2011. With the blossom of microarray and next generating sequencing, Dr. Yang changed his research interest to statistical genomics and its applications in genomic medicine and precision medicine. In 2018, Dr. Yang was promoted to a Full Research Fellow. With the advent of biotechnologies, a wealth of high-throughput, large-scale, various types of OMICS data were generated. Dr. Yang extended his research interests to the integrative study of statistical OMICS, electronic health records, medical images, and biobank research. Dr. Yang and his research team have devoted themselves to (1) developing novel statistical/bioinformatics methodologies and data analysis tools for medical images and OMICS including genomics, epigenomics, transcriptomics, metabolomics, and microbiomics as well as (2) answering practical biological and biomedical issues in precision health and smart through close collaborations with clinicians, epidemiologists, and geneticists.

Dr. Yang has won several titles, including the Career Development Award of Academia Sinica (2011); Significant research achievements of Academia Sinica (2008, 2011, 2017, 2020); Elected member of Global Young Academy (2013); Junior Research Investigators Award, Academia Sinica (2013); Outstanding Young Alumni Award of National Cheng Kung University (2016); Future Technology Breakthrough Award of Ministry of Science and Technology (2018); Elected member of International Statistical Institute (ISI) (2019); Contribution Award of Chinese Institute of Probability and Statistics (2019). Dr. Yang supports the editorial service for several international journals: *BMC Genomic Data*, *BMC Medical Research Methodology*, *Frontiers in Genetics – Statistical Genetics and Methodology*, *Frontiers in Genetics – Computational Genomics*, and *Frontiers in Systems Biology – Integrative Genetics and Genomics*. He has provided paper review service (>100 papers) for international journals (>40 journals).

**[Education]**

- 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

**[Present position]**

- 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  
2016.12 – 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 Chiao Tung University  
2018.08 – Present Joint Professor. Department of Statistics, National Cheng Kung University  
2021.08 – Present Core Faculty. Master of Public Health Program, National Yang Ming Chiao Tung University  
2021.08 – Present Joint Research Fellow. Biomedical Translation Research Center, Academia Sinica

**[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. Department of Statistics, National Cheng Kung University  
2016.02 – 2017.02 Adjunct Associate Professor. Institute of Statistics, National Tsing Hua University  
2019.07 – 2021.06 Coordinator. Bioinformatics Program, Taiwan International Graduate Program, Academia Sinica

**[Review service – Journal editorial board (> 80 papers)]**

1. BMC Genomic Data (Editorial Board Member: 2021/03 – Present)
2. BMC Medical Research Methodology (Associate Editor: 2012/11 – Present)
3. Computational Statistics (Associate Editor: 2013/10 – 2021/03)
4. Frontiers in Genetics – Statistical Genetics and Methodology (Review Editor: 2011/09 – Present)
5. Frontiers in Genetics – Computational Genomics (Review Editor: 2021/11 – Present)
6. Frontiers in Systems Biology – Integrative Genetics and Genomics (Review Editor: 2022/05 – Present)
7. Journal of the Chinese Statistical Association (Associate Editor: 2018/07 – 2021/06)
8. Statistica Sinica (Associate Editor: 2014/08 – 2017/07)
9. Statistica Sinica (Managing Editor: 2014/08 – 2017/07)

**[Review service – Journal review (> 110 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. Bioinformatics in Medicine Unlocked
7. Biomedical Journal
8. Biometrics
9. Biometrika
10. BMC Bioinformatics
11. BMC Genetics
12. BMC Medical Research Methodology
13. BMC Research Notes
14. BMC Supplements
15. Briefings in Bioinformatics
16. Cancer Informatics
17. Communications Biology
18. Computer Methods and Programs in Biomedicine
19. Computational and Structural Biotechnology Journal
20. Computational Statistics
21. Computational Statistics and Data Analysis
22. Current Cancer Drug Target
23. Diagnostics
24. Environmental Science and Pollution Research
25. Eurosurveillance

26. Evolutionary Bioinformatics
27. Expert Opinion on Drug Metabolism and Toxicology
28. Frontiers in Medicine
29. Frontiers in Nutrition
30. Frontiers in Oncology
31. Frontiers in Genetics – Statistical Genetics and Methodology
32. Frontiers in Genetics – Computational Genomics
33. Genetic Epidemiology
34. Genetics
35. Human Genetics
36. Human Molecular Genetics
37. Informatics in Medicine Unlocked
38. International Journal of Biostatistics
39. ISRN Bioinformatics
40. Journal of Clinical Bioinformatics
41. Journal of Data Science
42. Journal of Human Genetics
43. Journal of Medical Genetics
44. Journal of Medical Genetics and Genomics
45. Journal of Probability and Statistics
46. Kaohsiung Journal of Medical Sciences
47. Malaysian Journal of Medical Sciences
48. Molecular Ecology Resources
49. Neuroimmunomodulation
50. Nucleic Acids Research
51. PeerJ
52. PLoS Digital Health
53. PLoS ONE
54. Scientific Reports
55. Statistica Sinica
56. Statistics in Medicine
57. Test

**[Review service – Grant proposal]**

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

6. National Taiwan University

**[Review service – Recruitment and promotion]**

1. Academia Sinica
2. Kaohsiung Medical University
3. National Chung Hsing University
4. Feng Chia University
5. National Health Research Institute
6. National Taiwan University

**[Research interests]**

Data sciences for the multi-OMICS and precision & smart health studies

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

1. Zen, M. M.<sup>CA</sup> and [Yang, H.-C.](#) (1996). Estimating the sequential continuity of a semi-Markov process (以半馬可夫過程來探討持續性). *Journal of Chinese Statistical Association (中國統計學報)* **34**, 256-274. Publisher: Chinese Statistical Association. (In Chinese with English abstract)
2. Chao, A.<sup>CA</sup>, 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 (千禧年香港觀鳥大賽資料分析). *Journal of Chinese Statistical Association (中國統計學報)* **38**, 231-241. Publisher: Chinese Statistical Association. (In Chinese with English abstract)

**[Other publication --- Book chapter]**

1. Chao, A.<sup>CA</sup>, [Yang, H.-C.](#) and Yip, P. S. F. (2003). The use of capture-recapture methodology in epidemiological surveillance. pp. 711-739 in Y. Lu and J.-Q. Fang (Ed.), *Advanced Medical Statistics*. World Scientific Publishing Company, Singapore.
2. [Yang, H.-C.](#) and Fann, C. S. J.<sup>CA</sup> (2007). Association mapping using pooled DNA. pp. 161-175 in A. R. Collins (Ed.), *Linkage Disequilibrium and Association Mapping*, The Humana Press Inc., USA.
3. Chao, A.<sup>CA</sup>, Hsieh T. C. and [Yang, H.-C.](#) (2015). The use of capture-recapture methodology in epidemiological surveillance and ecological surveys. pp. 425-467 in Y. Lu, J.-Q. Fang, L. Tian and H. Jin (Ed.), *Advanced Medical Statistics*. 2nd Edition. World Scientific Publishing Company, Singapore.

**[Other publication --- Magazine, radio, and website interview]**

1. [Yang, H.-C.](#)<sup>CA</sup> (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. Publisher: Academia Sinica. (In Chinese) [[link](#)]
2. [Yang, H.-C.](#)<sup>CA</sup> (2017.09.16 – 2017.09.22). R becomes the main statistical language and plays a role on statistical disease gene mapping (滿足致病基因定位需求 R軟體成為統計分析市場主流). Publisher: *iThome (電週文化)* **834**, 13. (In Chinese) [[link](#)]
3. [Yang, H.-C.](#)<sup>CA</sup> (2019.05.24). Master in chromosomal aberration detection (染色體異常偵測大師). *Breakthrough Technologies (新科技大未來)*. Publisher: National Education Radio

(國立教育電台). (In Chinese) [\[link\]](#)

4. [Yang, H.-C.](#)<sup>CA</sup> and Chen, C.-W. (2019). Statistical gene mapping wars and precision medicine (統計基因定位大戰與精準醫療). *Science Development (科學發展)*. Publisher: Ministry of Science and Technology. (In Chinese) [\[link\]](#)
5. [Yang, H.-C.](#)<sup>CA</sup>. (2021.01.12). SARS-CoV-2 report (新冠病毒報導). *研之有物*. Publisher: Academia Sinica. (In Chinese) [\[link\]](#)
6. [Yang, H.-C.](#)<sup>CA</sup>. (2021.02.19). 【中研院團隊特寫】 跨領域專家攜手監測病毒突變 and 【中研院團隊解惑】 10個 Q&A 掌握變種病毒. Publisher: *Taiwan FactCheck Center (台灣事實查核中心)*. (In Chinese) [\[link\]](#)
7. [Yang, H.-C.](#)<sup>CA</sup>. (2021.05.19). 公共電視獨立特派員 – 五月風暴・疫苗SOS. Publisher: *Taiwan Public Television (公共電視)*. (In Chinese) [\[link\]](#)
8. [Yang, H.-C.](#)<sup>CA</sup>. (2021.09.29). 新冠病毒統計基因體分析與「病毒變異全球即時監測網」. *Natural Sciences and Sustainable Development Newsletter (自然科學與永續研究發展簡訊 and SPEC Monthly (科學推展中心月刊)*. Publisher: *Science Promotion & Engagement Center (科技部自然科學與永續研究推展中心)*. (In Chinese) [\[link\]](#)
9. [Yang, H.-C.](#)<sup>CA</sup>. (2021.09.30). 公共電視獨立特派員 – 變幻莫測的變種病毒，臺灣如何面對? Publisher: *Taiwan Public Television (公共電視)*. (In Chinese) [\[link\]](#)

#### [Other publication --- Scientific report]

1. Geffers, J., Beaudry, C., [Yang, H.-C.](#), Huang, F., Phanraksa, O., Dominik, M., Lin, Y.-C., Huang, M.-C., Komai, S., Lorimer, K., Piyawattanametha, W., Saengchantr, P., Saleh, H., Tagg, B. and Veerakumarasivam, A. (2017/01). *Global State of Young Scientists (GloSYS) in ASEAN – Creativity and Innovation of Young Scientists in ASEAN*. Publisher: Global Young Academy. Halle, Germany (ISBN: 978-3-8047-3709-9). Pages 1 – 97. [\[link\]](#)
2. [Yang, H.-C.](#)<sup>CA</sup>, Chen, C.-h., Wang, J.-H., Liao, H.-C., Yang, C.-T., Chen, C.-W., Lin, Y.-C., Kao, C.-H. and Liao, J. C.<sup>CA</sup> (2020/04). Genomic, geographic and temporal distributions of SARS-CoV-2 mutations. *bioRxiv* (doi: <https://doi.org/10.1101/2020.04.22.055863>)
3. [Yang, H.-C.](#)<sup>CA</sup>, Wang, J.-H., Yang, C.-T., Lin, Y.-C., Chen, P.-W., Liao, H.-C., Chen, C.-h. and Liao, J. C.<sup>CA</sup> (2022/04). Subtyping of major SARS-CoV-2 variants reveals different transmission dynamics. *bioRxiv* (doi: <https://doi.org/10.1101/2022.04.10.486823>)

#### [Other publication --- Degree thesis]

1. [Yang, H.-C.](#) (1996). *On Sequential Continuity Based on Semi-Markov Process*. Master thesis, Graduate 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)

#### [Other publication --- Online course]

1. [Yang, H.-C.](#) and lab members (2021/03). Fundamental Statistical Genomics. (17 video

clips). Publisher: MeDA Lab. [\[link\]](#)

**[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 Qian)
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 9<sup>th</sup> 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 2<sup>nd</sup> 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 59<sup>th</sup> ISI WSC and the 8<sup>th</sup> 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 11<sup>th</sup> 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 3<sup>rd</sup> 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/01-02). 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 10<sup>th</sup> ICSA International Conference on Global Growth of Modern Statistics in the 21<sup>st</sup> 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). 30<sup>th</sup> 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)
27. *Building on previous GloSYS instrument* (2019/Apr/29). GloSYS LAC Conceptual Workshop (Global Young Academy | Pre-Conference Workshop | AGM 2019), Halle, Germany. (Invited by Global Young Academy and Dr. Fatima Kareem)
28. *Ancestry-informative pharmacogenomic genes under homozygosity disequilibrium in global continents and populations* (2019/Oct/25). International Workshop on Biomathematics and Biostatistics, Department of Mathematics, Tamkang University, New Taipei City, Taiwan. (Invited by Prof. Jong-Shenq Guo)
29. *Responsible research: let statistics speak for themselves* (2020/Jan/15). Global Leadership Program, Institute of Statistical Science, Academia Sinica, Taipei, Taiwan. (Invited by Academia Sinica Data Science Statistical Cooperation Center)
30. *Genomic dissection of SARS-CoV-2 reveals a dominant strain type and newly emergent strains with strong allelic associations* (2021/Jul/07-09). Joint virtual conference of Data Science, Statistics & Visualization and the European Conference of Data Analysis (DSSV-ECDA 2021), the Erasmus University, Rotterdam, the Netherlands. (Invited by Profs. Chun-houh Chen and Andreas Alfons)
31. *Genomic dissection of SARS-CoV-2 reveals a dominant strain type and newly emergent strains with strong allelic associations* (2021/Sep/28). Statistics Explore 2021 (Theme: Global Economic Recovery Acceleration 2021: The Impact of Vaccination on Education and Health), Statistics Student Association (HIMASTA) Faculty of Mathematics and Science In Syiah Kuala University. (Invited by Prof. Hizir Sofyan)
32. *The convergence of artificial intelligence and biobank in precision medicine* (2022/Oct/08). 2022 International Precision Medicine Summit, Taichung Veterans General Hospital, Taichung, Taiwan. (Invited by Dr. Yi-Ming Chen)

**[Invited presentation in domestic conferences]**

1. *Population size estimation using local sample coverage for open populations* (2003/Jun/26). The 12<sup>th</sup> 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 13<sup>th</sup> Southern Taiwan Statistical Conference. Taipei, Taiwan. (Invited by Prof. Hung Chen)
3. *Disease gene mapping using pooled DNA experiments* (2006/Jul/29). The 5<sup>th</sup> 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 20<sup>th</sup> 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 22<sup>nd</sup> 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 9<sup>th</sup> 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. Hsinchu, 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 24<sup>th</sup> 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 25<sup>th</sup> 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. *Heterogeneity - easy to understand than done in statistics (統計上的知「異」行難)* (2018/Sep/30). Interdisciplinary Retreat for Researchers - Thinking Out of The Box: Heterogeneity and Healthy Longevity (跨領域研究人員交流會 - 跳脫框架思考：質性與健康長壽), National Center for Traditional Arts, Yi-Lan county, Taiwan. (Invited by Prof. Chau-Hwang Lee) (Keynote presentation)
21. *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)
22. *Precision diagnosis and treatment of autism spectrum disorders by using a genome-wide study of multiple phenotypes (利用多外表型為基礎之全基因體研究發展泛自閉症之精準診斷與治療)* (2018/Dec/19). Grand Challenge Seed Program Workshop, Academia Sinica, Taipei, Taiwan. (Invited by Grand Challenge Seed Program)
23. *Ancestry-informative pharmacogenomic loci in global populations* (2019/Jun/22). The 28<sup>th</sup> South Taiwan Statistical Conference, National Chung Hsing University, Taichung City, Taiwan. (Invited by Prof. Sheng-Ming Lee)
24. *Ancestry-informative pharmacogenomic genes under homozygosity disequilibrium in global continents and populations* (2019/Dec/14). The Annual Meeting of the Chinese Statistical Association and Statistical Symposium, Institute of Statistics, National Chiao Tung University, Hsinchu, Taiwan. (Invited by Prof. Wen-Ping Hsieh)
25. *Population pharmacogenomics: Enrichment of ancestry-informative markers in*

- pharmacogenetic loci* (2020/08/20-21). The 29<sup>th</sup> South Taiwan Statistical Conference, National Chung Cheng University, Chiayi City, Taiwan. (Invited by Prof. Yi Ting Hwang)
26. *Population pharmacogenomics: Enrichment of ancestry-informative markers in pharmacogenetic loci* (2020/11/14-15). 2020 Multiomics and Precision Medicine Joint Conference, Chang Gung University, New Taipei City, Taiwan. (Invited by Prof. Sunny Sun)
27. *Linking and applications of the Taiwan Biobank data with other health and environmental databases* (2020/Dec/07). The Joint Meeting of the 2<sup>nd</sup> Annual Meeting of Taiwan Biobanks and the Biobank Data Applications Workshop (第二屆臺灣人體生物資料庫學會會員大會暨人體生物資料庫應用研討會), National Biotechnology Research Park, Taipei, Taiwan. (Invited by Prof. Chun-houh Chen)
28. *Towards precision health through whole-genome medical genomics and population pharmacogenomics studies* (2020/12/10). The Workshop of Precision Medicine and Health Big Data. 2020 臺中榮總精準醫療及健康大數據研討會. Taichung Veterans General Hospital, Taichung, Taiwan. (Invited by Dr. Tzu-Hung Hsiao)
29. *Big data analytics of SARS-CoV-2 variants (COVID-19 病毒變異大數據分析)* (2021/04/17). The mini-symposium of COVID-19 in Taiwan Society for Virology and Vaccinology (社團法人台灣病毒暨疫苗學會 – 國內外 COVID-19 疫苗現況), National Taiwan University, Taipei, Taiwan. (Invited by Prof. Jen-Ren Wang)
30. *Big data applications in population genomics and precision medicine* (2021/07/24). Taiwan Precision Medicine Seed Training Program (臺灣精準醫療種子人才訓練計畫). Department of Research Planning and Development, National Health Research Institute, Taiwan. (Invited by Prof. Shih-Feng Tsai)
31. *Experience sharing of the data applications and analyses in biobank studies* (2021/08/05). 110 年度人體生物資料庫教育訓練系列課程. Joint Commission of Taiwan, Taiwan (Invited by Dr. Hou-Wei Chu)
32. *Big data analytics for SARS-CoV-2 genome sequences (大數據科學讓新冠病毒現形)* (2021/Oct/30). Open House, Institute of Statistical Science, Academia Sinica, Taipei, Taiwan. (Invited by Prof. Chun-houh Chen)
33. *Genomic dissection of SARS-CoV-2 reveals a dominant strain type and newly emergent strains with strong allelic associations (新冠病毒基因體研究發現至尊病毒株類型與新興變異株)* (2022/01/24-26). The artificial intelligence & data science workshop. Department of Applied Mathematics, National Dong Hwa University, Hualien, Taiwan. (Invited by Prof. Wen-Han Hwang)
34. *Big data applications in population genomics and precision medicine* (2022/07/23). Taiwan Precision Medicine Seed Training Program (臺灣精準醫療種子人才訓練計畫). Department of Research Planning and Development, National Health Research Institute, Taiwan. (Invited by Prof. Shih-Feng Tsai)

35. *Subtyping and transmission of SARS-CoV02* (2022/07/28-29). The 31<sup>st</sup> South Taiwan Statistical Conference, Feng Chia University, Taichung, Taiwan. (Invited by Prof. Shen-Ming Lee)
36. *Experience sharing of research and project execution* (2022/09/02-03). Joint Meeting of New Principal Investigators in the Department of Natural Sciences and Sustainable Development, National Science Council (國家科學及技術委員會自然處 2022 新進人員聯合研討會), Taichung, Taiwan. (Invited by Prof. Wen-Han Hwang)

**[Invited speech in domestic academic institutes]**

1. *Markov chain models for capture-recapture experiments* (2003/Mar/20). Graduate 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). Graduate 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). Institute of Population Health Sciences, 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)
43. *Analyzing genome-wide genotypes and hybridization intensities data from Affymetrix Axiom® SNP arrays for genomic medicine* (2018/Oct/09). Degree Program of Data Science, Academia Sinica & National Taiwan University, Taipei, Taiwan. (Invited by Prof. Da-Wei Wang)
44. *Careers for undergraduate students in Statistics* (2018/Oct/26). Department of Statistics, National Taipei University, Taipei, Taiwan. (Invited by Prof. Yi-Ting Hwang)
45. *Homozygosity disequilibrium and its applications* (2019/Apr/15). Institute of Cellular and Organismic Biology, Academia Sinica, Taipei, Taiwan. (Invited by Prof. Cheng-Fu Kao)
46. *Homozygosity disequilibrium and its applications* (2019/May/30). Department of Statistics, Tamkang University, Taipei, Taiwan. (Invited by Prof. Shuo-Jye Wu)
47. *OPATs: Omnibus p-value association tests* (2019/May/31). Department of Applied Statistics and Information Science, Ming Chuan University, Taipei, Taiwan. (Invited by Prof. Chen-Mao Liao)
48. *Analyzing genome-wide genotypes and hybridization intensities data from Affymetrix Axiom SNP arrays for genomic medicine* (2019/Jun/24). Master Program in Clinical Pharmacogenomics and Pharmacoproteomics, Taipei Medical University, Taipei, Taiwan. (Invited by Profs. Sung-Bau Lee and Wei-Chiao Chang)
49. *Responsible research: Let statistics speak for themselves* (2019/Sep/28). 2019 TIGP Ethics Course, Academia Sinica, Taipei, Taiwan. (Invited by Program for Promotion of Research Integrity (PPRI), Department of Academic Affairs and Instrument Service, Academia Sinica)
50. *Responsible research: Let statistics speak for themselves* (負責任的研究：讓數據說話) (2020/May/15). 2020 Research Ethics Course, Academia Sinica, Taipei, Taiwan. (Invited

- by Program for Promotion of Research Integrity (PPRI), Department of Academic Affairs and Instrument Service, Academia Sinica)
51. *Responsible research: Let statistics speak for themselves* (負責任的研究：讓數據說話) (2020/June/05). 2020 IRB-BM Committee Education Training Course, Academia Sinica, Taipei, Taiwan. (Invited by IRB on Biomedical Science Research, Department of Academic Affairs and Instrument Service, Academia Sinica)
  52. *Responsible research: Let statistics speak for themselves* (2020/Oct/24). 2019 TIGP Ethics Course, Academia Sinica, Taipei, Taiwan. (Invited by Program for Promotion of Research Integrity (PPRI), Department of Academic Affairs and Instrument Service, Academia Sinica)
  53. *Analysis of genomic distributions of SARS-CoV-2 reveals a dominant strain type with strong allelic associations* (2021/Jan/04). Institute of Statistical Science, Academia Sinica, Taipei, Taiwan. (Invited by Prof. Jing-Shiang Hwang)
  54. *Genomic dissection of SARS-CoV-2 reveals a dominant strain type and newly emergent strains with strong allelic associations* (2021/Mar/05). Degree Program of Data Science, Academia Sinica & National Taiwan University, Taipei, Taiwan. (Invited by Prof. Yi-Ping Tu)
  55. *Genomic dissection of SARS-CoV-2 by using big data analytics* (大數據科學讓新冠病毒現形) (2021/Apr/07). Tainan First Senior High School, Tainan, Taiwan. (Invited by Coordinator Mr. Anthony, C. F. Liu)
  56. *Nothing we don't sell in Data Science Statistical Cooperation Center – Creating and adding value from data* (什麼都賣的資料科學統計合作社 - 資料加值與創價) (2021/Apr/13). Taichung Veterans General Hospital, Taichung, Taiwan (Invited by Dr. Ching-Heng Lin)
  56. *Medical applications and added value of genomic data* (基因體資料的醫學應用與加值) (2021/Apr/28). Taipei Veterans General Hospital, Taipei, Taiwan (Invited by Drs. Shih-Hwa Chiou and Kung-Hao Liang)
  57. *Genomic dissection of SARS-CoV-2 reveals a dominant strain type with strong allelic associations* (2021/May/26). Institute of Statistics, National Kaohsiung University, Kaohsiung, Taiwan. (Invited by Prof. Hong-Ding Yang)
  58. *Genome research in precision and smart medicine* (2021/Nov/22). Department of Mathematics, Soochow University, Taipei, Taiwan. (Invited by Prof. Hui-Wen Lin)
  59. *Genomic dissection of SARS-CoV-2 by using big data analytics* (大數據科學讓新冠病毒現形) (2021/Dec/16). Department of Computer Science and Engineering, National Taiwan Ocean University, Keelung City, Taiwan. (Invited by Prof. Kuan Y. Chang)
  60. *Genomic dissection of SARS-CoV-2 reveals a dominant strain type and newly emergent strains with strong allelic associations* (新冠病毒基因體研究發現至尊病毒株類型與新興變異株) (2022/Apr/01). Institute of Statistics, National Tsing Hua University, Hsinchu, Taiwan. (Invited by Prof. Wen-Ping Hsieh)
  61. 大型資料庫申請案的審查應注意事項 - 以臺灣人體生物資料庫為例 (2022/Jun/20).

Institutional Review Board, National Health Research Institutes, Miaoli, Taiwan. (Invited by Dr. Shiu-Feng Kathy Huang)

**[Contributed presentation in international conferences]**

1. [Yang, H.-C.](#), Chen, C.-L. and Fann, C. S. J. (2003/Nov/04-08). *Estimation of allele frequencies with preferential amplification in a DNA-pooling study*. The 53<sup>rd</sup> 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/Sep/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/Oct/26-30). *Cost-benefit and high-throughput method for polymorphism validation*. The 54<sup>th</sup> Annual Meeting of American Society of Human Genetics, S1678. (Toronto, Canada)
4. Fann, C. S. J. and [Yang, H.-C.](#) (2004/Oct/26-30). *A haplotype regression model with errors*. The 54<sup>th</sup> 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/Dec/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/Apr/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/Oct/25-29). *A unified multilocus association test*. The 55<sup>th</sup> 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/Mar/06-10). *On preferential amplification in DNA-pooling studies*. Joint 6<sup>th</sup> Human Genome Organization (HUGO) Pacific Meeting & 7<sup>th</sup> Asia-Pacific Human Genetics Conference (HUGO-AP), S186. (Taipei, Taiwan)
9. [Yang, H.-C.](#), Lin, C.-Y. and Fann, C. S. J. (2006/Mar/06-10). *A sliding-window weighted linkage disequilibrium test*. Joint 6<sup>th</sup> Human Genome Organization (HUGO) Pacific Meeting & 7<sup>th</sup> 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/Aug/06-10). *A Microarray-based DNA pooling study based on 100K GeneChip*. The 11<sup>th</sup> 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/Nov/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/Sep/06-08). *Detection of allelic imbalance using accurate allele frequency estimation*. The 9<sup>th</sup> 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/Oct/23-27). *KBAT: Kernel-based association test*. The 57<sup>th</sup> 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/Sep/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/Sep/15-16). *Genomic dissection of preferential amplification/hybridization based on three large-scale genome projects*. The 17<sup>th</sup> 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/Nov/11-15). *Disease gene mapping of young-onset hypertension in the Taiwanese population*. The 58<sup>th</sup> 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/May/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)
  18. [Yang, H.-C.](#), Chen, J.-W., Liu, C.-M., Wen, C.-C., Liu, Y.-L., Chen, C.-H. and Hwu, H.-G. (2009/Oct/18-20). *The Taiwan schizophrenia genetic interaction study*. The 18<sup>th</sup> Annual Meeting of International Genetic Epidemiology Society, S67. (Hawaii, USA)
  19. [Yang, H.-C.](#), Chang, L.-C., Huggins, R., Chen, C.-H. and Mullighan, C.G. (2009/Oct/20-24). *LOHAS: Loss-of-heterozygosity analysis suite*. The 59<sup>th</sup> Annual Meeting of American Society of Human Genetics, S1241. (Hawaii, USA)
  20. [Yang, H.-C.](#) and Lin, H.-C. (2010/May/18-21). *SAQC: SNP array quality control*. The HUGO Journal 4, 153-154. (Montpellier, France)
  21. [Yang, H.-C.](#), Huang, M.-C., Kang, M.-J., and Pan, W.-H. (2010/Jun/02-05). *Pooled DNA analysis using Illumina human 660w-quad beadchip*. The Program Book of the 40<sup>th</sup> Annual Meeting of the Behavior Genetics Association, S12. (Seoul, South Korea)
  22. [Yang, H.-C.](#), Chang, L.-C., Liang, Y.-J. and Lin C.-H. (2010/Oct/10-12). *The excess of contiguous homozygous runs in the human major histocompatibility complex region in rheumatoid arthritis patients*. The 19<sup>th</sup> Annual Meeting of International Genetic Epidemiology Society, S202. (Boston, USA)
  23. [Yang, H.-C.](#) and Chen, J.-W. (2010/Oct/13-16). *Region-based and pathway-based QTL*

- mapping using a p-value combination method*. Proceeding of Genetic Analysis Workshop 17, G6. (Boston, USA)
24. [Yang, H.-C.](#), Liang, Y.-J., Chiang, K.-M., Chen, J.-W. and Pan, W.-H. (2010/Nov/02-06). *A genome-wide gene-based association study identifies SLC4A4, WWOX and COMMD7 as hypertension susceptibility genes in a Han Chinese population*. The 60<sup>th</sup> Annual Meeting of American Society of Human Genetics, S736. (Washington DC, USA)
  25. [Yang, H.-C.](#), Lin, C.-W., Chiang, K.-M., Liang, Y.-J., Chen, C.-W., Hwang, S.-M., Lynn, K.-S., Chen, J.-W. and Pan, W.-H. (2011/Oct/11-15). *An integrative pathway analysis using gene expression, single-nucleotide polymorphism and environmental factor successfully predicts disease status of hypertension*. The 12<sup>th</sup> International Congress of Human Genetics and the 61<sup>st</sup> Annual Meeting of American Society of Human Genetics, 365T. (Montreal, Canada)
  26. [Yang, H.-C.](#) and Chen, C.-W. (2012/Sep/06-08). *OPATs: Omnibus P-value Association Tests*. The 13<sup>th</sup> International Meeting on Human Genome Variation and Complex Genome Analysis, p123. (Shanghai, China)
  27. [Yang, H.-C.](#) and Han-Wei Li. (2012/Oct/14-17). *Study homozygosity disequilibrium using next-generation sequencing data*. Proceeding of Genetic Analysis Workshop 18. (Stevenson, USA)
  28. [Yang, H.-C.](#), Wang, P.-L., Lin, C.-W., Chen, C.-H. and Chen, C.-H. (2012/Oct/18-20). *Integrative analysis of single nucleotide polymorphisms and gene expression efficiently distinguishes samples from closely related ethnic populations*. The 20<sup>th</sup> Annual Meeting of International Genetic Epidemiology Society, S175. (Stevenson, USA)
  29. [Yang, H.-C.](#), Lin, C.-W., Chen, C.-W. and Chen, J. (2013/Apr/13-18). *A genome-wide gene-based mapping study of expression quantitative trait locus in humans*. Joint Conference of HGM 2013 and 21<sup>st</sup> International Congress of Genetics. S1342, 332-333 (Singapore)
  30. [Yang, H.-C.](#) and Chen, C.-W. (2013/Oct/22-26). *Identification of expression quantitative trait locus associated with drug biotransformation*. The 63<sup>rd</sup> Annual Meeting of American Society of Human Genetics, S720. (Boston, USA)
  31. [Yang, H.-C.](#) and Lin, Y.-T. (2014/May/31-2014/Jun/03). *Study homozygosity disequilibrium in human genome using the whole-genome sequencing data*. European Human Genetics Conference 2014, P17.44. (Milan, Italy)
  32. [Yang, H.-C.](#) and Lin, Y.-T. (2014/Aug/24-27). *Homozygosity disequilibrium and its regulatory genes*. Proceeding of Genetic Analysis Workshop 19. (Vienna, Austria)
  33. [Yang, H.-C.](#), Chu, S.-K., Wang, S.-C., Liu, S.-W., Ho, I.-K., Kuo, H.-W. and Liu, Y.-L. (2014/Aug/28-30). *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*. The 23<sup>rd</sup> Annual Meeting of International Genetic Epidemiology Society, S65. (Vienna, Austria)
34. [Yang, H.-C.](#) and Lin, Y.-T. (2015/Mar/14-17). *Homozygosity disequilibrium in the human genome*. The Conference of HGM 2015, 007. (Kuala Lumpur, Malaysia) (Selected as an oral presentation)
  35. [Yang, H.-C.](#) and Lin, Y.-T. (2015/May/25-29). *Homozygosity disequilibrium in the human genome*. The 5<sup>th</sup> International Conference for Young Scientists & General Assembly Meeting 2015 of the Global Young Academy. (Montebello, Québec, Canada) (Selected as an oral presentation)
  36. [Yang, H.-C.](#), Chen, J.-W., Lin, Y.-T and Chiu, S.-K. (2016/Apr/03-07). *Ancestry-informative pharmacogenomic loci*. The 13<sup>th</sup> International Congress of Human Genetics. (Kyoto, Japan) (Selected as an oral presentation)
  37. Liang, Y.-J., Lin, Y.-T., Chen, C.-W., Lin, C.-W., Chao, K.-M., Pan, W.-H. and [Yang, H.-C.](#) (2016/Oct/18-22) *SMART: Statistical Metabolomics Analysis – an R Tool*. The 66<sup>th</sup> Annual Meeting of American Society of Human Genetics, 501F. (Vancouver, Canada)
  38. [Yang, H.-C.](#) and Chen, C.-W. (2017/Mar/04-08) *Homozygosity disequilibrium associated with treatment response and its methylation regulation*. Proceeding of Genetic Analysis Workshop 20. (San Diego, USA)
  39. [Yang, H.-C.](#) (2017/May/15-19). *Statistical genomics and quantitative ecology*. The 7<sup>th</sup> International Conference for Young Scientists & General Assembly Meeting 2017 of the Global Young Academy. (Aviemore, Scotland, UK) (Selected as an oral presentation)
  40. [Yang, H.-C.](#) and Chu, S.-K. (2018/Mar/12-15). *Interethnic methylation difference on SLC7A5 explains ethnic disparity of response to tamoxifen therapy in breast cancer patients*. The Conference of HGM 2018, P120. (Yokohama, Japan)
  41. Chen, C.-W. and [Yang, H.-C.](#) (2018/July/06-10). *OPATs: Omnibus P-value Association Tests*. The 26<sup>th</sup> Conference on Intelligent Systems for Molecular Biology, A-378. (Chicago, USA)
  42. Huang, M.-C. Chen, C.-W. and [Yang, H.-C.](#) (2018/Oct/16-20). *An integrated analysis tool for big genomic data from a biobank*. The 68<sup>th</sup> Annual Meeting of American Society of Human Genetics, S2471. (San Diego, USA)
  43. [Yang, H.-C.](#), Chen, C.-W., Lin, Y.-T. and Chu, S.-K. (2019/Oct/15-19). *Study genetic ancestry and homozygosity disequilibrium in global populations*. The 69<sup>th</sup> Annual Meeting of American Society of Human Genetics, 2400W. (Huston, USA)
  44. [Yang, H.-C.](#), Chen, C.-W., Lin, Y.-T. and Chu, S.-K. (2020/Jul/01-04). *Population pharmacogenomics: Enrichment of ancestry-informative markers in pharmacogenetic loci*. The 29<sup>th</sup> Annual Meeting of International Genetic Epidemiology Society, S140. (Virtual Meeting)
  45. [Yang, H.-C.](#), Chen, C.-W., Wang, J.-H., Liao, H.-C., Chan, T.-C., Hwang, J.-S., Su, M.-W.,

Lee, T.-C., Lin, C.-W., and Chen, C.-h. (2021/Oct/18-22). *Genome-wide phenome-wide association study for important diseases & quantitative traits based on the Taiwan Biobank data*. The 71<sup>th</sup> Annual Meeting of American Society of Human Genetics, 2099. (Huston, USA)