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RESEARCH FOCUS:

My main research objectives are to utilize and develop statistics and machine learning methodologies for disease gene-mapping. In particular, I am interested in modeling the effect of gene-environment interactions on various diseases and traits. I am currently conducting polygenic risk scores (PRSs) for blood pressure and kidney functions and diseases, considering gene-environment interactions as predictors.

我的主要研究為基因型鑑定之品質管理和致病基因搜尋。在國家基因體醫學研究中心裡，我建立一套品管流程，並將此流程自動化與資訊化，確保本中心的高品質高效率產能。在致病基因搜尋方面，我參與「臺灣精準醫療計劃」，著重在以大數據分析找尋糖尿病、自體免疫及藥物基因學之相關危險因子。

PROFESSIONAL EXPERIENCE

2019-present Institute of Biomedical Science, Academia Sinica, Taipei, Taiwan
Research Scientist
2012-2019 Institute of Biomedical Science, Academia Sinica, Taipei, Taiwan
Associate Research Scientist
2004-2012 Institute of Biomedical Science, Academia Sinica, Taipei, Taiwan
Assistant Research Scientist

EDUCATION:

1998 Ph.D. in Applied Mathematics and Statistics
State University of New York, Stony Brook, New York.

RECENT PUBLICATIONS

1. Nicholson MW, Huang CY, Wang JY, Ting CY, Cheng YC, Chan DZH, Lee YC, Hsu CC, Hsu YH, Chang CMC, Hsieh ML, Cheng YY, Lin YL, Chen CH, Wu YT, Hacker TA, Wu JC, Kamp TJ, Hsieh PCH. Cardio- and Neurotoxicity of Selected Anti-COVID-19 Drugs. Pharmaceuticals (Basel). 2022 Jun 20;15(6):765. doi: 10.3390/ph15060765. PMID: 35745684; PMCID: PMC9231250.
2. Mahajan A, Spracklen CN, Zhang W, et al., Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nat Genet. 2022 May;54(5):560-572. doi: 10.1038/s41588-022-01058-3. Epub 2022 May 12. PMID: 35551307; PMCID: PMC9179018.
3. Huang CY, Nicholson MW, Wang JY, et al. Population-based high-throughput toxicity screen of human iPSC-derived cardiomyocytes and neurons. Cell Rep. 2022;39(1):110643.

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4. Wu CC, Chu YH, Shete S, Chen CH. Spatially varying effects of measured confounding variables on disease risk. Int J Health Geogr. 2021;20(1):45. Published 2021 Nov 11. doi:10.1186/s12942-021-00298-6
5. Lin WD, Cheng CF, Wang CH, et al. Genetic factors of idiopathic central precocious puberty and their polygenic risk in early puberty. Eur J Endocrinol. 2021;185(4):441-451. Published 2021 Aug 27. doi:10.1530/EJE-21-0424
6. Chen J, Spracklen CN, Marenne G, et al. The trans-ancestral genomic architecture of glycemic traits. Nat Genet. 2021;53(6):840-860. doi:10.1038/s41588-021-00852-9
7. Juang JJ, Lu TP, Su MW, et al. Rare variants discovery by extensive whole-genome sequencing of the Han Chinese population in Taiwan: Applications to cardiovascular medicine. J Adv Res. 2020;30:147-158. Published 2020 Dec 7. doi:10.1016/j.jare.2020.12.003
8. Wei CY, Yang JH, Yeh EC, et al. Genetic profiles of 103,106 individuals in the Taiwan Biobank provide insights into the health and history of Han Chinese. NPJ Genom Med. 2021;6(1):10. Published 2021 Feb 11. doi:10.1038/s41525-021-00178-9
9. Cheng CF, Hsieh AR, Liang WM, et al. Genome-Wide and Candidate Gene Association Analyses Identify a 14-SNP Combination for Hypertension in Patients With Type 2 Diabetes. Am J Hypertens. 2021;34(6):651-661. doi:10.1093/ajh/hpaa203
10. Cheng CF, Lin YJ, Lin MC, et al. Genetic risk score constructed from common genetic variants is associated with cardiovascular disease risk in type 2 diabetes mellitus. J Gene Med. 2021;23(2):e3305. doi:10.1002/jgm.3305
11. Lo YH, Cheng HC, Hsiung CN, et al. Detecting Genetic Ancestry and Adaptation in the Taiwanese Han People [published correction appears in Mol Biol Evol. 2021 Aug 21;:]. Mol Biol Evol. 2021;38(10):4149-4165. doi:10.1093/molbev/msaa276
12. Johnson TA, Mashimo Y, Wu JY, et al. Association of an IGHV3-66 gene variant with Kawasaki disease. J Hum Genet. 2021;66(5):475-489. doi:10.1038/s10038-020-00864-z
13. Spracklen CN, Horikoshi M, Kim YJ, et al. Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature. 2020;582(7811):240-245. doi:10.1038/s41586-020-2263-3
14. Jiang CL, Jen WP, Tsao CY, Chang LC, Chen CH, Lee YC. Glucose transporter 10 modulates adipogenesis via an ascorbic acid-mediated pathway to protect mice against diet-induced metabolic dysregulation. PLoS Genet. 2020;16(5):e1008823. Published 2020 May 26. doi:10.1371/journal.pgen.1008823
15. Lin YJ, Cheng CF, Wang CH, et al. Genetic Architecture Associated With Familial Short Stature. J Clin Endocrinol Metab. 2020;105(6):dgaa131. doi:10.1210/clinem/dgaa131
16. Yeh JK, Liu WH, Wang CY, et al. Targeted Next Generation Sequencing for Genetic Mutations of Dilated Cardiomyopathy. Acta Cardiol Sin. 2019;35(6):571-584. doi:10.6515/ACS.201911_35(6).20190402A
17. Chiang KM, Chang HC, Yang HC, et al. Genome-wide association study of morbid obesity in Han Chinese. BMC Genet. 2019;20(1):97. Published 2019 Dec 18. doi:10.1186/s12863-019-0797-x
18. Wong HS, Lin YJ, Lu HF, et al. Genomic interrogation of familial short stature contributes to the discovery of the pathophysiological mechanisms and pharmaceutical drug repositioning. J Biomed Sci. 2019;26(1):91. Published 2019 Nov 7. doi:10.1186/s12929-019-0581-2
19. Ko TM, Chang JS, Chen SP, et al. Genome-wide transcriptome analysis to further understand neutrophil activation and lncRNA transcript profiles in Kawasaki disease. Sci Rep. 2019;9(1):328. Published 2019 Jan 23. doi:10.1038/s41598-018-36520-y