YEN-CHEN ANNE FENG, MS, ScD

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📍 Institute of Health Data Analytics and Statistics, College of Public Health, National Taiwan University

CURRENT POSITION

08/2026 - Present **Associate Professor**
Institute of Health Data Analytics and Statistics
Institute of Epidemiology and Preventive Medicine
College of Public Health, National Taiwan University, Taipei, Taiwan

WORK EXPERIENCE

02/2022 – 07/2026 **Assistant Professor**
Institute of Health Data Analytics and Statistics
Institute of Epidemiology and Preventive Medicine
College of Public Health, National Taiwan University, Taipei, Taiwan

08/2021 - 01/2022 **Project Assistant Professor**
Division of Biostatistics and Data Science
Institute of Epidemiology and Preventive Medicine
College of Public Health, National Taiwan University, Taipei, Taiwan

11/2020 - 07/2021 **Vertex Fellow**, Innovation program
Vertex Pharmaceuticals, Boston, MA, USA

08/2017 - 11/2020 **Postdoctoral Fellow**
Center for Genomic Medicine, Massachusetts General Hospital, Boston, MA, USA
Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard, Cambridge, MA, USA
Mentors: Drs. Jordan Smoller and Benjamin Neale
Research focus: Contributions of common and rare genetic variation to disentangling the susceptibility and heterogeneity of neuropsychiatric disorders

EDUCATION

09/2012 - 05/2017 **Doctor of Science** in Genetic Epidemiology and Statistical Genetics
Department of Epidemiology
Harvard T.H. Chan School of Public Health, Boston, MA, USA
Advisor: Dr. Liming Liang; Committee: Drs. Peter Kraft, Andrea Baccarelli, Frank Hu
Dissertation: “Statistical Analysis and Methods for Human -*Omics* Data”

09/2011 - 06/2012 **Master of Science** in Epidemiology and Preventive Medicine
National Taiwan University, Taipei, Taiwan
Advisor: Dr. Chuhsing Kate Hsiao
Thesis: “Probabilistic Inference of DNA Hypermethylation Based on Global Methylation Profiling”

09/2006 - 06/2011 **Bachelor of Science** in Public Health & Biochemistry (dual major)
National Taiwan University, Taipei, Taiwan

TEACHING

02/2022 - Present **Ongoing courses**: *“HDAS 5001: Statistical Analysis of Genetics Data”; “HDAS 7003:*

	Seminar on Biomedical Statistics"; "PH 1011: Public Health"; "PH 0011: Analysis of Big Data in Health"; "PH 3007: Epidemiology"; "PH 3040: Essentials of Global Health"; "EPM7181: Special Topics in Genomic Studies"; "MolMed 7019: Principle of Statistical Genetics & Genome Data Interpretation"
08/2016 - Present	**Instructor**, *Summer Genomic Epidemiology Workshop*, Genomic Research Center, Academia Sinica, Taipei, Taiwan
07/2023 - 08/2023	**Instructor**, *Genome-Wide Association Studies (GWAS) & Polygenic Risk Prediction Workshop*, National Taiwan University Hospital, Taipei, Taiwan
09/2019 - 04/2020	**Teaching fellow**, *Global Initiative for Neuropsychiatric Genetics Education in Research (GINGER)* training program, Harvard T.H. Chan School of Public Health, Boston, MA, USA
11/2019 - 2020	**Instructor**, A short course on *A Practical Introduction to Statistical Genetics*, Massachusetts General Hospital Division of Clinical Research, Boston, MA, USA
12/2015	**Lecturer**, A short course on *Methods and Analysis of Genetic Studies*, Harvard Catalyst Biostatistics Seminar, Boston, MA, USA

PUBLICATIONS (Google Scholar)

1. **Feng, Y.-C. A.**, Lin, M.-C., Tseng, C.-H., Wu, C.-S., Tsai, M.-H.*, Wang, S.-H.* (2026). Paternal valproate exposure and offspring neurodevelopmental outcomes. *Neurology*, *107*(6), e218375.
2. Di Lorenzo, B., Camargo Tavares, L., Díaz-Muñoz, C., Heredia-Fernández, F., Bozzarelli, I., ..., **Feng, Y.-C. A.**, … D'Amato, M. (2026). Cross-definition GWAS of IBS in 2.8 million individuals reveals cardiometabolic and triglyceride-linked mechanisms. *Gut*, gutjnl-2026-338800.
3. Jen, Y., Yu, S.-L., Hsiao, P.-C., Kuo, P.-H., Liu, C.-M., Liu, C.-C., Hwang, T.-J., Hsieh, M. H., Chien, Y.-L., Lin, Y.-T., Huang, H., **Feng, Y.-C. A.**, Hsiao, C. K., Lin, Y.-F., Faraone, S. V., Neale, B., Glatt, S. J., Tsuang, M. T., Hwu, H.-G., & Chen, W. J. (2026). Identification of hub genes involved in early-onset schizophrenia: from genetic susceptibility to predicted regulated gene expression. *Molecular Psychiatry*, 1–13.
4. Ke, Y.-S., Tsai, M.-H., Ho, C.-R., Chou, C.-Y., Chen, H.-H., Stevelink, R., Chen, S., Chen, P. C.-H., Liu, Y.-T., Tung, H., Hsiao, T.-H., Tseng, S.-H., Chan, L., Lee, T.-H., Cheng, C.-K., Jeng, J.-S., Lin, C.-H., Hsu, C.-Y., Yang, Y.-H., … **Feng, Y.-C. A.*** (2026). Variability in epilepsy polygenic risk prediction across Taiwanese population and clinical cohorts. *Epilepsia*, *epi.70353*. https://doi.org/10.1002/epi.70353
5. Liu, R., Chen, T.-T., Xia, Y., Lin, S.-C., Ge, T., Chen, C.-Y.*, **Feng, Y.-C. A.***, Huang, H.*, & Lin, Y.-F.* (2026). Genetic regulation of methylation across East Asian and European populations. *Nature Communications*, *17*(1), 2616.
6. Lee, Y. H., Zhang, Y., Espinosa Dice, A. L., Li, J. H., Tubbs, J. D., **Feng, Y.-C. A.**, Ge, T., Maihofer, A. X., Nievergelt, C. M., Smoller, J. W., Koenen, K. C., Roberts, A. L., & Slopen, N. (2026). Towards scalable biomarker discovery in posttraumatic stress disorder: triangulating genomic and phenotypic evidence from a health system biobank. *Molecular Psychiatry*, 1–10.
7. He, Y.*, Lu, W., Jee, Y. H., Shih, M.-Y., Wang, Y., Tsuo, K., Qian, D. C., Diao, J. A., Huang, H., Patel, C. J., Byun, J., Pasaniuc, B., Atkinson, E. G., Amos, C. I., **Feng, Y.-C. A.**, Moll, M., Cho, M. H., Martin, A. R.* (2025). Multi-trait and multi-ancestry genetic analysis of comorbid lung diseases and traits improves genetic discovery and polygenic risk prediction. *Nature Genetics, 58*(2), 289–298.
8. Goleva, S. B., Leu, C., **Feng, Y.-C. A.**, Burstein, D., Venkatesh, S., Birnbaum, R., Rajagopal, V. M., Straub, P., Christensen, J., Bautista, J. F., Busch, R. M., Najm, I. M., Grove, J., Børglum, A. D., Voloudakis, G., Roussos, P., Smoller, J., Lal, D., & Davis, L. K. (2026). Multisite, multiancestry genome-wide association study meta-analysis of functional seizure disorder in a hospital sample of 675,680 patients. *Biological Psychiatry Global Open Science*, *6*(1), 100604.
9. Chen, P.-S., Liu, Y.-L., Chiang, P.-T., Tsai, H.-H., Lee, M.-J., Chang, Y.-Y., Lan, M.-Y., Wu, Y.-R., Hsiao, I.-T., Li, C.-H., Fan, S.-P., Tai, C.-H., Chiang, H.-L., Chen, C.-Y., Lee, T.-L., Chang, K., Lu, C.-S., Chang, H.-C., Ke, Y.-S., **Feng, Y.-C. A.**, Taiwan PSP/CBS consortium, Hsu, J. S., Lin, C.-H. (2025). Prevalence of NOTCH2NLC and FMR1

repeat expansions in atypical parkinsonism compared to asymptomatic elderly individuals. *Movement Disorders: Official Journal of the Movement Disorder Society*, *40*(9), 2002–2008.

10. Wang, L.-H., Shih, M.-Y., Lin, Y.-F., Kuo, P.-H., & **Feng, Y.-C. A.*** (2025). Polygenic dissection of treatment-resistant depression with proxy phenotypes in the UK Biobank. *Journal of Affective Disorders*, *381*, 350–359.
11. Pan, B.-Y., Tseng, I., **Feng, Y.-C.**, & Fang, C.-T. (2026). Impact of pre-Omicron COVID-19 vaccine boosters on the risk of Omicron variant infections: A systematic review and meta-regression. *Taiwan Yi Zhi [Journal of the Formosan Medical Association]*, 125(1):14-20.
12. **Feng, Y.-C. A.,** Chen, W. J., Lin, M.-C., Hsu, J. S., Cheng, C.-F., Liu, C.-M., Hwu, H.-G., Huang, Y.-T., Lu, T.-P., & Wang, S.-H. (2025). Paternal age, de novo mutation, and age at onset among co-affected schizophrenia sib-pairs: whole-genome sequencing in multiplex families. *Molecular Psychiatry*, *30*(8), 3560–3567.
13. Wang, S.-H., **Feng, Y.-C. A.**, Lin, M.-C., Cheng, C.-F., Su, M.-H., Chen, C.-Y., Wu, C.-S., & Fan, C. C. (2025). Incorporating polygenic liability and family history for predicting psychiatric diseases in the Taiwan Biobank. *Biological Psychiatry*, *98*(6), 485–493.
14. Chen, T.-T., Chen, C.-Y., Liu, C.-Y., Lee, J., Ganna, A., **Feng, Y.-C. A.**, & Lin, Y.-F. (2025). Genetic architectures of childhood maltreatment and causal influence of childhood maltreatment on health outcomes in adulthood. *Molecular Psychiatry*, *30*(8), 3404–3412.
15. Lee, Y. H., Zhang, Y., Kennedy, C. J., Mallard, T. T., Liu, Z., Vu, P. L., **Feng, Y.-C. A.**, Ge, T., Petukhova, M. V., Kessler, R. C., Nock, M. K., & Smoller, J. W. (2024). Enhancing suicide risk prediction with polygenic scores in psychiatric emergency settings: Prospective study. *JMIR Bioinformatics and Biotechnology*, *5*(1), e58357.
16. Epi25 Collaborative. (2024). Exome sequencing of 20,979 individuals with epilepsy reveals shared and distinct ultra-rare genetic risk across disorder subtypes. *Nature Neuroscience, 27*(10), 1864-1879.
17. Yuan, K., Longchamps, R. J., Pardiñas, A. F., Yu, M., Chen, T.-T., Lin, S.-C., Chen, Y., Lam, M., Liu, R., Xia, Y., Guo, Z., Shi, W., Shen, C., Schizophrenia Workgroup of Psychiatric Genomics Consortium, Daly, M. J., Neale, B. M., **Feng, Y.-C. A.**, Lin, Y.-F., Chen, C.-Y., O'Donovan, M., Ge, Tian, Huang, H. (2024). Fine-mapping across diverse ancestries drives the discovery of putative causal variants underlying human complex traits and diseases. *Nature Genetics*, *56*(9), 1841–1850.
18. Tseng, I., Pan, B.-Y., **Feng, Y.-C.**, & Fang, C.-T. (2024). Re-evaluating efficacy of vaccines against highly pathogenic avian influenza virus in poultry: A systematic review and meta-analysis. *One Health (Amsterdam, Netherlands)*, *18*(100714), 100714.
19. Kang, J., Castro, V. M., Ripperger, M., Venkatesh, S., Burstein, D., Linnér, R. K., Rocha, D. B., Hu, Y., Wilimitis, D., Morley, T., Han, L., Kim, R. Y., **Feng, Y.-C. A.**, Ge, T., Heckers, S., Voloudakis, G., Chabris, C., Roussos, P., McCoy, T. H., … Ruderfer, D. M. (2024). Genome-wide association study of treatment-resistant depression: Shared biology with metabolic traits. *The American Journal of Psychiatry*, *181*(7), 608–619.
20. Chen, T. T., Kim, J., ..., **Feng, Y.-C. A.**, Lin, Y.-F., Myung, W., Chen, C.-Y., Won, H.-H. (2024). Shared genetic architectures of educational attainment in East Asian and European populations. *Nature Human Behaviour*, *8*(3):562-575.
21. Chen, C.-Y.*, Chen, T.-T., **Feng, Y.-C. A.***, Yu, M., Lin, S.-C., Longchamps, R. J., Wang, S.-H., Hsu, Y.-H., Yang, H.-I., Kuo, P.-H., Daly, M. J., Chen, W. J., Huang, H.*, Ge, T.*, & Lin, Y.-F.* (2023). Analysis across Taiwan Biobank, Biobank Japan, and UK Biobank identifies hundreds of novel loci for 36 quantitative traits. *Cell Genomics*, *3*(12), 100436.
22. Guintivano, J., Byrne, E. M., Kiewa, J., Yao, S., Bauer, A. E., Aberg, K. A., Adams, M. J., Campbell, A., Campbell, M. L., Choi, K. W., Corfield, E. C., Havdahl, A., …, **Feng, Y.-C. A.**, … Sullivan, P. (2023). Meta-Analyses of Genome-Wide Association Studies for Postpartum Depression. *The American Journal of Psychiatry*, *180*(12), 884–895.
23. Campos, A. I., Namba, S., Lin, S.-C., Nam, K., Sidorenko, J., Wang, H., Kamatani, Y., Biobank Japan Project, Wang, L.-H., Lee, S., Lin, Y.-F., **Feng, Y.-C. A.**, Okada, Y., Visscher, P. M., & Yengo, L. (2023). Boosting the power of genome-wide association studies within and across ancestries by using polygenic scores. *Nature Genetics*, *55*(10), 1769–1776.

24. The COVID-19 Host Genetics Initiative. (2023). A second update on mapping the human genetic architecture of COVID-19. *Nature*, *621*(7977), E7-E26.

25. International League Against Epilepsy Consortium on Complex Epilepsies. (2023). GWAS meta-analysis of over 29,000 people with epilepsy identifies 26 risk loci and subtype-specific genetic architecture. *Nature Genetics*, *55*(9), 1471–1482.

26. Montanucci, L., Lewis-Smith, D., Collins, R. L., Niestroj, L.-M., Parthasarathy, S., Xian, J., Ganesan, S., Macnee, M., Brünger, T., Thomas, R. H., Talkowski, M., Epi25 Collaborative, Helbig, I., Leu, C., & Lal, D. (2023). Genome-wide identification and phenotypic characterization of seizure-associated copy number variations in 741,075 individuals. *Nature Communications*, *14*(1), 4392.

27. Lee, Y. H., Thaweethai, T., Sheu, Y.-H., **Feng, Y.-C. A.**, Karlson, E. W., Ge, T., Kraft, P., & Smoller, J. W. (2023). Impact of selection bias on polygenic risk score estimates in healthcare settings. *Psychological Medicine, 53*(15), 7435–7445.

28. Kanai, M., Elzur, R., Zhou, W., Global Biobank Meta-analysis Initiative, Daly, M. J., & Finucane, H. K. (2022). Meta-analysis fine-mapping is often miscalibrated at single-variant resolution. *Cell Genomics*, *2*(12), 100210.

29. **Feng, Y.-C. A.***, Chen, C.-Y., Chen, T.-T., Kuo, P.-H., Hsu, Y.-H., Yang, H.-I., Chen, W. J., Su, M.-W., Chu, H.-W., Shen, C.-Y., Ge, T., Huang, H., & Lin, Y.-F.* (2022). Taiwan Biobank: A rich biomedical research database of the Taiwanese population. *Cell Genomics*, *2*(11), 100197.

30. Zhou, W.*, Kana, M., Wu, K.-H. H., Humaira, R., Tsuo, K., Hirbo, J. B., …, **Feng, Y.-C. A.**, ..., Neale, B. M.* (2022). Global Biobank Meta-analysis Initiative: powering genetic discovery across human diseases. *Cell Genomics, 2*(10): 100192.

31. Su, M.-H., Lai, R.-Y., Lin, Y.-F., Chen, C.-Y., **Feng, Y.-C. A.**, Hsiao, P.-C., & Wang, S.-H. (2022). Evaluation of the causal relationship between smoking and schizophrenia in East Asia. *Schizophrenia (Heidelberg, Germany)*, *8*(1), 72.

32. The COVID-19 Host Genetics Initiative. (2022). A first update on mapping the human genetic architecture of COVID-19. *Nature*, *608*(7921), E1-E10.

33. Campbell, C., Leu, C., **Feng, Y.-C. A.**, Wolking, S., Moreau, C., Ellis, C., Ganesan, S., Martins, H., Oliver, K., Boothman, I., Benson, K., Molloy, A., Brody, L., Michaud, J. L., Hamdan, F. F., Minassian, B. A., Lerche, H., Scheffer, I. E., Sisodiya, S., … Cavalleri, G. L. (2022). The role of common genetic variation in presumed monogenic epilepsies. *eBioMedicine*, *81*, 104098.

34. **Feng, Y.-C. A.*,** Stanaway, I. B., Connolly, J. J., Denny, J. C., Luo, Y., Weng, C., Wei, W.-Q., Weiss, S. T., Karlson, E. W., & Smoller, J. W.* (2022). Psychiatric manifestations of rare variation in medically actionable genes: a PheWAS approach. *BMC Genomics, 23*(1), 385.

35. Wang, S.-H., Su, M.-H., Chen, C.-Y., Lin, Y.-F., **Feng, Y.-C. A.**, Hsiao, P.-C., Pan, Y.-J., & Wu, C.-S. (2022). Causality of abdominal obesity on cognition: a trans-ethnic Mendelian randomization study. *International Journal of Obesity (2005)*, *46*(8), 1487–1492.

36. Ge, T., Irvin, M. R., Patki, A., Srinivasasainagendra, V., Lin, Y.-F., Tiwari, H. K., Armstrong, N. D., Benoit, B., Chen, C.-Y., Choi, K. W., Cimino, J. J., Davis, B. H., Dikilitas, O., Etheridge, B., **Feng, Y.-C. A.**, Gainer, V., Huang, H., Jarvik, G. P., Kachulis, C., … Karlson, E. W. (2022). Development and validation of a trans-ancestry polygenic risk score for type 2 diabetes in diverse populations. *Genome Medicine*, *14*(1), 70.

37. Ruan, Y., Lin, Y.-F., **Feng, Y.-C. A.**, Chen, C.-Y., Lam, M., Guo, Z., Stanley Global Asia Initiatives, He, L., Sawa, A., Martin, A. R., Qin, S., Huang, H., & Ge, T. (2022). Improving polygenic prediction in ancestrally diverse populations. *Nature Genetics, 54*(5), 573–580.

38. Mars, N., Kerminen, S., **Feng, Y.-C. A.**, Kanai, M., Läll, K., Thomas, L. F., Skogholt, A. H., della Briotta Parolo, P., Neale, B. M., Smoller, J. W., Gabrielsen, M. E., Hveem, K., Mägi, R., Matsuda, K., Okada, Y., Pirinen, M., Palotie, A., Ganna, A., Martin, A. R., & Ripatti, S. (2022). Genome-wide risk prediction of common diseases across ancestries in one million people. *Cell Genomics*, *2*(4), 100118.

39. Sealock, J. M., Lee, Y. H., Moscati, A., Venkatesh, S., Voloudakis, G., Straub, P., Singh, K., **Feng, Y.-C. A.**, Ge, T., Roussos, P., Smoller, J. W., Chen, G., & Davis, L. K. (2021). Use of the PsycheMERGE network to investigate the

association between depression polygenic scores and white blood cell count. *JAMA Psychiatry (Chicago, Ill.)*, *78*(12), 1365–1374.

40. COVID-19 Host Genetics Initiative. (2021). Mapping the human genetic architecture of COVID-19. *Nature*, *600*(7889), 472-477.
41. Motelow, J. E., Povsil G., Dhinda, R. S., Stanley, K. E., Allen, A. S., **Feng, Y.-C. A.**, ... Goldstein, D. B. (Epi25 Collaborative). (2021). Sub-genic intolerance, ClinVar, and the epilepsies: A whole-exome sequencing study of 29,165 individuals. *The American Journal of Human Genetics*, *108*(6), 965–982.
42. **Feng, Y.-C. A.***, Guo, Y., Pain, L., Lathrop, G. M., Laprise, C., Moffatt, M. F., Cookson, W. O., & Liang, L.* (2021). Estimating cell-type-specific DNA methylation effects in heterogeneous cellular populations. *Epigenomics*, *13*(2), 87–97.
43. Rahman, M. L., **Feng, Y.-C. A.**, Fiehn, O., Albert, P. S., Tsai, M. Y., Zhu, Y., Wang, X., Tekola-Ayele, F., Liang, L., & Zhang, C. (2021). Plasma lipidomics profile in pregnancy and gestational diabetes risk: a prospective study in a multiracial/ethnic cohort. *BMJ Open Diabetes Research & Care*, *9*(1), e001551.
44. Dennis, J. K., Sealock, J. M., Straub, P., Lee, Y. H., Hucks, D., Actkins, K., Faucon, A., **Feng, Y.-C. A.**, Ge, T., Goleva, S. B., Niarchou, M., Singh, K., Morley, T., Smoller, J. W., Ruderfer, D. M., Mosley, J. D., Chen, G., & Davis, L. K. (2021). Clinical laboratory test-wide association scan of polygenic scores identifies biomarkers of complex disease. *Genome Medicine*, *13*(1), 6.
45. Lee, P. H., **Feng, Y.-C. A.**, & Smoller, J. W. (2021). Pleiotropy and Cross-Disorder Genetics Among Psychiatric Disorders. *Biological Psychiatry*, *89*(1), 20–31.
46. Dickey, A. K., Quick, C., Ducamp, S., Zhu, Z., **Feng, Y.-C. A.**, Naik, H., Balwani, M., Anderson, K. E., Lin, X., Phillips, J. E., Rebeiz, L., Bonkovsky, H. L., McGuire, B. M., Wang, B., Chasman, D. I., Smoller, J. W., Fleming, M. D., & Christiani, D. C. (2021). Evidence in the UK Biobank for the underdiagnosis of erythropoietic protoporphyria. *Genetics in Medicine: Official Journal of the American College of Medical Genetics*, *23*(1), 140–148.
47. Niestroj, L.-M., Perez-Palma, E., Howrigan, D. P., Zhou, Y., Cheng, F., Saarentaus, E., Nürnberg, P., Stevelink, R., Daly, M. J., Palotie, A., Lal, D., & Epi25 Collaborative. (2020). Epilepsy subtype-specific copy number burden observed in a genome-wide study of 17,458 subjects. *Brain: A Journal of Neurology*, *143*(7), 2106–2118.
48. Li, J., Guasch-Ferré, M., Chung, W., Ruiz-Canela, M., Toledo, E., Corella, D., Bhupathiraju, S. N., Tobias, D. K., Tabung, F. K., Hu, J., Zhao, T., Turman, C., **Feng, Y.-C. A.**, Clish, C. B., Mucci, L., Eliassen, A. H., Costenbader, K. H., Karlson, E. W., Wolpin, B. M., … Liang, L. (2020). The Mediterranean diet, plasma metabolome, and cardiovascular disease risk. *European Heart Journal*, *41*(28), 2645–2656.
49. Lee, P. H., Anttila, V., Won, H., **Feng, Y.-C. A.**, Rosenthal, J., Zhu, Z., ..., Smoller, J. W. (Cross-Disorder Group of the Psychiatric Genomics Consortium) (2019). Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. *Cell*, *179*(7), 1469-1482.e11.
50. Ge, T., Chen, C.-Y., Ni, Y., **Feng, Y.-C. A.**, & Smoller, J. W. (2019). Polygenic prediction via Bayesian regression and continuous shrinkage priors. *Nature Communications, 10*(1), 1776.
51. **Feng, Y.-C. A.**, Howrigan, D. P., Abbott, L. E., Tashman, K., Cerrato, F., Singh, T., Heyne, H., Byrnes, A., Churchhouse, C., Lal, D., Heinzen, E. L., Cavalleri, G. L., Fanous, A. H., McCarroll, S. A., Gupta, N., Gabriel, S. B., Daly, M. J., Lander, E. S., Lowenstein, D. H., … Neale, B. M. (Epi25 Collaborative). (2019). Ultra-rare genetic variation in the epilepsies: A whole-exome sequencing study of 17,606 individuals. *The American Journal of Human Genetics*, *105*(2), 267–282.
52. **Feng, Y.-C. A.**, Cho, K., Lindstrom, S., Kraft, P., Cormack, J., IGAP Consortium, Colorectal Transdisciplinary Study (CORECT), Discovery, Biology, and Risk of Inherited Variants in Breast Cancer (DRIVE), Elucidating Loci Involved in Prostate Cancer Susceptibility (ELLIPSE), Transdisciplinary Research in Cancer of the Lung (TRICL), Liang, L., & Driver, J. A. (2017). Investigating the genetic relationship between Alzheimer's disease and cancer using GWAS summary statistics. *Human Genetics*, *136*(10), 1341–1351.
53. Li, X., Liang, L., **Feng, Y.-C. A.**, De Vivo, I., Giovannucci, E., Tang, J. Y., & Han, J. (2017). Height, height-related SNPs, and risk of non-melanoma skin cancer. *British Journal of Cancer*, *116*(1), 134–140.

54. Chang, C.-W., Lu, T.-P., She, C.-X., **Feng, Y.-C.**, & Hsiao, C. K. (2016). Gene-set analysis with CGI information for differential DNA methylation profiling. *Scientific Reports*, *6*(1), 24666.
55. Wang, C.-H., Chueh, L.-H., Chen, S.-C., **Feng, Y.-C.**, Hsiao, C. K., & Chiang, C.-P. (2011). Impact of diabetes mellitus, hypertension, and coronary artery disease on tooth extraction after nonsurgical endodontic treatment. *Journal of Endodontics*, *37*(1), 1–5.

INVITED TALKS AND PRESENTATIONS

1. **Feng, Y.-C.A.** Polygenic Risk Prediction at Scale: Methods, Equity, and Public Health Applications. Taiwan International Graduate Program (TIGP), Institute of Statistical Science, Academia Sinica, May 21, 2026.
2. **Feng, Y.-C.A.** Biobank Polygenic Risk Scoring: Case Studies, Bias, and Clinical Impact. NTU Hospital Hsinchu Branch Precision Medicine Seminar, December 10, 2025.
3. **Feng, Y.-C.A.** Taiwan Biobank: A Resource to Empower Biomedical Research. East Asia Biobank Symposium. Virtual talk, Harvard Center Shanghai, November 5, 2025.
4. **Feng, Y.-C.A.** Genomic Profiling in Digestive Diseases. Taiwan Digestive Disease Week (TDDW; 台灣消化醫學週會議). National Taiwan University Hospital (NTUH) International Convention Center, Taipei, September 27, 2025.
5. **Feng, Y.-C.A.** Biobank Polygenic Risk Scoring: Case Studies, Bias, and Public-Health Impact. Conference on Health Data Analytics and Applications (健康數據資料分析及應用研討會), National Taiwan University Health Data Research Center, Taipei, June 6, 2025.
6. **Feng, Y.-C.A.** Applications of PRS Scoring in Epilepsy. TCVGH International Medical Conference (臺中榮民總醫院國際醫學研討會), Taichung, October 26, 2024.
7. **Feng, Y.-C.A.** Harnessing polygenic architectures for disease risk and health outcome prediction. Taiwan International Graduate Program (TIGP), Institute of Statistical Science, Academia Sinica, May 23, 2024.
8. **Feng Y.-C. A.** Harnessing the potential of polygenic prediction in improving population health. Graduate Institute of Biomedical Informatics, Taipei Medical University, September 28, 2023.
9. **Feng, Y.-C.A.** Harnessing the potential of polygenic prediction in improving population health. International Symposium on Evolutionary Genomics and Bioinformatics, National Tsing Hua University, June 29, 2023.
10. **Feng, Y.-C.A.** Development and applications of polygenic prediction in population health, Taichung Veterans General Hospital, June 15, 2023.
11. **Feng, Y.-C.A.** The era of population genomic health: leveraging genetic data to improve clinical care and public health. Biomedical Artificial Intelligence PhD program Colloquium, National Tsing Hua University, December 22, 2022.
12. **Feng, Y.-C.A.** Analytics and applications of genomic sciences in public health. National Taiwan University-University of Tokyo annual joint conference: A Symposium of Research Innovation in Public Health (virtual), December 9, 2022.
13. **Feng, Y.-C.A.** Informing population health through scalable genomic analysis, discovery, and prediction. Graduate Institute of Medical Genomics and Proteomics, National Taiwan University, November 14, 2022.
14. **Feng, Y.-C.A.** Scalable analysis of DNA sequence data and its application in brain-disorder studies. Pan-Asia Genetics of Brain Disorders Symposium, Singapore, November 3-5, 2022.
15. **Feng, Y.-C.A.** Development and applications of polygenic risk scores (PRS 的國外研究發展以及臨床應用展望). AI Labs, Taipei, Taiwan, September 27, 2022.
16. **Feng, Y.-C.A.** Biobank resources to empower genomic discovery and research. MS2 monthly seminar, Department of Psychiatry, National Taiwan University Hospital, Taipei, Taiwan, August 30, 2022.
17. **Feng, Y.-C.A.** & Lin, Y. F. Genetic analysis of quantitative traits in the Taiwan Biobank. Institute for Molecular Bioscience (IMB) from the University of Queensland (virtual), August 26, 2022.
18. **Feng, Y.-C.A.** Dissecting polygenic signals and rare-variant burden associated with psychiatric manifestations. The 33rd CINP World Congress of Neuropsychopharamcology, Taipei, Taiwan, June 9-12, 2022.

19. **Feng, Y.-C.A.**, Human genetics research at scale: opportunities, challenges, and its translational impact. Invited talk at the monthly seminar, Institute of Statistics, National Yang Ming Chiao Tung University, Hsinchu, Taiwan, November 19, 2021.
20. **Feng Y.-C. A.**, Human genetics research at scale: opportunities, challenges, and its translational impact. Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan, January 21, 2021.
21. **Feng, Y.-C.A.**, on behalf of the Epi25 Collaborative. Ultra-rare genetic variation in the epilepsies: Insights, Challenged, and Prospects. Invited talk at the inaugural Walter J. Burdette Trainee Symposium on Human Genomics, Yale School of Medicine, New Haven, CT, USA, December 2, 2019.
22. **Feng, Y.-C.A.**, Ge, T., Chen, C. Y., Smoller, J. W., Neale, B. M. Evaluating the age-of-onset-dependent genetic architecture of complex disorders in the UK Biobank. Platform talk at the American Society of Human Genetics (ASHG), Houston, TX, USA, October 15-19, 2019.
23. **Feng, Y.-C.A.**, Chu, S., Natarajan, P., Raychaudhuri, S., Weiss, S., Karlson, E. W., Smoller, J. W. A phenome-wide analysis of rare variant burden using *e*MERGEseq data: challenges and preliminary results. Selected talk at the *e*MERGE network steering committee meeting, Rockville, MD, USA, October 3-4, 2019.
24. **Feng, Y.-C.A.**, on behalf of the Epi25 Collaborative. Quantifying the impact of ultra-rare coding variation across the epilepsies. Invited talk at the Epilepsy Precision Medicine meeting, Washington, D.C., USA, September 16-17, 2019.
25. **Feng, Y.-C.A.**, Guo, Y., Pain, L., Lathrop, G. M., Laprise, C., Moffatt, M. F., Cookson, W. O. C. M., Liang, L. Estimating cell-type-specific DNA methylation effects in the presence of cellular heterogeneity. Seminar talk at the Program in Genetic Epidemiology and Statistical Genetics (PGSG), Harvard T.H. Chan School of Public Health, Boston, MA, USA, March, 2017.
26. **Feng, Y.-C.A.**, Cho, K., Lindstrom, S., Kraft, P., Cormack, J., IGAP Consortium, GAME-ON Network, Liang, L., & Driver, J. A*. Examining the genetic link between Alzheimer's disease and cancer using GWAS summary-level data. Invited talk at the Boston VA hospital, Boston, MA, USA, August, 2016.

GRANT AND JOURNAL REVIEWS

Ad-hoc grant reviewer	*National Science and Technology Council (NSTC) General Research Project; National Science and Technology Council (NSTC) Undergraduate Research Project; 台大醫院(總院)院內一般研究計畫; 台大醫院與台灣大學各學院合作計畫(UN); 台灣流行病學學會大專生參與專題研究計畫*
Ad-hoc journal reviewer	*American Journal of Medical Genetics Part B: Neuropsychiatric Genetics; PLOS One; Translational Psychiatry; Epigenetics; Scientific Reports; BMC Medical Genomics; Human Genetics and Genomics (HGG) Advances; Frontiers in Medicine; Frontiers in Pharmacology; European Journal of Human Genetics (ESHG); Journal of the Formosan Medical Association; American Journal of Human Genetics (AJHG); Psychological Medicine*
05/2026	Reviewer for The Israel Science Foundation (ISF) Personal Research Grants
09/2025	Reviewer for PTEN Research Foundation Grant Proposal
10/2022	Guest editor for *Frontiers in Genetics* special issue: "Linking Genetic Variation to Drug Response: Discovery and Challenges"
07/2022	Book reviewer for *Biometrics*: "Assessing COVID-19 and Other Pandemics and Epidemics using Computational Modelling and Data Analysis"
08/2017	Editor for a special issue of *Genes:* "Statistical Resources for the Interpretation and Integration of Human Genetic Association Studies" (ISSN 2073-4425)

HONORS AND AWARDS

08/2027	Ta-You Wu Memorial Award, National Science and Technology Council, Taiwan
08/2022 - 2027	Yushan Young Scholar, Ministry of Education, Taiwan
02/2022 - 07/2022	National Taiwan University Incentives for Newly Hired Exceptional Talent
11/2020	Vertex Pharmaceuticals fellowship
10/2019	Early Career Investigator (EICP) Poster award at the World Congress of Psychiatric Genetics (WCPG)
10/2017	Program in Quantitative Genomics (PQG) Student/Postdoc Travel Fund, Harvard T.H. Chan School of Public Health
10/2016	Reviewer's choice award at the American Society of Human Genetics (ASHG)
07/2015	Tuition Scholarship, Summer Institute in Statistical Genetics, University of Washington
09/2012 - 05/2015	Harvard Chan School scholarship
2012-2014	Studying Abroad Scholarship, Ministry of Education, Taiwan
06/2011	Member of the Phi Tau Phi Scholastic Honor Society of Taiwan
09/2006 - 06/2011	College Presidential awards

RESEARCH GRANTS (Principal Investigator)

2026/08 - 2029/07	**Research Project for Newly-Recruited Personnel, National Science and Technology Council** (115-2314-B-002-071-MY3)
2022/08 - 2027/07	**Yushan Young Scholar Fellowship, Ministry of Education** (MOE-111-YSFAG-0003-001-P1)
2024/01 - 2026/12	**Career Development Project, National Taiwan University** (NTU-113L7859)
2023/08 - 2026/07	**Research Project for Newly-Recruited Personnel, National Science and Technology Council** (112-2314-B-002-200-MY3)
2023/08 - 2024/07	**Seed Projects for Interdisciplinary Research, National Taiwan University** (NTU-113L8409)
2022/09 - 2023/08	**General Research Project, Ministry of Science and Technology** (111-2314-B-002-299)