

Charleston W.K. Chiang

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Curriculum Vitae

Academic Appointment

2024-present	Associate Professor <i>with tenure</i> , University of Southern California (<i>primary</i>) Center for Genetic Epidemiology, Department of Population and Public Health Sciences Keck School of Medicine
2024-present	Associate Professor, University of Southern California (<i>joint</i>) Department of Quantitative and Computational Biology Dornsife College of Letters, Arts, and Sciences
2023-present	Associate Director, Center for Genetic Epidemiology
2022-present	Member, USC Norris Comprehensive Cancer Center Cancer Epidemiology Program
2019-2024	Assistant Professor, University of Southern California (<i>joint</i>) Department of Quantitative and Computational Biology Dornsife College of Letters, Arts, and Sciences
2018-2024	Assistant Professor, University of Southern California (<i>primary</i>) Center for Genetic Epidemiology, Department of Population and Public Health Sciences Keck School of Medicine

Education and Training

parental leaves in 2013 and 2016 (and 2022).

2015-2017 [#]	Postdoctoral Research Fellow, UCLA Center for Neurobehavioral Genetics, Semel Institute
2011-2015 [#]	Ruth L. Kirschstein NRSA Postdoctoral Research Fellow, UCLA Department of Ecology and Evolutionary Biology
2005-2011	Ph.D., Genetics, Harvard University Division of Medical Sciences, Program in Biological and Biomedical Science Leder Human Biology and Translational Medicine Program Scholar Department of Genetics
2000-2005	B.S., Microbiology, Immunology, and Molecular Genetics, UCLA Mathematics (minor), Statistics (minor) Summa Cum Laude, College Honors Program Scholar

Funded Projects and Grants

Current

Years	Role	Source	Total Costs
2021-2026	PI (PI: Chiang)	NIGMS R35GM142783	\$2,035,683
An evolutionary framework to elucidate and interpret the genetic architecture of complex traits in diverse populations			
2022-2027	PI (PI: Chiang)	NHGRI R01HG011646	\$3,996,329
Leveraging the evolutionary history to improve identification of trait-associated alleles and risk stratification models in Native Hawaiians			
2023-2027	PI (PI: Chiang)	NHGRI R01HG012605	\$2,160,123
A genome-wide genealogical framework for statistical and population genetic analysis			

2021-2026	co-I	(PI: Mancuso)	NHGRI R01HG012133	\$4,205,166
Characterizing the evolutionary architecture of complex disease within and across diverse populations				
2022-2027	co-I	(PI: de Smith)	NCI R01CA248771	\$3,815,580
Understanding the increased risk of childhood acute lymphoblastic leukemia in Latinos				
2024-2029	co-I	(PI: Darst)	NHLBI R01HL174378	\$3,587,678
Leveraging metabolomics to identify factors contributing to health disparities in Native Hawaiian individuals				

Mentored Trainee Grants

2022-2024	Mentor	(PI: Bryan L. Dinh)	NHGRI F31HG012159	\$138,108
Genomic resources and references for genetic investigation of an understudied population				
2023-2027	Mentor	(PI: Jalen Langie)	NCI F31CA278359	\$190,776
Exploring the impact of genetic ancestry on acute lymphoblastic leukemia risk in Latino populations				

Publications

Numerically **bolded**: 12 (co-) first authorship, 19 (co-) corresponding or senior authorship

* equal contribution, † corresponding author, **bolded** name denotes group member

Through 2022, 28 out of 51 publications were in journals with impact factor (IF) > 8 at the year of publication.

Preprints and manuscripts in preparation

65. Agasaro O, Xu H, Sheng X, Fuller H, Albanes D, Conti DV, Haiman CA, **Chiang CWK**, Ye K, Darst BF. "Circulating metabolite levels vary by genetic ancestry in diverse populations." *In preparation*
64. Oleksyk TK*, Wolfsberger WW*, Huang YN, *et al.* "Challenges and recommendations in establishing national genomic projects" *In review at Cell*.
63. **Lo YC, Chan TF, Jeon S**, Wilkens LR, Le Marchand L, Haiman CA, **Chiang CWK**[†]. "Transferability of polygenic scores for anthropometric traits and Type II Diabetes to the Native Hawaiian population." *medRxiv* 2023: <https://www.medrxiv.org/content/10.1101/2023.12.25.23300499v1>. *In review at PLoS Genetics*.
62. Xu H, Sun Y, Francis M, Cheng CF, Modulla NTR, Brenna JT, **Chiang CWK**, Ye K. "Shared genetic basis informs the roles of polyunsaturated fatty acids in brain disorders." *medRxiv* 2023: <https://doi.org/10.1101/2023.10.03.23296500>. *In review at Biological Psychiatry*.
61. **Fan C, Cahoon JL, Dinh BL**, Ortega-Del Vecchyo VD, Huber CD, Edge MD, Mancuso N, **Chiang CWK**[†]. "A likelihood-based framework for demographic inference from genealogical trees." *bioRxiv* 2023: <https://www.biorxiv.org/content/10.1101/2023.10.10.561787v1>. *In revision at Nature Genetics*.

Peer-Reviewed and Published

60. Metayer C, Spector LG, Scheurer ME, **Jeon S**, Scott RJ, Takagi M, Clavel J, Manabe A, Ma X, Hailu EM, Lupo PJ, Milne E, Urayama KY, Bonaventure A, Kato M, Meirhaeghe A, **Chiang CWK**, Morimoto LM, Wiemels JL. "One carbon (folate) metabolism and development of childhood acute lymphoblastic leukemia: a genetic pathway analysis from the Childhood Cancer and Leukemia

International Consortium." *In press at Cancer Epidemiol Biomarkers Prev.*

59. **Cahoon JL, Rui X*, Tang E*, Simons C, Langie J, Chen M, Lo YC, Chiang CWK[†].** "Imputation Accuracy Across Global Human Populations." **Am J Hum Genet.** 2024 Apr 5:S0002-9297(24)00084-3. doi: 10.1016/j.ajhg.2024.03.011. Online ahead of print.
58. Hangai M, Kawagushi T, et al. "Genome-wide assessment of genetic risk loci for childhood acute lymphoblastic leukemia in Japanese patients." **Haematologica.** 2024 Apr 1;109(4):1247-1252. doi: 10.3324/haematol.2023.282914.
57. de Smith AJ*, Wahlster L*, **Jeon S***, Kachuri L, Yu F, Black S, **Langie J**, Cato LD, Nakatsuka N, **Chan TF**, Xia G, Mazumder S, Yang W, Gazal S, Eng C, Hu D, Buchard EG, Ziv E, Metayer C, Mancuso N, Yang JJ, Ma X, Wiemels JL, Yu F*, **Chiang CWK***, Sankaran VG*. "A noncoding regulatory variant in *IKZF1* increases acute lymphoblastic leukemia risk in Hispanic/Latino children." **Cell Genom.** 2024 Apr 10;4(4):100526. doi: 10.1016/j.xgen.2024.100526. Epub 2024 Mar 26.
56. Brandt DYC[†], Huber CD[†], **Chiang CWK[†]**, Ortega-Del Yecchy VD[†]. "The Promise of Inferring the Past using the Ancestral Recombination Graph." **Genome Biol Evol.** 2024 Feb 1;16(2):evae005. doi: 10.1093/gbe/evae005.
55. **Dinh BL, Tang E**, Taparra K, Nakatsuka N, Chen F, **Chiang CWK[†]**. "Recombination map tailored to Native Hawaiians may improve robustness of genomic scans for positive selection." **Hum Genet.** 2024 Jan;143(1):85-99. doi: 10.1007/s00439-023-02625-2. Epub 2023 Dec 29.
54. Link V, Schraiber JG, **Fan C, Dinh B**, Mancuso N, **Chiang CWK**, Edge MD. "Tree-based QTL mapping with expected local genetic relatedness matrices." **Am J Hum Genet.** 2023 Dec 7;110(12):2077-2091. doi: 10.1016/j.ajhg.2023.10.017.
53. **Chan TF, Rui X**, Conti DV, Fornage M, Graff M, Haessler J, Haiman C, Highland HM, Jung SY, Kenny E, Kooperberg C, Le Marchand L, North KE, Tao R, Wojcik G, Gignoux CR, PAGE Consortium, **Chiang CWK***, Mancuso N*. "Estimating heritability explained by local ancestry and evaluating stratification bias in admixture mapping from summary statistics." **Am J Hum Genet.** 2023 Nov 2;110(11):1853-1862. doi: 10.1016/j.ajhg.2023.09.012. Epub 2023 Oct 23.
52. **Jeon S, Lo YC**, Morimoto LM, Metayer C, Ma X, Wiemels JL, de Smith AJ, **Chiang CWK[†]**. "Evaluating Genomic Polygenic Risk Scores for Childhood Acute Lymphoblastic Leukemia in Latinos." **HGG Adv.** 2023 Sep 13:100239. doi: 10.1016/j.xhgg.2023.100239.
51. **Sheng X, Xia L, Cahoon JL**, Conti DV, Haiman CA, Kachuri L, **Chiang CWK[†]**. "Inverted genomic regions between reference genome builds in humans impact imputation accuracy and decrease the power of association testing." **HGG Adv.** 2022 Nov 11;4(1):100159. doi: 10.1016/j.xhgg.2022.100159. eCollection 2023 Jan 12.
50. Li S, **Chiang CWK**, Myint SS, Arroyo K, **Chan TF**, Morimoto L, Metayer C, de Smith AJ, Walsh KM, Wiemels JL. "Localized variation in ancestral admixture identifies pilocytic astrocytoma risk loci among Latino children." **PLoS Genet.** 2022 Sep 7;18(9):e1010388. doi: 10.1371/journal.pgen.1010388.
49. Qin X, **Chiang CWK**, Gaggiotti OE. "Deciphering signatures of natural selection via deep learning." **Brief Bioinform.** 2022 Sep 2:bbac354. doi: 10.1093/bib/bbac354.
48. Yu F, Cato LD, Weng C, Liggett LA, **Jeon S**, Xu K, **Chiang CWK**, Wiemels JL, Weissman JS, de Smith AJ, Sankaran VG. "Variant to function mapping at single-cell resolution through network propagation." **Nat Biotechnol.** 2022 Jun 6. doi: 10.1038/s41587-022-01341-y.

47. Qin X, **Chiang CWK**, Gaggiotti OE. “KLFDAPC: a supervised machine learning approach for spatial genetic structure analysis.” **Brief Bioinform.** 2022 Jun 2;bbac202. doi: 10.1093/bib/bbac202.
46. **Fan C[†]**, Mancuso N*, **Chiang CWK*[†]**. “A genealogical estimate of genetic relationships.” **Am J Hum Genet.** 2022 May 5;109(5):812-824. doi: 10.1016/j.ajhg.2022.03.016.
45. Fernandez-Rhodes L, Graff M, et al. “Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits – the Hispanic/Latino Anthropometry Consortium.” **HGG Adv.** 2022 Mar 11;3(2):100099. doi: 10.1016/j.xhgg.2022.100099.
44. **Jeon S**, de Smith AJ, Li S, **Chen M**, **Chan TF**, Muskens IS, Morimoto LM, Dewan AT, Mancuso N, Metayer C, Ma X, Wiemels JL[†], **Chiang CWK[†]**. “Genome-wide trans-ethnic meta-analysis identifies novel susceptibility loci for childhood acute lymphoblastic leukemia.” **Leukemia.** 2022 Mar;36(3):865-868. doi: 10.1038/s41375-021-01465-1.
43. Darst BF, Hughley R, et al. “A rare germline *HOXB13* variant contributes to risk of prostate cancer in men of African ancestry.” **Eur Urol.** 2022 Jan 11:S0302-2838(21)02271-5. doi: 10.1016/j.eururo.2021.12.023.
42. **Chen M[†]**, **Chiang CWK[†]**. “Allele frequency differentiation at height-associated SNPs among continental human populations.” **Eur J Hum Genet.** 2021 Oct;29(10):1542-1548. doi: 10.1038/s41431-021-00938-2.
41. Kachuri L, **Jeon S**, DeWan AT, Metayer C, Ma X, Witte JS, **Chiang CWK**, Wiemels JL, de Smith AJ. “Genetic determinants of blood cell traits influence susceptibility to childhood acute lymphoblastic leukemia.” **Am J Hum Genet.** 2021 Oct 7;108(10):1823-1835. doi: 10.1016/j.ajhg.2021.08.004.
40. **Chiang CWK[†]**. “The opportunities and challenges of integrating population histories into genetic studies for diverse populations: a motivating example from Native Hawaiians.” **Front Genet.** 2021 Sep 27;12:643883. doi: 10.3389/fgene.2021.643883.
39. Ganel L, Chen L, Christ R, Vangipurapu J, Young E, Das I, Kanchi K, Larson D, Regier A, Abel H, Kang CJ, Scott A, Havulinna A, **Chiang CWK**, Service S, Freimer N, Palotie A, Ripatti S, Kuusisto J, Boehnke M, Laakso M, Locke A, Stitzel NO, Hall IM. “Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences.” **Hum Genomics.** 2021 Jun 7;15(1):34. doi: 10.1186/s40246-021-00335-2.
38. Chen L, Abel HJ, Das I, Larson DE, Ganel L, Kanchi KL, Regier AA, Young EP, Kang CJ, Scott AJ, Chiang C, Wang X, Lu S, Christ R, Service SK, **Chiang CWK**, Havulinna AS, Kuusisto J, Boehnke M, Laakso M, Palotie A, Ripatti S, Freimer NB, Locke AE, Stitzel NO, Hall IM. “Association of structural variation with cardiometabolic traits in Finns.” **Am J Hum Genet.** 2021 Apr 1;108(4):583-596. doi: 10.1016/j.ajhg.2021.03.008.
37. Graff M, et al. “Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry.” **Am J Hum Genet.** 2021 Apr 1;108(4):564-582. doi: 10.1016/j.ajhg.2021.02.011.
36. **Sun H***, **Lin M***, Russell EM, Minster RL, **Chan TF**, **Dinh BL**, Naseri T, Reupena MS, Lum-Jones A, OLaGA Study Group, Cheng I, Wilkens LR, Le Marchand L, Haiman CA, **Chiang CWK[†]**. “The impact of global and local Polynesian genetic ancestry on complex traits in Native Hawaiians.” **PLoS Genet.** 2021 Feb 11; doi: 10.1371/journal.pgen.1009273.

35. Iksan OA, et al. "Analysis of the Kazakh tribe Baiuly based on the distribution of the Y-chromosome haplogroups." **Int J Biol Chem**. 2021 Jan; 13(2):80-87. doi: 10.26577/ijbch.2020.v13.i2.10.
34. Pua CJ, et al. "Genetic Studies of Hypertrophic Cardiomyopathy in Singaporeans Identify Variants in TNNI3 and TNNT2 that Are Common in Chinese Patients." **Cir Genom Precis Med**. 2020 Oct;13(5):424-434. doi: 10.1161/CIRCGEN.119.002823.
33. Chen MH, Raffield LM, Mousas A, et al. "Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 individuals from 5 Global Populations." **Cell**. 2020 Sep 3;182(5):1198-1213.e14. doi:10.1016/j.cell.2020.06.045.
32. **Lin M**, Caberto C, Wan P, Li Y, Lum-Jones A, Tiirikainen M, Pooler L, Nakamura B, Sheng X, Porcel J, Lim U, Setiawan VW, Le Marchand L, Wilkens LR, Haiman CA, Cheng I, **Chiang CWK**[†]. "Population-specific reference panels are crucial for the genetic analyses: an example of the *CREBRF* locus in Native Hawaiians." **Hum Mol Genet**. 2020 Aug 3;29(13):2275-2284. doi: 10.1093/hmg/ddaa083.
31. **Chen M**[†], Sidore C, Akiyama M, Ishigaki K, Kamatani Y, Schlessinger D, Cucca F, Okada Y, **Chiang CWK**[†]. "Evidence of Polygenic Adaptation in Sardinia at Height-Associated Loci Ascertained from the Biobank Japan." **Am J Hum Genet**. 2020 Jul 2;107(1):60-71. doi: 10.1016/j.ajhg.2020.05.014.
30. Marcus JH, Posth C, Ringbauer H, Lai L, Skeates R, Sidore C, Beckett J, Furtwangler A, Olivieri A, **Chiang CWK**, Al-asadi H, Dey K, Joseph TA, Liu CC, Der Sarkissian C, Radzeviciute R, Michel M, Gradoli MG, Marongiu P, Rubino S, Mazzarello V, Rovina D, La Fragola A, Serra RM, Bandiera P, Bianucci R, Pompianu E, Murgia C, Guirguis M, Orquin RP, Tuross N, van Dommelen P, Haak W, Reich D, Schlessinger D, Cucca F, Krause J, Novembre J. "Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia." **Nat Comm**. 2020 Feb 24;11(1):939. doi: 10.1038/s41467-020-14523-6.
29. de Smith AJ, Walsh KM, Morimoto LM, Francis SS, Hansen HM, **Jeon S**, Gonseth S, **Chen M**, **Sun H**, Luna-Fineman S, Antillón F, Girón V, Kang AY, Smirnov I, Shao X, Whitehead TP, Barcellos LF, Jolly KW, Healy J, Laverdière C, Sinnett D, Taub JW, Birch JM, Thompson PD, Pombo-de-Oliveira MS, Spector LG, DeWan AT, Mueller BA, **Chiang CWK**, Metayer C, Ma X, Wiemels JL. "Heritable variation at the chromosome 21 gene *ERG* is associated with acute lymphoblastic leukemia risk in children with and without Down syndrome." **Leukemia**. 2019 Nov;33(11):2746-2751. doi: 10.1038/s41375-019-0514-9.
28. Locke AE*, Steinberg KM*, **Chiang CWK***, Service S*, Havulinna A, Stell L, Pirinen M, Abel HJ, Chiang CC, Fulton RS, Jackson AU, Kang CJ, Kanchi KL, Koboldt DC, Larson DE, Nelson J, Nicholas TJ, Pietila A, Ramensky V, Ray D, Scott LJ, Stringham HM, Vangipurapu J, Welch R, Yajnik P, Yin X, Eriksson JG, Ala-Korpela M, Jarvelin MR, Manniko M, Laivouri H, FinnGen Project, Dutcher SK, Stitzel NO, Wilson RK, Hall IM, Sabatti C, Palotie A, Salomaa V, Laakso M, Ripatti S, Boehnke M, Freimer NB. "Exome sequencing of Finnish isolates enhances rare-variant association power." **Nature**. 2019 Aug;572(7769):323-328. doi: 10.1038/s41586-019-1457-z.
27. Sohail M, Maier RM, Ganna A, Bloemendal A, Martin AR, Turchin MC, **Chiang CWK**, Hirschhorn JN, Daly MJ, Patterson N, Neale B, Mathieson I, Reich D, Sunyaev SR. "Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies." **eLife**. 2019 Mar 21;8. Pii: e39702. doi: 10.7554/eLife.39702.
26. **Chiang CWK**[†], Mangul S, Robles C, Sankararaman S. "A comprehensive map of genetic variation in the world's largest ethnic group – Han Chinese." **Mol Bio Evol**. 2018 Nov 1;35(11):2736-2750. doi 10.1093/molbev/msy170.

25. **Chiang CWK**[†], Marcus J, Sidore C, Biddanda, A, Al-asadi H, Zoledziewska M, Pitzalis M, Busonero F, Maschio A, Pistis G, Steri M, Angius A, Lohmueller KE, Abecasis G, Schlessinger D, Cucca F, Novembre J[†]. “Genomic history of the Sardinian population.” **Nat Genet**. 2018 Oct;50(10):1426-1434. doi 10.1038/s41588-018-0215-8.
24. Ganna A, et al. “Quantifying the impact of rare and ultra-rare coding variation across the phenotypic spectrum.” **Am J Hum Genet**. 2018 Jun 7;102(6):1204-1211. doi: 10.1016/j.ajhg.2018.05.002.
23. Kim DS, et al. “Novel association of TM6SF2 rs58542926 genotype with increased serum tyrosine levels and decreased apoB-100 particles in Finns.” **J Lipid Res**. 2017 Jul;58(7):1471-1481. doi: 10.1194/jlr.P076034.
22. Ganel L, et al. “SVScore: an impact prediction tool for structural variation.” **Bioinformatics**. 2017 Apr 1;33(7):1083-1085. doi: 10.1093/bioinformatics/btw789.
21. Reid JS, Jeff J, et al. “A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape in >170,000 individuals of the GIANT Consortium.” **Nat Commun**. 2016 Nov 23;7:13357. doi: 10.1038/ncomms13357.
20. Chen CH, Yang JH, **Chiang CWK**, Hsiung CN, Wu PE, Chang LC, Chang J, Song IW, Yang SL, Chen YT, Liu FT, Shen CY. “Population structure of Han Chinese in the modern Taiwanese population based on 10,000 participants in the Taiwan Biobank project.” **Hum Mol Genet**. 2016 Dec 15;25(24):5321-5331. doi: 10.1093/hmg/ddw346.
19. **Chiang CWK**[†], Ralph, P, Novembre J[†]. “Conflations of short identity-by-descent segments bias their inferred length distribution.” **G3: Genes, Genomes, Genetics**. 2016 May 1; 6(5):1287-1296. doi: 10.1534/g3.116.027581.
18. Winkler TW, Justic AE, Graff M, Barata L, et al. “The influence of age and sex on genetic associations with body composition: a large-scale genome-wide interaction study.” **PLoS Genet**. 2015 Oct 1;11(10):e1005378. doi: 10.1371/journal.pgen.1005378. eCollection 2015 Oct.
17. Zoledziewska M*, Sidore C*, **Chiang CWK***, Sanna S*, Mulas A, Steri M, Busonero F, Marcus JH, Marongiu M, Maschio A, Del Vecchio DO, Floris M, Meloni A, Delitala A, Concas MP, Murgia F, Biino G, Vaccargiu S, Nagaraja R, Lohmueller KE; UK10K Consortium, Timpson NJ, Soranzo N, Tachmazidou I, Dedoussis G, Zeggini E; Understanding Society Scientific Group, Uzzau S, Jones C, Lyons R, Angius A, Abecasis GR, Novembre J, Schlessinger D, Cucca F. “Height-reducing variants and selection for short stature in Sardinia.” **Nat Genet**. 2015 Nov;47(11):1272-81. doi: 10.1038/ng.3368.
16. Sidore C, Busonero F, Maschio A, Porcu E, Naitza S, Zoledziewska M, Mulas A, Pistis G, Steri M, Danjou F, Kwong A, Ortega Del Vecchio VD, **Chiang CWK**, Bragg-Gresham J, Pitzalis M, Nagaraja R, Tarrier B, Brennan C, Uzzau S, Fuchsberger C, Atzeni R, Reinier F, Berutti R, Huang J, Timpson NJ, Toniolo D, Gasparini P, Malerba G, Dedoussis G, Zeggini E, Soranzo N, Jones C, Lyons R, Angius A, Kang HM, Novembre J, Sanna S, Schlessinger D, Cucca F, Abecasis GR. “Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers.” **Nat Genet**. 2015 Nov;47(11):1352-6. doi: 10.1038/ng.3403.
15. Yang WY, Platt A, **Chiang CWK**, Eskin E, Novembre J, Pasaniuc B. “Spatial localization of recent ancestors for admixed individuals.” **G3: Genes, Genomes, Genetics**. 2014 Nov 3; 4(12):2505-18. doi: 10.1534/g3.114.014274.
14. Wang SR, Agarwala V, Flannick J, **Chiang CWK**, Altshuler D, GoT2D Consortium, Hirschhorn JN. “Simulation of Finnish population history, guided by empirical genetic data, to assess power of rare

variant tests in Finland." **Am J Hum Genet.** 2014 May 1;94(5):710-20. doi: 10.1016/j.ajhg.2014.03.019.

13. Olalde I, Sanchez-Quinto F, Datta D, Marigorta UM, **Chiang CWK**, Rodriguez JA, Fernandez-Callejo M, Gonzalez I, Montfort M, Matas-Lalueza L, Civit S, Luiselli D, Charlier P, Pettener D, Ramirez O, Navarro A, Himmelbauer H, Marques-Bonet T, Lalueza-Fox C. "Genomic analysis of the blood attributed to Louis XVI (1754-1793), king of France." **Sci Rep.** 2014 Apr 24;4:4666. doi: 10.1038/srep04666.
12. Olalde I, Allentoft ME, Sanchez-Quinto F, Santpere G, **Chiang CWK**, DeGiorgio M, Prado-Martinez J, Rodriguez JA, Quilez J, Rasmussen S, Ramirez O, Marigorta UM, Fernandez-Callejo M, Prada ME, Encinas JM, Nielsen R, Netea MG, Novembre J, Sturm RA, Sabeti P, Marques-Bonet T, Navarro A, Willerslev E, Lalueza-Fox C. "Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European." **Nature.** 2014 Mar 13;507(7491):225-8. doi: 10.1038/nature12960.
11. Monda KL, Chen GK, Taylor KC, Palmer CD, et al. "A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry." **Nat Genet.** 2013 Jun;45(6):690-6. doi: 10.1038/ng.2608.
10. Turchin MC*, **Chiang CWK***, Palmer CD, Sankararaman S, Reich D, Genetic Investigation of Anthropometric Traits (GIANT) Consortium, Hirschhorn JN. "Evidence of widespread selection on standing variation in Europe at height-associated SNPs." **Nat Genet.** 2012 Sep;44(9):1015-9. doi: 10.1038/ng.2368.
9. **Chiang CWK**, Liu CT, Lettre G, Lange LA, Jorgensen NW, Keating BJ, Vedantam S, Nock NL, Franceschini N, Reiner AP, Demerath EW, Boerwinkle E, Rotter JI, Wilson JG, North KE, Papanicolaou GJ, Cupples LA, Genetic Investigation of Anthropometric Traits (GIANT) consortium, Murabito JM, Hirschhorn JN. "Ultraconserved elements in the human genome: association and transmission analyses of highly constrained single-nucleotide polymorphisms." **Genetics.** 2012 Sep;192(1):253-66.
8. Dauber A, Yu Y, Turchin MC, **Chiang CWK**, Meng Y, Demerath EW, Patel SR, Rich SS, Rotter JI, Schreiner PJ, Wilson JG, Shen Y, Wu BL, Hirschhorn JN. "Genome-wide association of copy number variation reveals an association between short stature and the presence of low frequency genomic deletions." **Am J Hum Genet.** 2011 Dec 9;89(6):751-9.
7. **Chiang CWK**, Gajdos ZKZ, Korn JM, Butler JL, Hackett R, Guiducci C, Nguyen T, Wilks R, Forrester T, Henderson KD, Le Marchand L, Henderson BE, Haiman CA, Cooper RS, Lyon HN, Zhu X, McKenzie CA, Palmert MR, Hirschhorn JN. "The efficacy of detecting variants with small effects on the Affymetrix 6.0 platform using pooled DNA." **Hum Genet.** 2011 Nov;130(5):607-21.
6. Zhu X, Young JH, Fox E, et al. "Combined admixture mapping and association analysis identifies a novel blood pressure genetic locus on 5p13: contributions from the CARE consortium." **Hum Mol Genet.** 2011 Jun 1;20(11):2285-95.
5. Kang SJ*, **Chiang CWK***, Palmer CD*, Tayo BO, Lettre G, Butler JL, Hackett R, Adeyemo AA, Guiducci C, Berzins I, Nguyen TT, Feng T, Luke A, Shriner D, Ardlie K, Rotimi C, Wilks R, Forrester T, McKenzie CA, Lyon HN, Cooper RS, Zhu X, Hirschhorn JN. "Genome wide association of anthropometric traits in African and African derived populations." **Hum Mol Genet.** 2010 Jul 1;19(13):2725-38.
4. **Chiang CWK**, Gajdos ZKZ, Korn JM, Kuruvilla FG, Butler JL, Hackett R, Guiducci C, Nguyen T, Wilks R, Forrester T, Haiman C, Henderson KD, Le Marchand L, Henderson BE, Palmert MR,

McKenzie CA, Lyon HN, Cooper RS, Zhu X, Hirschhorn JN. "Rapid assessment of genetic ancestry in populations of unknown origin by genome-wide genotyping of pooled samples." **PLoS Genet.** 2010;6(3):e1000866.

3. **Chiang CWK***, Derti A*, Schwartz D, Chou MF, Hirschhorn JN, Wu C-t. "Ultraconserved elements: Analyses of dosage sensitivity, motifs, and boundaries." **Genetics.** 2008 Dec;180(4):2277-93.
2. Keating BJ, Tischfield S, Murray SS, *et al.* "Concept, Design and Implementation of a Cardiovascular Gene-centric 50K SNP Array for Large-scale Genomic Association Studies." **PLoS ONE.** 2008;3(10):e3583.
1. Dewing P, **Chiang CWK**, Sinchak K, Sim H, Fernagut P, Kelly S, Chesselet M, Micevych P, Albrecht KH, Harley VR, Vilain E. "Direct regulation of adult brain function by the male-specific factor SRY." **Curr Biol.** 2006, Feb 21;16(4): 415-420.

Contributed Abstracts: Talks

bolded name denotes group member.

28. **Chiang CWK** and Fan C. "A genealogy-based framework to estimate population structure and demographic history." Society of Molecular Biology and Evolution (SMBE), Puerto Vallarta, Mexico, Jul 2024.
27. **Chiang CWK** and Fan C. "A genealogy-based framework to estimate population structure and demographic history." The Allied Genetics Conference (TAGC), Washington DC, Mar 2024.
26. **Cahoon JL**, Mathieson I, **Chiang CWK**, Mathieson S. "Leveraging deep learning to infer archaic human introgression from ancestral recombination graphs." The Allied Genetics Conference (TAGC), Washington DC, Mar 2024. (withdrawn due to inability to attend)
25. **Chiang CWK**. "A genealogy-based framework to estimate population structure and demographic history." The 3rd AsiaEvo Conference, Singapore, Dec 2023.
24. **Chiang CWK**, **Cahoon JL**, **Rui X**, **Tang E**, **Simons C**, **Langie J**, **Chen M**, **Lo YC**. "Imputation Efficacy Across Diverse Global Human Populations." International Genetic Epidemiology Society (IGES), Nashville, TN, Nov 2023. Poster Highlight Talk / Best Poster Award
23. **Langie J**, **Jeon S**, Ma X, Metayer C, de Smith AJ, Wiemels JL, **Chiang CWK**. "Identifying Acute Lymphoblastic Leukemia Risk Loci in Latino Children via Admixture Mapping." American Society of Human Genetics (ASHG), Washington DC, Nov 2023.
22. **Chiang CWK**, **Cahoon JL**, **Rui X**, **Tang E**, **Simons C**, **Langie J**, **Chen M**, **Lo YC**. "Imputation Efficacy Across Diverse Global Human Populations." International Society for Evolution, Medicine & Public Health (ISEMPH), Irvine, CA, Aug 2023.
21. **Cahoon JL**, **Rui X**, **Tang E**, **Simons C**, **Langie J**, **Chen M**, **Lo YC**, **Chiang CWK**. "Imputation Efficacy Across Global Human Populations." Southern California Evolutionary Genetics and Genomics Meeting (ScalE), Irvine, CA, May 2023.
20. **Dinh BL**, **Tang E**, Wilkens LR, Le Marchand L, Haiman CA, **Chiang CWK**. "Population-specific Recombination Maps Reduce False Positive Findings in Genomic Scans of Adaptations." Southern California Evolutionary Genetics and Genomics Meeting (ScalE), Irvine, CA, May 2023.
19. **Jeon S**, Gazal S, Mancuso N, Meyayer C, Ma X, Wiemels JL, **Chiang CWK**, de Smith AJ. "Risk

allele associated with childhood acute lymphoblastic leukemia at the *IKZF1* locus is associated with Indigenous American ancestry and absent in European-ancestry populations.” American Society of Human Genetics (ASHG), Los Angeles, CA, Oct 2022.

18. Link V, **Fan C**, **Chiang CWK**, Mancuso N, Edge MD. “ARG-based association mapping.” Society of Molecular Biology and Evolution (SMBE) Everywhere Symposium, virtual, Sep 2022.
17. **Fan C**, Mancuso N, **Chiang CWK**. “A likelihood-based framework for demographic inference from genealogical trees.” Society of Molecular Biology and Evolution (SMBE) Everywhere Symposium, virtual, Sep 2022.
16. Link V, **Fan C**, **Chiang CWK**, Mancuso N, Edge MD. “ARG-based association mapping.” Population, Evolutionary, and Quantitative Genetics (PEQG), Pacific Grove, CA, Jun 2022.
15. Hughley R, Darst BF, Andrews C, Berndt SI, Sheng X, Kote-Jaral Z, Lachance J, **Chiang CWK**, Jalloh M, Abediyi A, Aisuodionoe-Shadrac O, Adusei B, Mante S, Mensah J, Adjei A, Chanock SJ, Watya S, Eeles RA, Rebbeck TR, Conti DV, Haiman CA, MADCaP Consortium, PRACTICAL Consortium, and African Ancestry Prostate Cancer Consortium. “Germline *HOXB13* variant contributes to risk of prostate cancer in men of African ancestry.” American Society of Human Genetics (ASHG), virtual, Oct 2021.
14. **Chiang CWK**, **Fan C**, Mancuso N. “A genealogical estimate of genetic relationships to improve detection of population structure over time.” International Genetic Epidemiology Society (IGES), virtual, Oct 2021.
13. **Jeon S**, de Smith AJ, Musken IS, Metayer C, Ma X, Wiemels JL, **Chiang CWK**. “Multi-ethnic genome-wide association study of Acute Lymphoblastic Leukemia.” International Genetic Epidemiology Society (IGES), Seoul, Korea, July 2020 (Online due to COVID-19). Best Poster/Lightning Talk Award.
12. **Chen M**, Sidore C, Akiyama M, Ishigaki K, Kamatani Y, Schlessinger D, Cucca F, Okada Y, **Chiang CWK**. “Evidence of polygenic adaptation at height-associated loci in mainland Europeans and Sardinians.” Bay Area Population Genetics Meeting (BAPG), Berkeley, California, Nov 2019.
11. **Chen M**, Sidore C, Akiyama M, Ishigaki K, Kamatani Y, Schlessinger D, Cucca F, Okada Y, **Chiang CWK**. “Re-examining the evidence of polygenic adaptation at height loci in mainland European and Sardinia.” Southern California Evolution Meeting (Scale), Irvine, California, Oct 2019.
10. Lettre G, Chen MH, Raffield L, Mousas A, Jiang T, Akbari P, Sakaue S, Bao EL, Lareau CA, **Chen M**, **Chiang CWK**, Okada Y, Sankaran VG, Soranzo N, Reiner A, Johnson AD, Auer P, Blood-Cell Consortium. “The genetic architecture of hematological traits within and between populations.” American Society of Human Genetics (ASHG), Houston, TX, Oct 2019.
9. **Lin M**, Caberto C, Wan P, Lum-Jones A, Tiirikainen M, Le Marchand L, Wilkens L, Haiman C, Cheng I, **Chiang CWK**. “Oceanian reference panels are crucial for understanding the impact of a Polynesian-specific variant on adiposity in Native Hawaiians.” 23andMe Genome Research Day, Mountain View, California, Jun 2019.
8. **Chiang CWK**, Mangul S, Robles C, Kretschmar WW, Cai N, Kendler KS, Sankararaman S, Flint J. “A comprehensive map of genetic variation in the world’s largest ethnic group – Han Chinese.” Society for Molecular Biology & Evolution (SMBE), Yokohama, Japan, Jul 2018.
7. **Chiang CWK**, Locke AE, Steinberg KM, Service S, Abel H, Havulinna AS, Chiang C, Stell L, Stringham HM, Jackson AU, Pirinen M, Ray D, Larson DE, Koboldt DC, Scott LJ, Fulton RS, Nelson

J, Nicholas TJ, Yajnik P, Ramensky V, Stitzel NO, Wilson RK, Hall IM, Sabatti C, Ripatti S, Salomaa V, Palotie A, Laakso M, Boehnke M, Freimer NB. "Insights to the population structure and genetic architecture of cardiometabolic traits in 20,029 Finnish exomes." American Society of Human Genetics (ASHG) Orlando, FL, Oct 2017.

6. **Chiang CWK**, Locke AE, Steinberg KM, Service S, Abel H, Havulinna AS, Chiang C, Stell L, Stringham HM, Jackson AU, Pirinen M, Ray D, Larson DE, Koboldt DC, Scott LJ, Fulton RS, Nelson J, Nicholas TJ, Yajnik P, Ramensky V, Stitzel NO, Wilson RK, Hall IM, Sabatti C, Ripatti S, Salomaa V, Palotie A, Laakso M, Boehnke M, Freimer NB. "Insights to the genetic architecture of cardiometabolic traits empowered by 20,000 exomes and the history of Finland." Gordon Research Conference (GRC), Human Genetics & Genomics, Stowe, VT, Jul 2017.
5. **Chiang CWK**, Sidore C, Zoledziwska M, Marcus JH, Al-asadi H, Abecasis GR, Schlessinger D, Cucca F, Novembre J. "Population genetic insight to the study of human height." International Society for Evolution, Medicine & Public Health (ISEMPH), Durham, NC, Jun 2016.
4. Novembre J, **Chiang CWK**, Marcus J, Sidore C, Zoledziwska M, Steri M, Al-asadi H, Sanna S, Abecasis G, Schlessinger D, Cucca F. "The population structure and demographic history of Sardinia in relationship to neighboring populations." American Society of Human Genetics (ASHG), San Diego, CA, Oct 2014.
3. **Chiang CWK**, Ralph P, Novembre J. "Conflations of short IBD blocks can bias inferred length of IBD blocks." Society for Molecular Biology & Evolution (SMBE), San Juan, PR, Jun 2014.
2. Turchin MC, **Chiang CWK**, Palmer CD, Hirschhorn JN, GIANT consortium. "Intra-European allele frequency differences at height-associated SNPs suggest widespread selection on standing variation." Cold Spring Harbor Laboratory (CSHL), The Biology of Genomes, Cold Spring Harbor, NY, May 2011.
1. **Chiang CWK**, Dewing P, Vilain E. "The genetic effect of the male-determining gene Sry on brain sexual dimorphism and function." Southern California Conference of Undergraduate Research (SCCUR), Whittier College, Whittier, CA, Nov. 2004.

Contributed Abstracts: Posters (Last 2 Years)

From 2016-2023, 9 of 24 submitted abstracts at ASHG received the Reviewer's Choice Award or Platform Talk. **bolded** name denotes group member.

56. Streicher SA, Park SY, **Chiang CWK**, Sheng X, Bogumi D, Conti DV, Haiman CA, Wilkins LR, Le Marchand L. "Characterizing cancer patterns in Okinawan vs. mainland Japanese Americans: The Multiethnic Cohort." American Association for Cancer Research (AACR), San Diego, CA, Apr 2024.
55. **Dinh BL**, **Wang X**, Sheng X, **Tang E**, Chen F, Young E, Taparra K, Castel SE, Merriman TR, Wilkins LR, Le Marchand L, Hall IM, Stitzel N, Haiman CA, **Chiang CWK**. "A reference panel to improve genotype imputation for Native Hawaiians." Pacific Symposium on Biocomputing (PSB), Kona, HI, Jan 2024.
54. **Chiang CWK**, **Cahoon JL**, **Dinh BL**, Ortega-Del Vecchyo D, Huber CD, Edge MD, Mancuso N, **Fan C**. "A likelihood-based framework for demographic inference from genealogical trees." American Society of Human Genetics (ASHG), Washington DC, Nov 2023.
53. **Dinh BL**, Sheng X, **Tang E**, Chen F, Young E, Taparra K, Wilkins LR, Le Marchand L, Hall IM, Stitzel N, Haiman CA, **Chiang CWK**. "A reference panel to improve genotype imputation for Native

Hawaiians.” American Society of Human Genetics (ASHG), Washington DC, Nov 2023.

52. **Malomane DK**, Mangul S, Abedalthagafi MA, **Chiang CWK**. “Patterns of population structure and genetic variation within the Saudi Arabian population.” American Society of Human Genetics (ASHG), Washington DC, Nov 2023.
51. **Jeon S, Dinh BL, Fan C**, Sheng X, Chen F, Wilkens L, Le Marchand L, Haiman CA, **Chiang CWK**. “Pattern of genetic variation and population structure in Native Hawaiians.” American Society of Human Genetics (ASHG), Washington DC, Nov 2023. *Reviewer’s Choice Abstract* (withdrawn due to inability to attend)
50. Agasaro O, Xu H, Sheng X, Fuller H, Albanes D, Conti DV, Haiman CA, **Chiang CWK**, Ye K, Darst BF. “Circulating metabolite levels vary by genetic ancestry in individuals of African ancestry.” American Society of Human Genetics (ASHG), Washington DC, Nov 2023.
49. **Chiang CWK, Cahoon JL, Rui X, Tang E, Simons C, Langie J, Chen M, Lo YC**. “Imputation Efficacy Across Diverse Global Human Populations.” Gordon Research Conference (GRC), Human Genetics & Genomics, Waterville, NH, Jul 2023.
48. **Langie J, Jeon S**, Ma X, Metayer C, de Smith AJ, Wiemels JL, **Chiang CWK**. “Identifying Acute Lymphoblastic Leukemia Risk Loci in Latino Children via Admixture Mapping.” American Association for Cancer Research (AACR), Orlando, FL, Apr 2023.
47. **Cahoon JL, Rui X, Tang E, Simons C, Langie J, Chen M, Lo YC, Chiang CWK**. “Imputation around the world: Assessing imputation quality across diverse global populations.” Gordon Research Conference (GRC), Quantitative Genetics & Genomics, Ventura, CA, Feb 2023.
46. **Langie J, Jeon S**, Ma X, Metayer C, de Smith AJ, Wiemels JL, **Chiang CWK**. “Identifying Acute Lymphoblastic Leukemia Risk Loci in Latino Children via Admixture Mapping.” Gordon Research Conference (GRC), Quantitative Genetics & Genomics, Ventura, CA, Feb 2023.
45. **Lo YC, Jeon S**, Wilkens L, Le Marchand L, Haiman CA, **Chiang CWK**. “Transferability of polygenic scores for anthropometric traits to the Native Hawaiian population.” Pacific Symposium on Biocomputing (PSB), Kona, HI, Jan 2023.
44. de Smith A, Wahlster L, **Jeon S**, Yu F, Black S, Gazal S, Mancuso N, Metayer C, Ma X, Wiemels JL, **Chiang CWK**, Sankaran VG. “Racial and ethnic disparities in childhood acute lymphoblastic leukemia risk due to an *IKZF1* noncoding regulatory variant.” American Society of Hematology (ASH), New Orleans, LA, Dec 2022.
43. **Fan C**, Mancuso N, **Chiang CWK**. “A likelihood-based framework for demographic inference from genealogical trees.” American Society of Human Genetics (ASHG), Los Angeles, CA, Oct 2022.
42. Kachuri L, **Jeon S**, Mak ACY, Dewan AT, Metayer C, Ma X, Ziv E, Burchard EG, Mancuso N, **Chiang CWK**, Wiemels JL, de Smith AJ. “Transcriptome-wide association study identifies novel susceptibility genes for childhood acute lymphoblastic leukemia in Latinos.” American Society of Human Genetics (ASHG), Los Angeles, CA, Oct 2022.
41. **Lo YC, Jeon S**, Wilkens L, Le Marchand L, Haiman CA, **Chiang CWK**. “Transferability of polygenic scores for anthropometric traits to the Native Hawaiian population.” American Society of Human Genetics (ASHG), Los Angeles, CA, Oct 2022.
40. **Chan TF**, Rui X, Haiman CA, Conti DV, Le Marchand L, Wojcik G, Graff M, Highland HM, North K, Tao R, Haessler J, Kooperberg C, Gignoux CR, Jung SY, Fornage M, Kenny E, PAGE Consortium,

Chiang CWK, Mancuso N. “Estimating heritability explained by local ancestry and stratification bias in admixture mapping from summary statistics.” American Society of Human Genetics (ASHG), Los Angeles, CA, Oct 2022.

39. **Chiang CWK**, Xia L, **Cahoon JL**, Conti DV, Haiman CA, Kachuri L, **Sheng X**. “Inverted genomic regions between reference genome builds in humans impact imputation accuracy and decrease the power of association testing.” American Society of Human Genetics (ASHG), Los Angeles, CA, Oct 2022.
38. **Dinh BL**, Wilkens LR, Le Marchand L, Haiman CA, **Chiang CWK**. “Population-specific recombination maps reduce false positive findings in genomic scans of adaptations.” American Society of Human Genetics (ASHG), Los Angeles, CA, Oct 2022.
37. **Cahoon JL**, **Rui X**, **Tang E**, **Simons C**, **Langie J**, **Chen M**, **Lo YC**, **Chiang CWK**. “Imputation around the world: Assessing imputation quality across diverse global populations.” American Society of Human Genetics (ASHG), Los Angeles, CA, Oct 2022.

Invited Talks and Colloquia

- 2024.02.22 Department of Biomolecular Engineering
University of California, Santa Cruz, Santa Cruz, CA.
- 2024.02.09 Institute for Genomic Health
Icahn School of Medicine at Mount Sinai, New York, NY
- 2023.12.21 Institute for Genome Sciences, Department of Life Sciences
National Yang Ming Chiao Tung University, Taipei, Taiwan.
- 2023.12.14 Institute of Epidemiology and Preventive Medicine
National Taiwan University, Taipei, Taiwan.
- 2023.07.19 Department of Genetics
University of Pennsylvania, Philadelphia, PA.
- 2023.06.30 Genomic Medicine Institute Seminar, Department of Biomedical Sciences
Seoul National University College of Medicine, Seoul, Korea.
- 2023.02.07 Department of Molecular and Human Genetics
Baylor College of Medicine, Houston, TX.
- 2022.11.02 Population Biology Seminar Series
University of Southern California, Los Angeles, CA.
- 2022.11.01 Gerardo Heiss Cardiovascular Epidemiology Seminar
University of North Carolina at Chapel Hill, Chapel Hill, NC.
- 2022.07.15 Native Hawaiian Community Advisory Board (*outreach*)
University of Hawai'i Cancer Center, Honolulu, HI.
- 2021.10.06 American Association for Cancer Research (AACR) Conference on The Science of
Cancer Health Disparity.
Session on “Heterogeneity Within the Asian and Pacific Islander Diaspora”
- 2020.01.22 Department of Genetics
University of Georgia, Athens, GA.
- 2019.09.09 International Laboratory of Human Genome Research (LIIGH)
National University of Mexico (UNAM), Queretero, Mexico.
- 2019.08.29 Quantitative Computational Biology Section, Department of Biological Sciences
University of Southern California, Los Angeles, CA.
- 2018.06.08 Informatics Center for Neurogenetics and Neurogenomics (ICNN) Symposium
University of California, Los Angeles (UCLA), Los Angeles, CA.
- 2018.04.18 Asian Evo Conference, Symposium on “Human Evolution and Adaptation”
China National GeneBank, Shenzhen, China.

2018.04.13	Institute of Biomedical Sciences (IBMS) Academia Sinica, Taipei, Taiwan.
2017.04.13	Center for Genetic Epidemiology, Department of Preventive Medicine University of Southern California, Los Angeles, CA.
2017.02.23	Virginia Institute for Psychiatric and Behavioral Genetics Virginia Commonwealth University, Richmond, VA.
2017.01.26	Department of Anthropology University of Utah, Salt Lake City, UT.
2015.05.06	CAS-MPG Partnered Institute of Computational Biology Chinese Academy of Science, Shanghai, China.
2015.04.30	Center for Genomic Sciences University of Hong Kong, Hong Kong, SAR, China.
2015.04.09	Institute of Biomedical Sciences (IBMS) Academia Sinica, Taipei, Taiwan.

Academic Awards and Recognitions

2023	Human Genetics and Genomics Advances Early Career Investigator Award
2020	Undergraduate Research Associate Program Award, USC (To support undergraduate researchers S. Rashid and S. Sommerer in AY 2020-21)
2017	ASHG Charles J. Epstein Trainee Award for Excellence in Human Genetics Research (Semifinalist)
2013-2015	National Institute of Health NRSA Postdoctoral Fellowship, F32
2010	Summer Institute in Statistical Genetics Travel Scholarship
2007-2010	National Science Foundation Graduate Fellowship
2005	Director's Fellowship, Yale University (declined)
2005	Phi Beta Kappa Society
2004	Ira J. and Shirley Spoon Honors Collegium Scholarship, UCLA
2003	Golden Key International Honour Society
2001	CRC Press Freshmen Chemistry Achievement Award
2001	The National Society of Collegiate Scholar
2001	Alpha Lambda Delta Honor Society
2001	Phi Eta Sigma Honor Society

Mentored Student, Staff, and Postdocs

Abbreviations: **PIBBS**, Programs in Biomedical and Biological Sciences PhD program; **CBB**, Computational Biology and Bioinformatics PhD program; **MBBO**, Marine Biology and Biological Oceanography PhD program; **QB**, Quantitative Biology undergraduate program, USC; **HB**, Human Biology undergraduate program, USC; **CS**, Computer Science undergraduate program, USC.

Year	Name	Program	Role
<i><u>Current Trainee</u></i>			
2022-current	Dorcus Malomane, Ph.D.	Postdoctoral Fellow, USC	Postdoc advisor
2023-current	Ji Tang, Ph.D.	Postdoctoral Fellow, USC	Postdoc advisor
2023-current	Indu Sharma, Ph.D.	Postdoctoral Fellow, USC	Postdoc advisor
2019-current	Tsz Fung Chan	Ph.D. student, Epidemiology, USC	PhD co-advisor
2020-current	Bryan Dinh	Ph.D. student, CBB, USC	PhD advisor
2021-current	Jalen Langie	Ph.D. student, Epidemiology, USC	PhD advisor
2023-current	He Tian	Ph.D. student, Epidemiology, USC	PhD advisor
2023-current	Xinran Wang	Program Analyst I	--
2023-current	Eunice Lee, Ph.D.	Senior Research Associate	--

Graduate Student Committees

2019-2023	Olzhas Iksan	Ph.D. student, Genetics, Kazakh National University	Ph.D. Dissertation (ext. member)
2020	Maria Ruggeri	Ph.D. student, MBBO, USC	Qualifying Exam (ext. member)
2021-2022	Qianxi Feng	Ph.D. student, Epidemiology, USC	Ph.D. Dissertation
2021	Changqing Su	M.S. student, Biostatistics, USC	M.S. Thesis
2021-2022	Shaobo Li	Ph.D. student, PIBBS, USC	Ph.D. Dissertation
2022-2023	Yating Zeng	M.S. student, Biostatistics, USC	M.S. Thesis
2022-current	Huifang Xu	Ph.D. student, Genetics, University of Georgia	Ph.D. Dissertation (ext. member)
2023	Michaela Ince	Ph.D. student, PIBBS, USC	Qualifying Exam
2023	Bida Gu	Ph.D. student, CBB, USC	Qualifying Exam

Former Trainee

2018-2019	Hanxiao Sun	M.S. student, Biostatistics, USC	MS advisor
2018-2020	Meng Lin, Ph.D.	Postdoctoral Fellow, USC	Postdoc advisor
2018-2021	Minhui Chen, Ph.D.	Postdoctoral Fellow, USC	Postdoc advisor
2018-2023	Soyoung Jeon	Ph.D. student, PIBBS, USC Postdoctoral Fellow, USC	PhD co-advisor Postdoc advisor
2019-2020	Samuel Sommerer	B.S. student, QB/CS, USC	--
2019-2023	Caoqi Fan	Ph.D. student, CBB, USC	PhD advisor
2020-2021	Sydney Rashid	B.S. student, QB, USC	--
2020-2022	Xinyue Rui	M.S. student, Biostatistics, USC B.S. student, Mathematics, USC USC Provost Fellowship (2020, 21), Jennifer Battat USC Scholarship	MS advisor
2021-2023	Ying-Chu Lo, Ph.D.	USC-Taiwan Postdoc Fellow, USC	Postdoc advisor
2021-2023	Christopher Simons	B.S. / M.S. student, QB, USC	--
2021-2023	Echo Tang	B.S. student, QB, USC	--
2021-2024	Jordan Cahoon	B.S. student, CS, USC USC Viterbi Fellowship (2020-24) Barry Goldwater Scholarship (2023) Discovery Fellowship (2024) QCB Google Alumni Award (2024)	--
2023	Melody McBride	B.S. student, HB, USC	--

Rotation and Other Visiting Students

2018 Spr	Kuochang Tseng	Rotation student, PIBBS, USC	--
2018 Spr	Charles Bramlett	Rotation student, PIBBS, USC	--
2018 Fall	Audrey Nickle	Rotation student, PIBBS, USC	--
2021 Sum	Dandan Peng	Rotation student, CBB, USC	--
2022 Spr	Ilkwon Cho	Rotation student, CBB, USC	--
2023 Sum	Zachary Chang	High school intern	--
2023 Fall	Yinqiao Wang	Rotation student, Epidemiology, USC	--
2024 Spr	Yifan Zhang	Rotation student, Epidemiology, USC	--
2024 Spr	Juanita Quino	Rotation student, Epidemiology, USC	--
2024 Spr	Matthew Williams	Visiting postdoc from Penn State U	--
2024 Sum	Evelyn Kim	High school intern	--

Teaching

2021-present	Course Director, University of Southern California PM 534 (Statistical Genetics: Introduction to Medical Population Genetics) 3 units, Fall Term
2020	Guest Lecturer, University of Southern California PM 533 (Genetic and Molecular Epidemiology), 1hr/term, Fall Term
2020	Guest Lecturer, University of Hawai'i Cancer Center Multiethnic Cohort T32 Postdoctoral Fellowship Seminar Series, 1hr, Spring Term
2019-2021	Guest Lecturer, University of Southern California BISC 577A (Computational Biology Laboratory), 2hrs/term, Fall Term
2009	Teaching Assistant, Harvard University. LS1B (Genetics, Genomics, and Evolution), Spring Term
2008	Guest Lecturer, Harvard Medical School. Genetics 228 (Genetics in Medicine; "Using Genetics Databases"), Fall Term
2007	Teaching Assistant, Harvard Medical School. Genetics 228 (Genetics in Medicine), Fall Term

Departmental and University Service

Abbreviations: **CGE**, Center for Genetic Epidemiology; **PIBBS**, Programs in Biomedical and Biological Sciences PhD program; **DPPHS**, Department of Population and Public Health Sciences, USC; **QCB**, Department of Quantitative Computational Biology, USC.

Year	Role	Service
2023-present	Leader	Genetic Epidemiology Track, Epidemiology Ph.D. program, DPPHS
2023-present	Member	DPPHS IT/Computing Committee
2021	Member	CGE Scientific Review Committee
2021-2022	Member	DPPHS Junior Faculty Committee
2021-present	Member	DPPHS Statistical Genetics Curriculum Committee
2020-present	Chair	CGE Seminar Series
2020-present	Webmaster	CGE webpage design and launch
2019-present	Member, Co-chair	DPPHS Epidemiology Ph.D. Admission Committee
2019-2020	Member	PIBBS Ph.D. Admission Committee
2019	Member	QCB Faculty Search Committee
2018	Member	DPPHS Biostatistics Ph.D. Admission Committee

Professional Services and Scientific Communities

Editorship and Editorial Board:

Guest Associate Editor (PLoS Genetics, 2023)
Associate Editor (Frontier in Genetics, 2021-current)
Review Editor (Frontier in Genetics, 2018-2021)

Invited Manuscript Reviewer:

Nature	Nature Genetics	Nature Communications
Science	Science Advances	PNAS
Am J Hum Genet	HGG Advances	Cell Genomics
Genetics	G3: Genes, Genomes, Genetics	Molecular Biology and Evolution
PLoS Genetics	PLoS Computational Biology	PLoS ONE
npj Genomic Medicine	Genome Medicine	Eur J Hum Genet
Human Molecular Genetics	Human Genetics	iScience

Bioinformatics
Human Genomics
Nutrition and Diabetes

Evol Med Public Health
Frontiers in Genetics

BMC Genomics
Scientific Reports

American Society of Human Genetics (ASHG):

Member, 2007-present

Judge, DNA Day Essay Contest, 2014, 2015, 2017, 2021

Program Abstract Reviewer, Evolutionary and Population Genetics, 2017

Mentor, Trainee-Mentor Luncheon, Evolution and Population Genetics, 2019

Member, Awards Committee, 2021-2023

Grant Reviewer (*ad hoc*):

Human Frontier Science Program (Reviewer, 2018)

Medical Research Council NIRG (Reviewer, 2019)

NSF CAREER Award (Reviewer, 2021)

German Israeli Foundation (GIF) for Scientific Research and Development (Reviewer, 2022)

NIH Genetic Variation and Evolution (GVE) study section (Reviewer, Jun 2024)

Symposia Organizer:

1st AsiaEvo Conference, "Human Evolution and Adaptation" (2018)

Society of Molecular Biology and Evolution, "Using Ancestral Recombination Graphs (ARGs) to infer Evolutionary Processes" (2022)

Grand Rounds Panelist:

Genomic Screening and Preventive Health by Noura Abul-Husn, DPPHS (2024)

Membership:

American Society for Human Genetics (ASHG)

Society for Molecular Biology & Evolution (SMBE)

International Society of Evolution Medicine and Public Health (ISEMPH)

American Association of Physical Anthropologists (AAPA)

International Genetic Epidemiology Society (IGES)

Genetic Society of America (GSA)

Media Appearances, Engagement, and Coverage

"Filling in genomic blanks for disease studies works better for some groups than others"

Keck School of Medicine News, Apr 10, 2024

<https://keck.usc.edu/news/filling-in-genomic-blanks-for-disease-studies-works-better-for-some-groups-than-others/>

"IKZF1 Genetic Variant May Contribute to Disparities in Risk of ALL in Pediatric Hispanic and Latino Patients"

The ASCO (American Society of Clinical Oncology) Post, Apr 2, 2024

https://ascopost.com/news/march-2024/ikzf1-genetic-variant-may-contribute-to-disparities-in-risk-of-all-in-pediatric-hispanic-and-latino-patients/#new_tab

"USC researchers find genetic variant contributing to disparities in childhood leukemia risk"

Keck School of Medicine News, Mar 26, 2024

<https://keck.usc.edu/news/usc-researchers-find-genetic-variant-contributing-to-disparities-in-childhood-leukemia-risk/>

"Inside HGG Advances: A Chat with Charleston Chiang"

Human Genetics and Genomics Advances, Jan 20, 2023

<https://www.ashg.org/hgga/inside-hgga-with-charleston-chiang/>

“COVID-19 vaccine eligibility expands to anyone over the age of 16 in L.A. county”

USC Annenberg Media, Apr 13, 2021

<https://www.uscannenbergmedia.com/2021/04/13/covid-19-vaccine-eligibility-expands-to-anyone-over-the-age-of-16-in-la-county/>

“Polynesian ancestry linked to obesity in study of Native Hawaiians”

Genetic Obesity News, Feb 15, 2021

<https://geneticobesitynews.com/2021/02/15/polynesian-ancestry-linked-obesity-diabetes-heart-disease-risk-study/>

“Native Hawaiian genetic ancestry linked to metabolic diseases”

The Academic Times, Feb 11, 2021

<https://academictimes.com/native-hawaiian-genetic-ancestry-linked-to-metabolic-diseases/>

“Global, Local Polynesian Ancestry Influence Disease Risk Among Native Hawaiians”

Genomeweb, Feb 11, 2021

<https://www.genomeweb.com/genetic-research/global-local-polynesian-ancestry-influence-disease-risk-among-native-hawaiians#.YCWPKBNkIBI>

“Genetic ancestry linked to diabetes, heart failure and obesity among Native Hawaiians”

Keck School of Medicine News, Feb 11, 2021

<https://keck.usc.edu/genetic-ancestry-linked-to-diabetes-heart-failure-and-obesity-among-native-hawaiians/>

“Polynesian ancestry linked to obesity, diabetes in Native Hawaiians”

Honolulu Star Advertiser, Feb 11, 2021

<https://www.staradvertiser.com/2021/02/11/breaking-news/polynesian-ancestry-linked-to-obesity-diabetes-in-native-hawaiians/>

“Genetics contributes to diabetes, HF, obesity risk in Native Hawaiian individuals”

Healio, Feb 11, 2021

https://www.healio.com/news/cardiology/20210211/genetics-contributes-to-diabetes-hf-obesity-risk-in-native-hawaiian-individuals?utm_medium=social&utm_source=twitter&utm_campaign=scheduledpost

“Accuracy of Genotyping Chips Called into Question”

The Scientist, Jul 24, 2019

<https://www.the-scientist.com/news-opinion/accuracy-of-genotyping-chips-called-into-question--66198>

“Hidden Stories of Chinese Migration and Culture Found in Giant Genetic Study”

The New York Times, Oct 5, 2018

<https://www.nytimes.com/2018/10/05/science/china-genetics.html>

Outreach, Community Engagements and Services

Hoyt Art Gallery, USC

Community outreach pairing local visual artist with biomedical researcher to collaborate for innovative artistic representation of ongoing research at Keck School of Medicine

2018, 2022, 2023 Partnered Biomedical Researcher

“A PhD is Not Enough” book club seminar series, Graduate Society in Biostatistics and Epidemiology (GSBE), Department of Population and Public Health Sciences, USC
2022 Faculty Panelist

“How to get a postdoc” workshop, Department of Ecology and Evolutionary Biology, UCLA
2015 Panelist

Science in the News, Boston, MA.

Science in the News is a free evening seminar series for the public aimed at explaining and discussing today's hottest scientific topics without the hype or exaggeration often introduced by media coverage.

2005-2006 Lecture Coordinator
“Stem Cells: Hope or Hype?” lecture series (2005)
“Obesity and Diabetes” lecture series (2006)

MATHCOUNTS, Suzanne Middle School, Walnut, CA

MATHCOUNTS is a nation-wide program for 6th to 8th grade students designed to elicit interest in mathematics through teamwork and competition.

2003-2005 Head Coach, Suzanne Middle School
1999-2003 Assistant Coach, Suzanne Middle School
2006, 2008, 2013 Volunteer, East San Gabriel Valley Chapter, CA