

# Charleston W.K. Chiang

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Curriculum Vitae

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## Academic Appointment

2018-present      Assistant Professor, University of Southern California  
Center for Genetic Epidemiology, Department of Preventive Medicine  
Keck School of Medicine

## Education

2011              Ph.D., Genetics, Harvard University  
Division of Medical Sciences, Program in Biological and Biomedical Science  
Leder Human Biology and Translational Medicine Program Scholar

2005              B.S., Microbiology, Immunology, and Molecular Genetics, UCLA  
Mathematics (minor), Statistics (minor)  
Summa Cum Laude, College Honors Program Scholar

## Past Employment / Research Experience

<sup>#</sup> include parental leaves in 2013 and 2016.

2015-2017<sup>#</sup>      Postdoctoral Research Fellow, UCLA  
Center for Neurobehavioral Genetics, Semel Institute for Neuroscience  
Advisor: Nelson B. Freimer, M.D.

2011-2015<sup>#</sup>      Postdoctoral Research Fellow, UCLA  
Department of Ecology and Evolutionary Biology  
Advisor: John Novembre, Ph.D.

2005-2011      Graduate student, Harvard Medical School, Broad Institute  
Department of Genetics  
Thesis Advisor: Joel N. Hirschhorn, M.D. Ph.D.

2002-2005      Undergraduate Research Assistant, UCLA  
Department of Human Genetics  
Advisor: Eric Vilain, M.D. Ph.D.

## Publications

**11** (co-) first authorship (numerically bolded), **3** (co-) corresponding authorship (numerically bolded)

\* equal contribution, <sup>†</sup> corresponding author, **bolded** name denotes group member

27. 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, Sarkissian CD, Radzeviciute R, Giuseppina G, Haak W, Reich D, Schlessinger D, Cucca F, Krause J, Novembre J. "Population history from the Neolithic to present on the Mediterranean island of Sardinia: An ancient DNA perspective." *In review* at Nat. Comm. bioRxiv 2019: <https://www.biorxiv.org/content/10.1101/583104v1>. doi: 10.1101/583104
26. de Smith AJ, Walsh KM, Morimoto LM, Francis SS, Gonseth S, **Jeon S**, **Chen M**, **Sun H**, Luna-Fineman S, Antillon F, Hansen HM, Kang AY, Smirnov I, Xiao X, Whitehead T, Barcellos LF, Sender L, Healy J, Laverdiere C, Sinnett D, Taub JW, Birch JM, Thompson P, 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.” *Accepted at Leukemia*.

25. Locke AE\*, Steinberg KM\*, **Chiang CWK\***, Service S\*, Havulinna A, Stell L, Pirinen M, Abel HJ, Chiang C, Fulton RS, Jackson AU, Kang CJ, Kanchi K, Koboldt DC, Larson D, Nelson J, Nicholas TJ, Pietila A, Ramensky V, Ray D, Scott LJ, Stringham HM, Vangipurapu J, Welch R, Yajnik P, Yin X, Eriksson J, Ala-Korpela M, Jarvelin MR, Manniko M, Laivouri H, Dutcher SK, Stitzel NO, Wilson RK, Hall IM, Sabatti C, Palotie A, Salomaa V, Laakso M, Ripatti S, Boehnke M, Freimer NB. “Exome sequencing identifies high-impact trait-associated variants enriched in Finns.” *In revision at Nature*. bioRxiv 2018: <https://www.biorxiv.org/content/early/2018/11/07/464255>. doi: 10.1101/464255
24. 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.
23. **Chiang CWK**<sup>†</sup>, 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.
22. **Chiang CWK**<sup>†</sup>, Marcus J, Sidore C, Biddanda A, Al-asadi H, Zoledziwska M, Pitzalis M, Busonero F, Maschio A, Pistis G, Steri M, Angius A, Lohmueller KE, Abecasis G, Schlessinger D, Cucca F, Novembre J<sup>†</sup>. “Genomic history of the Sardinian population.” *Nat Genet* 2018 Oct;50(10):1426-1434. doi 10.1038/s41588-018-0215-8.
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**<sup>†</sup>, Ralph P, Novembre J<sup>†</sup>. “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. Zoledziwska 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, Zoledziwska 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**

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 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**

**bolded** name denotes group member

19. **Sun H, Lin M**, Wilkens L, Le Marchand L, Haiman CA, **Chiang CWK**. “The impact of global and local Polynesian genetic ancestry on complex traits in Native Hawaiians.” Biology of Genomes, CSHL, Cold Spring Harbor, NY, May 2019.
18. **Chen M**, Akiyama M, Sidore C, Ishigaki K, Okada Y, Kamatani Y, Schlessinger D, **Chiang CWK**. “Re-examining the evidence of polygenic adaptation at height-associated loci in mainland Europe and Sardinia.” Biology of Genomes, CSHL, Cold Spring Harbor, NY, May 2019.
17. **Chiang CWK**, Mangul S, Robles C, Sankararaman S. “A comprehensive map of genetic variation in the world’s largest ethnic group – Han Chinese.” American Society of Human Genetics (ASHG), San Diego, CA, Oct 2018.
16. Noursome D, Jiang X, McKean-Cowdin R, **Chiang CWK**, Burkemper B, Torres M, Varma R. “Admixture and genome-wide association mapping of the retinal nerve fiber layer thickness in a multiethnic population.” Association for Research in Vision and Ophthalmology (ARVO), Honolulu, HI. Apr 2018.
15. **Chiang CWK**, Marcus J, Sidore C, Zoledziwska M, Steri M, Al-asadi H, Sanna S, Abecasis GR, Schlessinger D, Cucca F, Novembre J. “Using whole-genome sequencing to shed insight on the complex prehistory of Sardinia.” American Society of Human Genetics (ASHG), Vancouver, Canada, Oct 2016. *Reviewer’s Choice Abstract*
14. Marcus JH, **Chiang CWK**, Novembre J. “Testing directional selection on polygenic traits using ancient DNA.” American Society of Human Genetics (ASHG), Vancouver, Canada, Oct 2016.
13. **Chiang CWK**, Locke AE, Steinberg KM, Service S, Abel H, Ramensky V, Pirinen M, Stell L, Stringham HM, Jackson AU, Yajnik P, Ray D, Larson DE, Koboldt DC, Scott LJ, Fulton RS, Nelson J, Nicholas TJ, Stitzel NO, Hall IM, Sabatti C, Ripatti S, Salomaa V, Palotie A, Laakso M, Boehnke M, Wilson RK, Freimer NB. “Insights to the genetic architecture of cardiometabolic traits and population structure in 20,029 Finnish exomes.” UCLA Cardiovascular Symposium, Los Angeles, CA, Sep. 2016.
12. **Chiang CWK**, Novembre J. “Conflation of short IBD blocks can bias inferred length of IBD blocks.” American Society of Human Genetics (ASHG), Boston, MA, Oct 2013.



11. **Chiang CWK**, Li J, Ehm MG, Nelson MR, Novembre J. "A population genetic measure of the *de novo* mutation rate using identity-by-descent estimates." American Society of Human Genetics (ASHG), San Francisco, CA, Nov 2012.
10. **Chiang CWK**, Turchin MC, Palmer CD, Sankararaman S, Reich D, GIANT consortium, Hirschhorn JN. "Evidence of widespread selection on standing variation in Europe at height-associated SNPs." 1000 Genomes Community Meeting, Ann Arbor, MI, Jul 2012.
9. **Chiang CWK**, Turchin MC, Palmer CD, Sankararaman S, Reich D, GIANT consortium, Hirschhorn JN. "Intra-European allele frequency differences at height-associated SNPs suggest widespread selection on standing variation." Gordon Research Conferenec (GRC), Human Genetics & Genomics, Newport, RI, Jul. 2011.
8. Wang SR, **Chiang CWK**, Daly MJ, Palotie A, Salomaa V, Hirschhorn JN. "Assessing the Finnish founder effect using next-generation sequencing data." Gordon Research Conference (GRC), Human Genetics & Genomics, Newport, RI, Jul. 2011.
7. **Chiang CWK**, Nguyen TT, Palmer CD, Kang SJ, Hassanein MT, Lyon HN, McKenzie CA, Henderson B, Cooper RS, Zhu X, Haiman CA, Hirschhorn JN. "Genome-wide association and signal fine-maping for variants associated with BMI in African-derived populations." Smith Family Awards Program for Excellence in Biomedical Research Scientific Poster Session, Boston, MA, May 2010.
6. **Chiang CWK**, Kang SJ, Tayo B, Palmer CD, Lettre G, Butler JL, Hackett R, Guiducci C, Nguyen T, Adeyemo A, Rotimi C, Luke A, Lyon HN, Cooper R, Hirschhorn JN, Zhu X. "A genome-wide survey of SNPs and CNVs for association to body mass index in 1,931 individuals from African-derived populations." American Society of Human Genetics (ASHG), Honolulu, HI, Oct. 2009.
5. Gajdos ZKZ, **Chiang CWK**, Korn JM, Kuruvilla FG, Butler JL, Hackett R, Guiducci C, Nguyen T, Lyon HN, Henderson KD, Haiman C, Le Marchand L, Henderson B, Palmert MR, Wilks R, Forrester T, McKenzie CA, Cooper RS, Zhu X, Hirschhorn JN. "Genome-wide genotyping of pooled samples for ancestry assessment of population of unknown origin." American Society of Human Genetics (ASHG), Honolulu, HI, Oct. 2009.
4. **Chiang CWK**, Gajdos ZKZ, Kuruvilla FG, Korn JM, Butler JL, Hackett R, Guiducci C, Nguyen T, Lyon HN, Wilks R, Forrester T, Haiman C, Henderson KD, Le Marchand L, Henderson BE, Palmert MR, McKenzie CA, Cooper RS, Zhu X, Hirschhorn JN. "Rapid assessment of genetic ancestry in populations of unknown origin by genome-wide genotyping of pooled samples." Gordon Research Conferenec (GRC), Human Genetics & Genomics, Biddeford, ME, Jul. 2009.
3. **Chiang CWK**, Gajdos ZKZ, Kuruvilla FG, Korn JM, Hackett R, Butler JL, Guiducci C, Lyon H, Henderson KD, Cooper R, Zhu X, Le Marchand L, Henderson BE, Palmert MR, Hirschhorn JN. "Empirical evaluation of genome-wide allelotyping on pooled DNA samples." American Society of Human Genetics (ASHG), Philadelphia, PA, Nov. 2008.
2. Kang SJ, Tayo B, **Chiang CWK**, Feng T, Adeyemo A, Rotimi C, Luke A, Cooper R, Hirschhorn J, Zhu X, Lyon H. "A Genome-wide association study of body mass index (BMI) in African-origin samples." American Society of Human Genetics (ASHG), Philadelphia, PA, Nov. 2008.
1. **Chiang CWK**, Derti A, Hirschhorn JN, Wu C-t. "Depletion Analysis of Ultraconserved Elements among Copy Number Variants." American Society of Human Genetics (ASHG), San Diego, CA, Oct. 2007.

## **Invited Talks and Colloquia**

2019	Institute Seminar, International Laboratory of Human Genome Research (LIIGH) National University of Mexico (UNAM), Queretero, Mexico. Sep 9
2018	Informatics Center for Neurogenetics and Neurogenomics (ICNN) Symposium University of California, Los Angeles (UCLA), Los Angeles, CA. Jun 8
2018	Asian Evo Conference, Symposium on "Human Evolution and Adaptation" China National GeneBank, Shenzhen, China. Apr 18
2018	Institute Seminar, Institute of Biomedical Sciences (IBMS) Academia Sinica, Taipei, Taiwan. Apr 13
2017	Department Seminar, Center for Genetic Epidemiology University of Southern California, Los Angeles, CA. Apr 13
2017	Department Seminar, Virginia Institute for Psychiatric and Behavioral Genetics (VIPBG) Virginia Commonwealth University, Richmond, VA. Feb 23
2017	Department Seminar, Department of Anthropology University of Utah, Salt Lake City, UT. Jan 26
2015	Institute Seminar, CAS-MPG Partnered Institute of Computational Biology Chinese Academy of Science, Shanghai, China. May 6
2015	Department Seminar, Center for Genomic Sciences University of Hong Kong, Hong Kong, SAR, China. Apr 30
2015	Institute Seminar, Institute of Biomedical Sciences (IBMS) Academia Sinica, Taipei, Taiwan. Apr 9

## **Academic Awards and Recognitions**

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 and Postdocs**

2018-current	Minhui Chen, Ph.D.	Postdoctoral Fellow, USC
2018-current	Meng Lin, Ph.D.	Postdoctoral Fellow, USC
2018-current	Soyoung Jeon	Ph.D. student, PIBBS, USC
2018-current	Hanxiao Sun	M.S. student, Biostatistics, USC
2018 Fall	Audrey Nickle	Rotation student, PIBBS, USC
2018 Spring	Kuochang Tseng	Rotation student, PIBBS, USC
2018 Spring	Charles Bramlett	Rotation student, PIBBS, USC

## **Teaching**

- 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**

- 2019 Quantitative Computational Biology section Faculty Search Committee, Department of Biological Sciences, USC
- 2019 Epidemiology Ph.D. Admission Committee
- 2019 Program in Biomedical and Biological Sciences (PIBBS) Ph.D. Admission Committee
- 2018 Biostatistics Ph.D. Admission Committee

## **Professional Services and Scientific Communities**

**Editorship and Editorial Board:** Review Editor (Frontier in Genetics, 2018-current)

**Invited Manuscript Reviewer:** Nature Genetics, American Journal of Human Genetics; PLoS Genetics; Proceedings of National Academy of Science; Human Molecular Genetics; Molecular Biology and Evolution; Bioinformatics; Genetics; European Journal of Human Genetics; Human Genetics; PLoS ONE; G3: Genes, Genomes, Genetics; Nutrition and Diabetes; Frontier in Genetics; Scientific Report

**Invited Abstract Reviewer:** American Society of Human Genetics (Evolutionary and Population Genetics, 2017)

**Invited Grant Reviewer:** Human Frontier Science Program (Mail-in Reviewer, 2018)

**Symposia Organizer:** 1st AsiaEvo Conference (2018)

**Member:** Society for Molecular Biology & Evolution; American Society for Human Genetics

## **Outreach and Community 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 Partnered Biomedical Researcher

**DNA Day Essay Contest,** American Society of Human Genetics (ASHG)

2014-2015, 2017 Second-round Judge

**“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