Qi Yan

(205) 396-6942 | qy2253@cumc.columbia.edu
622 West 168th Street, New York, NY 10032
https://qiyanpitt.github.io/

Immigration Status

U.S. Permanent Resident

Research Interests

Statistical methods in genomic, epigenomic and transcriptomic data analysis, mediation analysis, causal inference, machine learning/deep learning in disease risk prediction, study design and statistical analysis in clinical trials, bioinformatics pipelines in next-generation sequencing, and genetic data analysis in childhood asthma, age-related macular degeneration, and adverse pregnancy outcomes.

Work Experience

- **Department of Obstetrics and Gynecology - Biostatistics, Columbia University**, New York, NY
  Assistant Professor (tenure-track) 2020-
- **Department of Pediatrics, University of Pittsburgh**, Pittsburgh, PA
  Research Assistant Professor 2018-2020
- **Department of Pediatrics, University of Pittsburgh**, Pittsburgh, PA
  Research Instructor 2017-2018

Education

- **Department of Pediatrics, University of Pittsburgh**, Pittsburgh, PA
  Post-doctoral fellow (mentors: Wei Chen and Daniel E. Weeks) 2014-2016
- **Department of Biostatistics, University of Alabama at Birmingham**, Birmingham, AL
  Ph.D. and Master of science (mentor: Nianjun Liu) 2009-2014
- **Department of Biomedical Engineering, University of Alabama at Birmingham**, Birmingham, AL
  Master of Science 2007-2009
- **Department of Biomedical Engineering, Beijing Institute of Technology**, Beijing, China
  Bachelor of Science 2003-2007

Teaching Experience

- *Invited Lecturer*, OBGYN and Genetic Counseling Education (Clinical data analysis, RCT) 2022,2023
- *Invited Lecturer*, Statistical Genetics, University of Pittsburgh 2020
- *Invited Lecturer*, Foundations of Translational Bioinformatics, University of Pittsburgh 2019
- *Invited Lecturer*, Applied mixed model analysis, University of Pittsburgh 2016
- *Invited Lecturer*, Introductory high-throughput genomic data analysis I: data mining and applications, University of Pittsburgh 2015,2016,2017

Peer Reviewed Publications

† *corresponding author*; * *co-first author*

1. Clark-Sevilla A, Lin Y, Saxena A, **Yan Q**, Wapner R, Raja A, Pe'er I, Salleb-Aouissi A. Diving into CDC pregnancy data in the United States: longitudinal study and interactive application. *JAMIA Open 2024*.
2. Schuermans A, Truong B, Ardissino M, Bhukar R, Slob EAW, Nakao T, Dron JS, Small AM, Cho SMJ, Yu Z, Hornsby W, Antoine T, Lannery K, Postupaka D, Gray KJ, **Yan Q**, Butterworth AS, Burgess S, Wood MJ, Scott NS, Harrington CM, Sarma AA, Lau ES, Roh JD, Januzzi JL, Jr., Natarajan P, Honigberg MC. Genetic associations of circulating cardiovascular proteins with gestational hypertension and preeclampsia. *JAMA Cardiol 2024*.
3. **Yan Q**, Blue NR, Truong B, Zhang Y, Guerrero RF, Liu N, Honigberg MC, Parry S, McNeil RB, Simhan HN, Chung J, Mercer

BM, Grobman WA, Silver R, Greenland P, Saade GR, Reddy UM, Wapner RJ, Haas DM. Genetic associations with dynamic placental proteins identify causal biomarkers for hypertension in pregnancy. Under revision in *Am J Obstet Gynecol. MedRxiv 2023;* 10.1101/2023.05.25.23290460

4. **Yan Q**, Guerrero RF, Khan RR, Surujnarine AA, Wapner RJ, Hahn MW, Raja A, SallebAouissi A, Grobman WA, Simhan H, Blue NR, Silver R, Chung JH, Reddy UM, Radivojac P, Pe'er I, Haas DM. Searching and visualizing genetic associations of pregnancy traits by using GnuMoM2b. *Genetics 2023;* doi: 10.1093/genetics/iyad151.
5. Freud LR, Galloway S, Crowley TB, Moldenhauer J, Philip-Sarles N, Swillen A, Breckpot J, Borrell A, Vora NL, Cuneo B, Hoffman H, Gilbert L, Nowakowska B, Geremek M, Kutkowska-Kaźmierczak A, Vermeesch JR, Devriendt K, Busa T, Sigaudy S, Vigneswaran T, Simpson JM, Dungan J, Gotteiner N, Gloning K-P, Springer A, Digilio MC, Unolt M, Putotto C, Marino B, Repetto G, Fadic M, Garcia-Minaur S, Buil AA, Thomas MA, Fruitman D, Beecroft T, Keyes A, Hui PW, Oskarsdottir S, Bradshaw R, Criebaum A, Norton ME, Lee T, Geiger M, Dunnington L, Isaac J, Wilkins-Haug L, Hunter L, Izzi C, Ullemar V, Toscano M, Ghi T, McGlynn J, Grati FR, Emanuel BS, Gaiser K, Gaynor JW, Goldmuntz E, McGinn DE, Schindewolf E, Tran O, Zackai EH, **Yan Q**, Bassett A, Wapner R, McDonald-McGinn DM. Prenatal versus postnatal diagnosis of 22q11.2 deletion syndrome and perinatal and infant outcomes. *Am J Obstet Gynecol 2024;* 230: 368.e1-368.e12.
6. Tang I, Mallia D, **Yan Q**, Pe'er I, Raja A, Salleb-Aouissi A, Wapner R. A scoping review of preterm birth risk factors. *Am J Perinatol 2023*.
7. Zhang Y, **Yan Q**, Angley M, Lu L, Miller EC, Judd SE, Field RW, Kahe K. Smoking Modifies the Association Between Radon Exposure and Incident Ischemic Stroke: The REGARDS Study. *Stroke 2023*; 54:2737-2744.
8. Kim S, Xu Z, Forno E, Qin Y, Park HJ, Yue M, **Yan Q**, Manni ML, Acosta-Perez E, Canino G, Chen W, Celedon JC. Cis- and trans-eQTM analysis reveals novel epigenetic and transcriptomic immune markers of atopic asthma in airway epithelium. *J Allergy Clin Immunol 2023*.
9. Honigberg MC, Truong B, Khan RR, Xiao B, Bhatta L, Vy HMT, Guerrero RF, Schuermans A, Selvaraj MS, Patel AP, Koyama S, Cho SMJ, Vellarikkal SK, Trinder M, Urbut SM, Gray KJ, Brumpton BM, Patil S, Zollner S, Antopia MC, Saxena R, Nadkarni GN, Do R, **Yan Q,** Pe'er I, Verma SS, Gupta RM, Haas DM, Martin HC, van Heel DA, Laisk T, Natarajan P. Polygenic prediction of preeclampsia and gestational hypertension. *Nat Med 2023*; 29: 1540-1549.
10. Herrera-Luis E, Ortega VE, Ampleford EJ, Sio YY, Granell R, Roos E, Terzikhan N, Vergara EE, Hernandez-Pacheco N, Perez-Garcia J, Martin-Gonzalez E, Lorenzo-Diaz F, Hashimoto S, Brinkman P, Jorgensen AL, **Yan Q**, Forno E, Vijverberg, SJ, Lethem R, Espuela-Ortiz A, Gorenjak M, Eng C, González-Pérez R, Hernández-Pérez JM, Poza-Guedes P, Sardón O, Corcuera P, Hawkins GA, Marsico A, Bahmer T, Rabe KF, Hansen G, Kopp MV, Rios R, Cruz MJ, González-Barcala FJ, Olaguibel JM, Plaza V, Quirce S, Canino G, Cloutier M, Pozo V, Rodriguez-Santana JR, Korta-Murua J, Villar J, Potočnik U, Figueiredo C, Kabesch M, Mukhopadhyay S, Pirmohamed M, Hawcutt DB, Melén E, Palmer CN, Turner S, Maitland-van der Zee AH, Mutius E, Celedó, JC, Brusselle G, Chew FT, Bleecker E, Meyers D, Burchard EG, Pino-Yanes M. Multi-ancestry genome-wide association study of asthma exacerbations. *Pediatr Allergy Immunol 2022*; 33: e13802.
11. Han YY, **Yan Q**, Chen W, Celedón JC. Child maltreatment, anxiety and depression, and asthma among British adults in the UK Biobank. *Eur Respir J* 2022.
12. Ye Z, Mo C, Ke H, **Yan Q**, Chen C, Kochunov P, Hong LE, Mitchell BD, Chen S, Ma T. Meta-Analysis of Transcriptome-Wide Association Studies across 13 Brain Tissues Identified Novel Clusters of Genes Associated with Nicotine Addiction. *Genes* 2021; 13.
13. Yang K, Chen C, **Yan Q**, Shen X, Jiang L, Ma R, Lu L, Zhu J, Tian Y, Cai W, D'Alton ME, Zhang J, Kahe K. Combined association of early exposure to long-chain n-3 polyunsaturated fatty acids, mercury and selenium with cognitive performance in 1-year-old infants. *Environ Res* 2021; 207, 112186.
14. Castellanos CA, Ren X, Gonzalez SL, Li HK, Schroeder AW, Liang HE, Laidlaw BJ, Hu D, Mak ACY, Eng C, Rodríguez-Santana JR, LeNoir M, **Yan Q**, Celedón JC, Burchard EG, Zamvil SS, Ishido S, Locksley RM, Cyster JG, Huang X, Shin JS.

Lymph Node Resident Dendritic Cells Drive TH2 Cell Development Involving MARCH1. *Sci Immunol* 2021; 6, eabh0707.

15. **Yan Q**†, Forno E, Celedón JC, Chen W, Weeks DE. CHIT: an allele-specific method for testing the association between molecular quantitative traits and phenotype-genotype interaction. *Bioinformatics* 2021; doi: 10.1093/bioinformatics/btab554.
16. **Yan Q**†, Forno E, Celedón JC, Chen W. A region-based method for causal mediation analysis of DNA methylation data. *Epigenetics* 2021; 17, 286-296.
17. **Yan Q**, Forno E, Cardenas A, Qi C, Han YY, Acosta-Perez E, Kim S, Zhang R, Boutaoui N, Canino G, Vonk JM, Xu C, Chen W, Marsland A, Oken E, Gold DR, Koppelman GH, Celedón JC. Exposure to violence, chronic stress, nasal DNA methylation, and atopic asthma in children. *Pediatr Pulmonol* 2021; 56: 1896-1905.
18. **Yan Q**, Ding Y, Weeks DE, Chen W. AMD Genetics: Methods and Analyses for Association, Progression, and Prediction. *Adv Exp Med Biol* 2021; 1256: 191-200.
19. Camiolo M, Zhou X, Oriss T, **Yan Q**, Gorry M, Horne W, Trudeau J, Scholl K, Chen W, Kolls J, Ray P, Weisel F, Weisel N, Aghaeepour N, Wenzel S, Nadeau K, Ray A. High dimensional profiling clusters asthma severity by lymphoid and non-lymphoid status. *Cell Rep* 2021; 35: 108974.
20. **Yan Q**, Jiang Y, Huang H, Swaroop A, Chew EY, Weeks DE, Chen W, Ding Y. Genome-Wide Association Studies-based Machine Learning for Prediction of Age-Related Macular Degeneration Risk. *Transl Vis Sci Technol*. 2021; 10: 29.
21. Han YY, **Yan Q**, Chen W, Forno E, Celedón JC. Serum insulin-like growth factor-1, asthma, and lung function among British adults. Ann Allergy Asthma Immunol 2021; 126: 284-291 e282.
22. Mirizio E, Liu C, **Yan Q**, Waltermire J, Mandel R, Schollaert-Fitch K, Konnikova L, Wang X, Chen W, Torok KS. Genetic signatures from RNA sequencing of pediatric localized scleroderma (LS) skin. *Front Pediatr* 2021.
23. Yang G, Han YY, Forno E, **Yan Q**, Rosser F, Chen W, Celedón JC. Glycated Hemoglobin A1c, Lung Function, and Hospitalizations Among Adults with Asthma. *J Allergy Clin Immunol Pract* 2020.
24. **Yan Q**†, Weeks DE, Xin H, Swaroop A, Chew EY, Huang H, Ding Y, Chen W. Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression. *Nat Mach Intell* 2020; 2: 141-150.
25. **Yan Q**[*], Forno E[*], Yang G, Herrera-Luis E, Pino-Yanes M, Oh SS, Acosta-Pérez E, Hu D, Eng C, Huntsman S, Rodriguez-Santana J, Cloutier MM, Canino G, Burchard E, Chen W, Celedón JC. A genome-wide association study of asthma hospitalizations in adults. *J Allergy Clin Immunol* 2020. **Chosen by the Editors to be highlighted in the AAAAI website.**
26. **Yan Q**[*], Forno E[*], Herrera-Luis E[*], Pino-Yanes M, Qi C, Rios R, Han YY, Kim S, Oh S, Acosta-Perez E, Zhang R, Hu D, Eng C, Huntsman S, Avila L, Boutaoui N, Cloutier MM, Soto-Quiros ME, Xu CJ, Weiss ST, Lasky-Su J, Kiedrowski MR, Figueiredo C, Bomberger J, Barreto ML, Canino G, Chen W, Koppelman GH, Burchard EG, Celedón JC. A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. *Eur Respir J* 2020.
27. Xin H, Lian Q, Jiang Y, Luo J, Wang X, Erb C, Xu Z, Zhang X, Heidrich-O'Hare E, **Yan Q**, Duerr RH, Chen K, Chen W. GMM-Demux: sample demultiplexing, multiplet detection, experiment planning, and novel cell-type verification in single cell sequencing. *Genome Biol* 2020; 21: 188.
28. So J, Ningappa M, Glessner J, Min J, Ashokkumar C, Ranganathan S, Higgs BW, Li D, Sun Q, Schmitt L, Biery AC, Dobrowolski S, Trautz C, Fuhrman L, Schwartz MC, Klena NT, Fusco J, Prasadan K, Adenuga M, Mohamed N, **Yan Q**, Chen W, Horne W, Dhawan A, Sharif K, Kelly D, Squires RH, Gittes GK, Hakonarson H, Morell V, Lo C, Subramaniam S, Shin D, Sindhi R. Biliary-Atresia-Associated Mannosidase-1-Alpha-2 Gene Regulates Biliary and Ciliary Morphogenesis and Laterality. *Front Physiol* 2020; 11: 538701.
29. Kim S, Forno E, Zhang R, Park HJ, Xu Z, **Yan Q**, Boutaoui N, Acosta-Perez E, Canino G, Chen W, Celedón JC. Expression Quantitative Trait Methylation Analysis Reveals Methylomic Associations With Gene Expression in Childhood Asthma. *Chest* 2020.

30. Kim S, Forno E, **Yan Q**, Jiang Y, Zhang R, Boutaoui N, Acosta-Perez E, Canino G, Chen W, Celedón JC. SNPs identified by GWAS affect asthma risk through DNA methylation and expression of cis-genes in airway epithelium. *Eur Respir J* 2020; 55.
31. Jiang Y, Chiu C-Y, **Yan Q**, Chen W, Gorin MB, Conley YP, Lakhal-Chaieb MHL, Cook RJ, Amos CI, Wilson AF, Bailey-Wilson JE, McMahon FJ, Vazquez AI, Yuan A, Zhong X, Xiong M, Weeks DE, Fan R. Gene-Based Association Testing of Dichotomous Traits With Generalized Functional Linear Mixed Models Using Extended Pedigrees: Applications to Age-Related Macular Degeneration. *Journal of the American Statistical Association* 2020: 1-15.
32. Han YY, **Yan Q**, Yang G, Chen W, Forno E, Celedón JC. Serum free testosterone and asthma, asthma hospitalisations and lung function in British adults. *Thorax* 2020; 75: 849-854.
33. Forno E, Zhang R, Jiang Y, Kim S, **Yan Q**, Ren Z, Han YY, Boutaoui N, Rosser F, Weeks DE, Acosta-Perez E, Colon-Semidey A, Alvarez M, Canino G, Chen W, Celedón JC. Transcriptome-wide and differential expression network analyses of childhood asthma in nasal epithelium. *J Allergy Clin Immunol* 2020; 146: 671-675.
34. **Yan Q**†, Liu N, Forno E, Canino G, Celedón JC, Chen W. An integrative association method for omics data based on a modified Fisher's method with application to childhood asthma. *PLoS Genet* 2019; 15: e1008142.
35. Rajakumar K, **Yan Q**, Khalid AT, Feingold E, Vallejo AN, Demirci FY, Kamboh MI. Gene Expression and Cardiometabolic Phenotypes of Vitamin D-Deficient Overweight and Obese Black Children. *Nutrients* 2019; 11.
36. Mandel J, Wang H, Normolle DP, Chen W, **Yan Q**, Lucas PC, Benos PV, Prochownik EV. Expression patterns of small numbers of transcripts from functionally-related pathways predict survival in multiple cancers. *BMC Cancer* 2019; 19: 686.
37. Kamboh MI*, Fan KH*, **Yan Q***, Beer JC, Snitz BE, Wang X, Chang CH, Demirci FY, Feingold E, Ganguli M. Population-based genome-wide association study of cognitive decline in older adults free of dementia: identification of a novel locus for the attention domain. *Neurobiol Aging* 2019; 84: 239 e215-239 e224.
38. Forno E, Wang T, Qi C, **Yan Q**, Xu CJ, Boutaoui N, Han YY, Weeks DE, Jiang Y, Rosser F, Vonk JM, Brouwer S, Acosta-Perez E, Colon-Semidey A, Alvarez M, Canino G, Koppelman GH, Chen W, Celedón JC. DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. *Lancet Respir Med* 2019; 7: 336-346.
39. **Yan Q**, Nho K, Del-Aguila JL, Wang X, Risacher SL, Fan KH, Snitz BE, Aizenstein HJ, Mathis CA, Lopez OL, Demirci FY, Feingold E, Klunk WE, Saykin AJ, Alzheimer's Disease Neuroimaging I, Cruchaga C, Kamboh MI. Genome-wide association study of brain amyloid deposition as measured by Pittsburgh Compound-B (PiB)-PET imaging. *Mol Psychiatry* 2018.
40. **Yan Q**†, Fang Z, Chen W. KMgene: a unified R package for gene-based association analysis for complex traits. *Bioinformatics* 2018; 34: 2144-2146.
41. **Yan Q***, Ding Y*, Liu Y, Sun T, Fritsche LG, Clemons T, Ratnapriya R, Klein ML, Cook RJ, Liu Y, Fan R, Wei L, Abecasis GR, Swaroop A, Chew EY, Group AR, Weeks DE, Chen W. Genome-wide analysis of disease progression in age-related macular degeneration. *Hum Mol Genet* 2018; 27: 929-940.
42. Wen X*, Liu Y*, **Yan Q***, Liang M, Tang M, Liu R, Pan J, Liu Q, Chen T, Guo S, Liang J, Lu L, Ding X, Chen W, Wei L. Association of IGFN1 variant with polypoidal choroidal vasculopathy. *J Gene Med* 2018; 20: e3007.
43. Fang Z, Ma T, Tang G, Zhu L, **Yan Q**, Wang T, Celedón JC, Chen W, Tseng GC. Bayesian integrative model for multi-omics data with missingness. *Bioinformatics* 2018; 34: 3801-3808.
44. Burkart KM, Sofer T, London SJ, Manichaikul A, Hartwig FP, **Yan Q**, Soler Artigas M, Avila L, Chen W, Davis Thomas S, Diaz AA, Hall IP, Horta BL, Kaplan RC, Laurie CC, Menezes AM, Morrison JV, Oelsner EC, Rastogi D, Rich SS, Soto-Quiros M, Stilp AM, Tobin MD, Wain LV, Celedón JC, Barr RG. A Genome-Wide Association Study in Hispanics/Latinos Identifies Novel Signals for Lung Function. The Hispanic Community Health Study/Study of Latinos. *Am J Respir Crit Care Med* 2018; 198: 208-219.

45. **Yan Q**, Brehm J, Pino-Yanes M, Forno E, Lin J, Oh SS, Acosta-Perez E, Laurie CC, Cloutier MM, Raby BA, Stilp AM, Sofer T, Hu D, Huntsman S, Eng CS, Conomos MP, Rastogi D, Rice K, Canino G, Chen W, Barr RG, Burchard EG, Celedón JC. A meta-analysis of genome-wide association studies of asthma in Puerto Ricans. *Eur Respir J* 2017; 49. **With an accompanying Editorial.**
46. Wang L, Pan D, **Yan Q**, Song Y. Activation mechanisms of alphaVbeta3 integrin by binding to fibronectin: A computational study. *Protein Sci* 2017; 26: 1124-1137.
47. Forno E, Wang T, **Yan Q**, Brehm J, Acosta-Perez E, Colon-Semidey A, Alvarez M, Boutaoui N, Cloutier MM, Alcorn JF, Canino G, Chen W, Celedón JC. A Multiomics Approach to Identify Genes Associated with Childhood Asthma Risk and Morbidity. *Am J Respir Cell Mol Biol* 2017; 57: 439-447.
48. Forno E, Sordillo J, Brehm J, Chen W, Benos T, **Yan Q**, Avila L, Soto-Quiros M, Cloutier MM, Colon-Semidey A, Alvarez M, Acosta-Perez E, Weiss ST, Litonjua AA, Canino G, Celedón JC. Genome-wide interaction study of dust mite allergen on lung function in children with asthma. *J Allergy Clin Immunol* 2017; 140: 996-1003 e1007.
49. Ding Y, Liu Y, **Yan Q**, Fritsche LG, Cook RJ, Clemons T, Ratnapriya R, Klein ML, Abecasis GR, Swaroop A, Chew EY, Weeks DE, Chen W, Group AR. Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. *Genetics* 2017; 206: 119-133.
50. Danila MI, Laufer VA, Reynolds RJ, **Yan Q**, Liu N, Gregersen PK, Lee A, Kern M, Langefeld CD, Arnett DK, Bridges SL, Jr. Dense Genotyping of Immune-Related Regions Identifies Loci for Rheumatoid Arthritis Risk and Damage in African Americans. *Mol Med* 2017; 23: 177-187.
51. Chen W, Wang T, Pino-Yanes M, Forno E, Liang L, **Yan Q**, Hu D, Weeks DE, Baccarelli A, Acosta-Perez E, Eng C, Han YY, Boutaoui N, Laprise C, Davies GA, Hopkin JM, Moffatt MF, Cookson W, Canino G, Burchard EG, Celedón JC. An epigenome-wide association study of total serum IgE in Hispanic children. *J Allergy Clin Immunol* 2017; 140: 571-577.
52. **Yan Q**, Chen R, Sutcliffe JS, Cook EH, Weeks DE, Li B, Chen W. The impact of genotype calling errors on family-based studies. *Sci Rep* 2016; 6: 28323.
53. Fan R[*], Wang Y[*], **Yan Q**[*], Ding Y, Weeks DE, Lu Z, Ren H, Cook RJ, Xiong M, Swaroop A, Chew EY, Chen W. Gene-Based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions. *Genet Epidemiol* 2016; 40: 133-143.
54. **Yan Q**, Weeks DE, Tiwari HK, Yi N, Zhang K, Gao G, Lin WY, Lou XY, Chen W, Liu N. Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. *Hum Hered* 2015; 80: 126-138.
55. **Yan Q**, Weeks DE, Celedón JC, Tiwari HK, Li B, Wang X, Lin WY, Lou XY, Gao G, Chen W, Liu N. Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. *Genetics* 2015; 201: 1329-1339. **Chosen by the GENETICS Editors as one of the December 2015 Highlights.**
56. **Yan Q**, Tiwari HK, Yi N, Gao G, Zhang K, Lin WY, Lou XY, Cui X, Liu N. A Sequence Kernel Association Test for Dichotomous Traits in Family Samples under a Generalized Linear Mixed Model. *Hum Hered* 2015; 79: 60-68.
57. Limdi NA, Brown TM, **Yan Q**, Thigpen JL, Shendre A, Liu N, Hill CE, Arnett DK, Beasley TM. Race influences warfarin dose changes associated with genetic factors. *Blood* 2015; 126: 539-545. **With an accompanying Editorial.**
58. Chen W, Brehm JM, Manichaikul A, Cho MH, Boutaoui N, **Yan Q**, Burkart KM, Enright PL, Rotter JI, Petersen H, Leng S, Obeidat M, Bosse Y, Brandsma CA, Hao K, Rich SS, Powell R, Avila L, Soto-Quiros M, Silverman EK, Tesfaigzi Y, Barr RG, Celedón JC. A genome-wide association study of chronic obstructive pulmonary disease in Hispanics. *Ann Am Thorac Soc* 2015; 12: 340-348.
59. Brehm JM, Man Tse S, Croteau-Chonka DC, Forno E, Litonjua AA, Raby BA, Chen W, **Yan Q**, Boutaoui N, Acosta-Perez E, Avila L, Weiss ST, Soto-Quiros M, Cloutier MM, Hu D, Pino-Yanes M, Wenzel SE, Spear ML, Kolls JK, Burchard EG, Canino G, Celedón JC. A Genome-Wide Association Study of Post-bronchodilator Lung Function in Children with Asthma. *Am J Respir Crit Care Med* 2015; 192: 634-637.

60. **Yan Q**, Tiwari HK, Yi N, Lin WY, Gao G, Lou XY, Cui X, Liu N. Kernel-machine testing coupled with a rank-truncation method for genetic pathway analysis. *Genet Epidemiol* 2014; 38: 447-456. **2014 Best Paper Award - UAB from the Science Unbound Foundation.**
61. **Yan Q**, McDonald JM, Zhou T, Song Y. Structural insight for the roles of fas death domain binding to FADD and oligomerization degree of the Fas-FADD complex in the death-inducing signaling complex formation: a computational study. *Proteins* 2013; 81: 377-385.
62. Shrestha S, **Yan Q**, Joseph G, Arnett DK, Martinson JJ, Kingsley LA. Replication of RYR3 gene polymorphism association with cIMT among HIV-infected whites. *AIDS* 2012; 26: 1571-1573.
63. Makowsky R, **Yan Q**, Wiener HW, Sandel M, Aissani B, Tiwari HK, Shrestha S. The utility of mitochondrial and y chromosome phylogenetic data to improve correction for population stratification. *Front Genet* 2012; 3: 301.
64. **Yan Q**, Murphy-Ullrich JE, Song Y. Molecular and structural insight into the role of key residues of thrombospondin-1 and calreticulin in thrombospondin-1-calreticulin binding. *Biochemistry* 2011; 50: 566-573.
65. Pan D, **Yan Q**, Chen Y, McDonald JM, Song Y. Trifluoperazine regulation of calmodulin binding to Fas: a computational study. *Proteins* 2011; 79: 2543-2556.
66. **Yan Q**, Murphy-Ullrich JE, Song Y. Structural insight into the role of thrombospondin-1 binding to calreticulin in calreticulin-induced focal adhesion disassembly. *Biochemistry* 2010; 49: 3685-3694.

BOOK CHAPTERS

1. Novel Methods for Family-Based Genetic Studies (pages 135-144), Genetic Epidemiology (Methods and Protocols). Springer, 2018.
2. Automated Segmentation of Cervical Anatomy to Interrogate Preterm Birth (pages 48-59), Perinatal, Preterm and Paediatric Image Analysis. Springer, 2022.

INVITED PRESENTATIONS

1. Multi-omics data analysis in complex human diseases. Workshop of Statistical Methods in Genetic/Genomic Studies. Institute for Mathematical Sciences at National University of Singapore. Jan 14 2022
2. Statistical method and application in omics data analysis. MFM Research Meeting. Columbia University Irving Medical Center. Aug 20, 2021
3. An “incomplete” overview of omics data analysis. Seminar Series. UMD-BRIGHT at the University of Maryland. May 5, 2021.
4. A region-based method for causal mediation analysis of DNA methylation data. Seminar Series. Department of Biostatistics, University of Pittsburgh. October 22, 2020.
5. Convolutional neural network with application in AMD progression prediction. Seminar Series. Department of Preventive Medicine, University of Tennessee Health Science Center. July 13, 2020.
6. Multi-omics data analysis in asthma in Puerto Rican children. Lecture Series. Department of Biomedical Informatics, University of Pittsburgh. March 9, 2019.

CONTRIBUTED PRESENTATIONS

1. Genetic associations with dynamic placental proteins identify biomarkers for hypertension in pregnancy. STATGEN. Platform talk. May 2, 2024.
2. The ongoing nuMoM2b-HHS WGS analysis. NHLBI TOPMed annual meeting. Platform talk. February 14, 2024.
3. GWAS and Mendelian randomization analysis for placental proteins in early pregnancy. ICSA Conference. Platform talk. June 12, 2023.
4. Placenta fraction of maternal blood cell-free RNA associates with pre-eclampsia during pregnancy. ASHG Conference. Poster. October 25-29, 2022.
5. Allele-specific method for testing the association between gene expression and phenotype-genotype interaction. ASHG Virtual Conference. Poster. October 27-30, 2020.

6. Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression. ASHG Conference. Poster. October 17, 2019.
7. KMgene: a unified R package for gene-based association analysis for complex traits. ASHG Conference. Poster. October 19, 2018.
8. Genome-wide analysis of age-related macular degeneration progression. ASHG Conference. Poster. October 19, 2017.
9. An Omnibus Test for Gene-Level Effects of Multi-Omics Data with Application to Childhood Asthma. ICSA Conference (Shanghai, China). Platform talk. December 22, 2016.
10. Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. ICSA Conference (Atlanta, GA). Platform talk. June 13, 2016.
11. Set-based Methods for DNA Methylation Analysis. ASHG Conference. Poster. October 8, 2015.
12. Rare-Variant Kernel Machine Test for Longitudinal Data for Population and Family Samples. JSM Conference. Platform talk. August 12, 2015.
13. Sequence kernel association test for multivariate quantitative phenotype in family samples. ASHG Conference. Platform talk. October 19, 2014.
14. Kernel Machine Testing Coupled with Rank Truncation Method for Genetic Pathway Analysis. JSM Conference. Platform talk. August 4, 2013.

GRANTS

- NIH/NHLBI, R01 HL171376, Predicting Post-Covid Pulmonary Fibrosis with Explainable Deep Learning and Optimal Biomarker Discovery (PI: Bagci), 07/01/2024-06/30/2029 (role: co-I)
- NIH/NIA, R01 AG077255, Radon Exposure in Relation to the Risk of Cognitive Impairment and Mitochondrial Function (PI: Kahe), 12/01/2022-11/30/2027 (role: co-I)
- NIH, R03 OD034501, Integration of GTEx and HuBMAP Data to Gain Population-level Cell-type-specific Insights (MPI: Wang and Yan), 09/20/2022-09/19/2023 (role: PI)
- Columbia University, SIRS, Artificial Intelligence Based Spontaneous Preterm Birth Prediction Using Ultrasound and EMR Data (PI: Myers), 07/01/2021-06/30/2022 (role: co-PI)
- NIH/NINDS, R01 NS122449, Residential Radon Exposure and Stroke Risk: the REGARDS Study (PI: Kahe), 07/01/2021-06/30/2026 (role: co-I)
- NIH/NHLBI, K01 HL138098, Novel Methods for Analysis of Genetic and Epigenetic Studies of Childhood Asthma (PI: Yan), 04/15/2018-03/31/2023 (role: PI)
- UPMC/University of Pittsburgh, RAC, Novel Methods for Analysis of Genetic and Epigenetic Studies of Childhood Asthma (PI: Yan), 01/01/2016 – 12/31/2016 (role: PI)

Pending

- NIH/NHLBI, R01 HL173330, Multi-omics investigation of preeclampsia and long-term postpartum hypertension: insights from the nuMoM2b and nuMoM2b-HHS cohorts (MPI: Yan and Blue), score: 45, percentile: 35, pending resubmission
- NIH/NHLBI, R21 HL165385, Novel Methods for Estimating Hispanic Specific Genetic Effects on Childhood Asthma Using Summary Statistics (MPI: Yan and Wang), score: 35, percentile: 23, pending resubmission
- NIH/NHLBI, R03 HL171432, Cord blood metabolites and the risk of childhood asthma: the nuMoM2b and nuMoM2b-HHS studies (PI: Yan), score 36, pending resubmission
- NIH/NEI, R21 EY036974, Novel multimodal data based clinical risk calculator, deep learning models and model fairness for late AMD risk prediction (MPI: Zhang and Yan).

PROFESSIONAL SERVICES

- **Topic Editor**: statistical approaches in omics data association studies, *Frontiers in Genetics* 2020-
- **Editorial Board**: *Frontiers in Genetics* 2014-
- **Guest Editor**: the supplement of *Big Data Analytics for Health* 2015
- **Reviewer**: *Pediatric Pulmonology* (2023, 2021), *Nature Genetics* (2022), *eLife* (2022), *Briefings in Bioinformatics* (2021), *Patterns* (2020), *European Respiratory Journal* (2019, 2022), *Chest* (2019, 2020, 2021), *Frontiers in Genetics*

(2019), *Plos One* (2015, 2018), *Meta Gene* (2017), *Scientific Reports* (2016, 2018), *Human Heredity* (2016), *Bioinformatics* (2015), *Human Genetics* (2015, 2017, 2018), *Genetic Epidemiology* (2015, 2018), *Statistics and Its Interface* (2015), *International Journal of Cancer* (2015), *Mediators of Inflammation* (2015), *Biometrics & Biostatistics International Journal* (2015), *Annals of Nutrition and Metabolism* (2014), *Annals of Human Genetics* (2014), *Colombian Journal of Statistics* (2014).

SOFTWARE

- Searching and visualizing genetic associations of pregnancy traits by using GnuMoM2b
  - *R Shiny app: https://gnumom2b.cumcobgyn.org/*
- Allele-specific method for association between molecular quantitative traits and phenotype-genotype interaction
  - *Python source code: https://github.com/QiYanPitt/CHIT*
- A region-based method for causal mediation analysis
  - *R package: https://cran.r-project.org/web/packages/MRmediation/index.html*
- Deep-learning-based prediction of late age-related macular degeneration progression
  - *Website: http://52.90.194.108/calculator/*
  - *Python source code: https://github.com/QiYanPitt/AMDprogressCNN*
- GWAS-based machine learning for prediction of age-related macular degeneration risk
  - *R Shiny app: https://yang.shinyapps.io/no_vs_amd_NN/*
- An integrative association method for omics data based on a modified Fisher's method
  - *R package: https://cran.r-project.org/web/packages/OmnibusFisher/index.html*
- KMgene: a unified R package for gene-based association analysis for complex traits
  - *R package: https://cran.r-project.org/web/packages/KMgene/index.html*

TECHNICAL SKILLS

- ***Proficient*** in R, Bash, Python, Keras | *Basic* in SAS, SQL, Perl

PROFESSIONAL MEMBERSHIPS

- American Society of Human Genetics 2014-