

Curriculum Vitae

Qi Yan

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<https://qiyanpitt.github.io/>

IMMIGRATION STATUS

U.S. Permanent Resident

ACADEMIC APPOINTMENTS

- 2020-** Assistant Professor (tenure track) in Biostatistics
Department of Obstetrics & Gynecology
Columbia University Irving Medical Center, Columbia University, New York, NY
- 2018-2020** Research Assistant Professor in Biostatistics
Department of Pediatrics
UPMC Children's Hospital of Pittsburgh, University of Pittsburgh, Pittsburgh, PA
- 2017-2018** Research Instructor in Biostatistics
Department of Pediatrics
UPMC Children's Hospital of Pittsburgh, University of Pittsburgh, Pittsburgh, PA

EDUCATION

- 2014-2016** Post-Doctoral Fellow in Pediatrics (Mentors: Daniel E. Weeks and Wei Chen)
UPMC Children's Hospital of Pittsburgh, University of Pittsburgh, Pittsburgh, PA
- 2011-2014** Ph.D. of Science in Biostatistics (Mentor: Nianjun Liu)
University of Alabama at Birmingham, Birmingham, AL
Dissertation: Statistical Methods for Set-based Association Tests in Genetic Studies
- 2009-2011** Master of Science in Biostatistics
University of Alabama at Birmingham, Birmingham, AL
- 2007-2009** Master of Science in Biomedical Engineering (Bioinformatics)
University of Alabama at Birmingham, Birmingham, AL
- 2003-2007** Bachelor of Science in Biomedical Engineering
Beijing Institute of Technology, Beijing, China

AWARDS

- 2015** 2014 Best Paper Award - UAB from the Science Unbound Foundation
- 2011** Research Fellowship Award from Department of Biostatistics
- 2009** Research Fellowship Award from Department of Biomedical Engineering
- 2007** Research Fellowship Award from Department of Biomedical Engineering

PROFESSIONAL EXPERIENCE

- 2017-2020** Department of Pediatrics, University of Pittsburgh, PA
Research Assistant Professor/Research Instructor
My active research projects include: 1. Development of statistical and computational methods for high throughput genetic and genomic data; 2. Genetic studies of Age-related Macular Degeneration (AMD),

Asthma, Chronic Obstructive Pulmonary Disease (COPD) and Alzheimer Disease; 3. Transcriptome (RNAseq) studies in Asthma and Localized Scleroderma (LS); 4. Deep-learning in AMD risk prediction.

- Develop statistical algorithms and related software packages.
- Write independent research grants.
- Collaborate with several research teams, perform statistical analysis and write scientific manuscripts.

2014-2016 Department of Pediatrics, University of Pittsburgh, PA
Postdoctoral Research

My research projects included: 1. Development of statistical and computational methods for high throughput genetic and genomic data; 2. Genetic studies of AMD; 3. Genetic studies of Asthma and COPD in Hispanics; 4. Investigation of the impact of sequencing errors on family-based gene mapping; 5. DNA-seq, RNA-seq and Methylation analysis

- Develop statistical algorithms and related software packages.
- Collaborate with several research teams, perform statistical analysis and write scientific manuscripts.

2011-2014 Department of Biostatistics, University of Alabama at Birmingham, Birmingham, AL
Doctoral Dissertation Research

This dissertation research focuses on developing statistical methods for set-based association tests at both pathway and gene levels in genetic studies. In the first study, we proposed a novel way for pathway analysis that assesses the effects of genes using the sequence kernel association test (SKAT) and the effects of pathways via an extended adaptive-rank-truncated product statistic. In the second study, we proposed an analytical method based on kernel machine regression to be applicable for longitudinal data. In the third study, we proposed an analytical method to be applicable for familial data with various types of phenotypes based on generalized linear mixed model.

- Collaborate with mentor to develop statistical algorithms and associated software packages.
- Perform data analysis and write professional manuscripts.

2013-2014 Department of Biostatistics, University of Alabama at Birmingham, Birmingham, AL
NSF Graduate Research

We try to determine whether genetic markers of autoimmunity validated in European and Asian populations influence the occurrence of Rheumatoid Arthritis (RA) in African Americans, determine whether genetic markers of RA susceptibility play a role in radiographic severity in African Americans and develop and test predictive models for RA risk and outcome using clinical and genomic data in African Americans.

- Conducted statistical analysis of GWAS at marker and gene levels.
- Reported research results at internal meetings.

2010-2011 Department of Biostatistics, University of Alabama at Birmingham, Birmingham, AL
Master's Thesis Research

We evaluated the influence of race and gender on therapeutic warfarin dose, anticoagulation control and most importantly risk of major hemorrhage from prospective inception cohort of chronic warfarin users.

- Conducted research in interdisciplinary groups
- Reported research results at internal meetings.
- Provided statistical support to medical doctors with their projects and grant preparation.

2010-2011 Department of Epidemiology, University of Alabama at Birmingham, Birmingham, AL
Research Assistant

I participated in two projects. 1. A genome-wide association study (GWAS) of carotid atherosclerosis in HIV-infected men. 2. A Comparison of Principal Component Analysis Using Autosomal Variants with Phylogeny Based on Y-chromosome and Mitochondrial Markers.

- Provided insight, regular and ad-hoc reporting backed by solid analysis and documentation.
- Manipulated and maintained large-scale genetic data.

- Worked on multiple large projects to perform in a cross-functional team.

2007-2009 Department of Biomedical Engineering, University of Alabama at Birmingham, Birmingham, AL
Research Assistant
 We investigated the structural insights for Thrombospondin-1 binding to Calreticulin by using Molecular Dynamics technique.

- Worked with supervisor to investigate the properties of Molecular Dynamics of proteins.
- Reported research results in the manuscripts professionally.

TEACHING EXPERIENCE

2020 spring Invited Lecturer
Statistical Genetics (HUGEN 2080)
 Genetic Rare Variant Test; Convolutional Neural Network (4 hours)
Department of Human Genetics, University of Pittsburgh, Pittsburgh, PA

2019 spring Invited Lecturer
Foundations of Translational Bioinformatics (BIOINF 2016)
 Genome-wide Association Study; Analysis of Next Generation Sequence Data (2 hours)
Department of Biomedical Informatics, University of Pittsburgh, Pittsburgh, PA

2017 winter Invited Lecturer
Introductory high-throughput genomic data analysis I: data mining and applications (BIOST 2055)
 Genome-wide Association Study; Analysis of Next Generation Sequence Data; Lab (3 hours)
Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA

2016 spring Invited Lecturer
Introductory high-throughput genomic data analysis I: data mining and applications (BIOST 2055)
 Genome-wide Association Study; Analysis of Next Generation Sequence Data; Lab (3 hours)
Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA

2016 spring Invited Lecturer
Applied mixed models analysis (BIOST 2086)
 Rare-Variant Kernel Machine Test (1 hour)
Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA

2015 spring Invited Lecturer
Introductory high-throughput genomic data analysis I: data mining and applications (BIOST 2055)
 Genome-wide Association Study; Analysis of Next Generation Sequence Data; Lab (3 hours)
Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA

2013 fall Graduate Teaching Assistant
Inter Statistical Analysis II (BST612)
Department of Biostatistics, University of Alabama at Birmingham, Birmingham, AL

2012 spring Graduate Teaching Assistant
Inter Statistical Analysis I (BST611)
Department of Biostatistics, University of Alabama at Birmingham, Birmingham, AL

PEER REVIEWED PUBLICATIONS

1. **Yan Q**, Jiang Y, Huang H, Swaroop A, Chew EY, Weeks DE, Chen W, Ding Y. “GWAS-based Machine Learning for Prediction of Age-Related Macular Degeneration Risk”. Accepted in *TVST*. Preprint is available at medRxiv (doi: <https://doi.org/10.1101/19006155>)
2. Han YY, **Yan Q**, Chen W, Forno E, Celedón JC. “Serum insulin-like growth factor-1, asthma, and lung function among British adults”. Accepted in *Annals of Allergy, Asthma and Immunology*.
3. Yang G, Han YY, Forno E, **Yan Q**, Rosser F, Chen W, Celedon JC. Glycated Hemoglobin A1c, Lung Function, and Hospitalizations Among Adults with Asthma. *J Allergy Clin Immunol Pract* 2020.
4. **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.
5. **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, Celedon 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.**
6. **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, Celedon JC. A genome-wide association study of severe asthma exacerbations in Latino children and adolescents. *Eur Respir J* 2020.
7. 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.
8. 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, Prasad 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.
9. Kim S, Forno E, Zhang R, Park HJ, Xu Z, **Yan Q**, Boutaoui N, Acosta-Perez E, Canino G, Chen W, Celedon JC. Expression Quantitative Trait Methylation Analysis Reveals Methylomic Associations With Gene Expression in Childhood Asthma. *Chest* 2020.
10. Kim S, Forno E, **Yan Q**, Jiang Y, Zhang R, Boutaoui N, Acosta-Perez E, Canino G, Chen W, Celedon JC. SNPs identified by GWAS affect asthma risk through DNA methylation and expression of cis-genes in airway epithelium. *Eur Respir J* 2020; 55.
11. 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.
12. Han YY, **Yan Q**, Yang G, Chen W, Forno E, Celedon JC. Serum free testosterone and asthma, asthma hospitalisations and lung function in British adults. *Thorax* 2020; 75: 849-854.
13. 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, Celedon JC. Transcriptome-wide and differential expression network analyses of childhood asthma in nasal epithelium. *J Allergy Clin Immunol* 2020; 146: 671-675.

14. **Yan Q**, Liu N, Forno E, Canino G, Celedon 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.
15. 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.
16. 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.
17. 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.
18. 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, Celedon JC. DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. *Lancet Respir Med* 2019; 7: 336-346.
19. **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.
20. **Yan Q**, Fang Z, Chen W. KMGene: a unified R package for gene-based association analysis for complex traits. *Bioinformatics* 2018; 34: 2144-2146.
21. **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.
22. 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.
23. Fang Z, Ma T, Tang G, Zhu L, **Yan Q**, Wang T, Celedon JC, Chen W, Tseng GC. Bayesian integrative model for multi-omics data with missingness. *Bioinformatics* 2018; 34: 3801-3808.
24. 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, Celedon 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.
25. **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, Celedon JC. A meta-analysis of genome-wide association studies of asthma in Puerto Ricans. *Eur Respir J* 2017; 49. **With an accompanying Editorial.**
26. 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.
27. 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, Celedon JC. A Multiomics Approach to Identify Genes Associated with Childhood Asthma Risk and Morbidity. *Am J Respir Cell Mol Biol* 2017; 57: 439-447.
28. 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, Celedon 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.

29. 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.
30. 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.
31. 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, Celedon JC. An epigenome-wide association study of total serum IgE in Hispanic children. *J Allergy Clin Immunol* 2017; 140: 571-577.
32. **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.
33. 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.
34. **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.
35. **Yan Q**, Weeks DE, Celedon 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.**
36. **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.
37. 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.**
38. 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, Celedon JC. A genome-wide association study of chronic obstructive pulmonary disease in Hispanics. *Ann Am Thorac Soc* 2015; 12: 340-348.
39. 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, Celedon 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.
40. **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.**
41. **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.
42. 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.
43. 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.

44. **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.
45. 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.
46. **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.

MANUSCRIPTS UNDER REVIEW OR REVISION

1. **Qi Yan**, Erick Forno, Andres Cardenas, Cancan Qi, Yueh-Ying Han, Edna Acosta-Pérez, Rong Zhang, Nadia Boutaoui, Glorisa Canino, Judith M. Vonk, Cheng-jian Xu, Wei Chen, Emily Oken, Diane R. Gold, Gerard H. Koppelman, Juan C. Celedón. “Exposure to violence, chronic stress, nasal DNA methylation, and asthma in children”. Under review in *Pediatric Pulmonology*.
2. **Qi Yan**, Erick Forno, Juan C. Celedón and Wei Chen. “A region-based method for causal mediation analysis of DNA methylation data”. Under revision in *Epigenetics*.

READY FOR SUBMISSION

1. **Qi Yan**, Erick Forno, Edna Acosta-Perez, Glorisa Canino, Juan C. Celedón, Wei Chen and Daniel E. Weeks. “Allele-specific method for testing the association between gene expression and phenotype-genotype interaction”.

PRESENTATIONS

1. **Yan Q**. “Allele-specific method for testing the association between gene expression and phenotype-genotype interaction” ASHG Virtual Conference. Poster. October, 2020
2. **Yan Q**. “Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression” ASHG Conference. Poster. October 17, 2019
3. **Yan Q**. “KMgene: a unified R package for gene-based association analysis for complex traits” ASHG Conference. Poster. October 19, 2018
4. **Yan Q**. “Genome-wide analysis of age-related macular degeneration progression” ASHG Conference. Poster. October 19, 2017
5. **Yan Q**. “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
6. **Yan Q**. “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
7. **Yan Q**. “Set-based Methods for DNA Methylation Analysis” ASHG Conference. Poster. October 8, 2015
8. **Yan Q**. “Rare-Variant Kernel Machine Test for Longitudinal Data for Population and Family Samples” JSM Conference. Platform talk. August 12, 2015
9. **Yan Q**. “Sequence kernel association test for multivariate quantitative phenotype in family samples” ASHG Conference. Platform talk. October 19, 2014
10. **Yan Q**. “Kernel Machine Testing Coupled with Rank Truncation Method for Genetic Pathway Analysis” JSM Conference. Platform talk. August 4, 2013

REVIEWS

Guest editor, the supplement of Big Data Analytics for Health, 2015
Editorial Board, Frontiers in Genetics, 2014

Reviewer, Patterns, 2020
 Reviewer, European Respiratory Journal, 2019
 Reviewer, Chest, 2019, 2020
 Reviewer, Frontiers in Genetics, 2019
 Reviewer, Plos One, 2015, 2018
 Reviewer, Meta Gene, 2017
 Reviewer, Scientific Reports, 2016, 2018
 Reviewer, Human Heredity, 2016
 Reviewer, Bioinformatics, 2015
 Reviewer, Human Genetics, 2015, 2017, 2018
 Reviewer, Genetic Epidemiology, 2015, 2018
 Reviewer, Statistics and Its Interface, 2015
 Reviewer, International Journal of Cancer, 2015
 Reviewer, Mediators of Inflammation, 2015
 Reviewer, Biometrics & Biostatistics International Journal, 2015
 Reviewer, Annals of Nutrition and Metabolism, 2014
 Reviewer, Annals of Human Genetics, 2014
 Reviewer, Colombian Journal of Statistics, 2014

GRANTS

K01 HL138098 (NHLBI)	Principal Investigator	04/15/2018 – 03/31/2023
<i>Novel Methods for Analysis of Genetic and Epigenetic Studies of Childhood Asthma</i>		
Total cost: \$714,630		

RAC UPMC/University of Pittsburgh	Principal Investigator	01/01/2016 – 12/31/2016
<i>Novel Methods for Analysis of Genetic and Epigenetic Studies of Childhood Asthma</i>		
Total cost: \$45,100		

TECHNICAL SKILLS

Proficiency with R programming
 Proficiency with UNIX environment and related programming languages: Shell, Python, Perl

SOFTWARE

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1. KMGene: a unified R package for gene-based association analysis for complex traits
<https://cran.r-project.org/web/packages/KMgene/index.html>)
 2. An integrative association method for omics data based on a modified Fisher's method
<https://cran.r-project.org/web/packages/OmnibusFisher/index.html>)
 3. Late AMD Fundus Image Prediction
<http://www.pitt.edu/~qiy17/amdprediction.html>); (<https://github.com/QiYanPitt/AMDprogressCNN>)
 4. Computer-Aided Risk Estimation for Any Age-related Macular Degeneration in Caucasians
https://yanq.shinyapps.io/no_vs_amd_NN/)
 5. DoubleWeightSKAT-ARTP: Pathway Based Method Testing the Significance of a Pathway
<http://www.pitt.edu/~qiy17/Softwares/DoubleWeightSKAT-ARTP.zip>)

PROFESSIONAL ORGANIZATIONS

Member, American Society of Human Genetics, 2014-.
 Member, American Statistical Association, 2013-.
 Member, Professional Development Committee in Department of Biostatistics at UAB, 2012-2014.
 Vice President, Chinese Student and Scholar Association at UAB, 2012-2013.