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 **Obstetrics & Gynecology** **Columbia University Irving Medical Center, Columbia University, New York, NY**
2018-2020	**Research Assistant Professor** in **Pediatrics** **UPMC Children's Hospital of Pittsburgh, University of Pittsburgh, Pittsburgh, PA**
2017-2018	**Research Instructor** in **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-	**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. Jiang, Y.*, Chiu, C.*, **Yan, Q.**, Chen, W., Gorin, M.B., Conley, Y.P., Lakhal-Chaieb, M.L., Cook, R.J., Amos, C.I., Wilson, A.F., et al. (2020). Gene-based Association Testing of Dichotomous Traits with Generalized Linear Mixed Models Using Extended Pedigrees. Accepted in *JASA*.

2. Han, Y.Y., **Yan, Q.**, Yang, G., Chen, W., Forno, E., Celedón, J.C. (2020) Serum free testosterone and asthma, asthma hospitalizations, and lung function in British adults. Accepted in *Thorax*.

3. Xin, H., Lian, Q., Jiang, Y., Luo, J., Wang, X., Erb, C., Xu, Z., Zhang, X., Heidrich-O'Hare, E., **Yan, Q.**, Duerr, R., Chen, K., and Chen, W. (2020) GMM-Demux: sample demultiplexing, multiplet detection, experiment planning and novel cell type verification in single cell sequencing. Accepted in *Genome Biology*.

4. Yang, G., Han, Y.Y., Forno, E., **Yan, Q.**, Rosser, F., Chen, W., Celedón, J.C. (2020) Glycated hemoglobin A1c, lung function, and hospitalizations among adults with asthma. Accepted in *J Allergy Clin Immunol: In Practice*.

5. Kim, S., Forno, E., Zhang, R., Xu, Z., Park, H., **Yan, Q.**, Boutaoui, N., Acosta-Perez, E., Canino, G., Chen, W., Celedón, J.C. (2020) Expression quantitative trait methylation analysis reveals methylomic associations with gene expression in childhood asthma. Accepted in *CHEST*.

6. **Yan, Q.**, Weeks, D.E., Xin, H., Swaroop, A., Chew, E.Y., Huang, H., Ding, Y., and Chen, W. (2020). Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression. *Nature Machine Intelligence* doi.org/10.1038/s42256-020-0154-9.

7. Forno, E., Zhang, R., Jiang, Y., Kim, S., **Yan, Q.**, Ren, Z., Han, Y.Y., Boutaoui, N., Rosser, F., Weeks, D.E., Acosta-Pérez, E., Colón-Semidey, A., Alvarez, M., Canino, G., Chen, W., Celedón, J.C. (2020). Transcriptome-wide and differential expression network analyses of childhood asthma in nasal epithelium. *J Allergy Clin Immunol* doi: 10.1016/j.jaci.2020.02.005.

8. Kim, S., Forno, E.; **Yan, Q.**, Jiang, Y., Zhang, R., Boutaoui, N., Acosta-Perez, E., Canino, G., Chen, W., Celedon, J.C. (2019). SNPs identified by GWAS affect asthma risk through DNA methylation and expression of *cis*-genes in airway epithelium. *Eur Respir J* doi:10.1183/13993003.02079-2019.

9. **Yan, Q.**, Liu, N., Forno, E., Canino, G., Celedon, J.C., and Chen, W. (2019). An integrative association method for omics data based on a modified Fisher's method with application to childhood asthma. *PLoS Genet* 15, e1008142.

10. Mandel, J., Wang, H., Normolle, D.P., Chen, W., **Yan, Q.**, Lucas, P.C., Benos, P.V., and Prochownik, E.V. (2019). Expression patterns of small numbers of transcripts from functionally-related pathways predict survival in multiple cancers. *BMC Cancer* 19, 686.

11. Rajakumar, K., **Yan, Q.**, Khalid, A.T., Feingold, E., Vallejo, A.N., Demirci, F.Y., and Kamboh, M.I. (2019). Gene Expression and Cardiometabolic Phenotypes of Vitamin D-Deficient Overweight and Obese Black Children. *Nutrients* 11.

12. Kamboh, M.I.*, Fan, K.H.*, **Yan, Q.**,*, Beer, J.C., Snitz, B.E., Wang, X., Chang, C.H., Demirci, F.Y., Feingold, E., and Ganguli, M. (2019). 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*. *co-first-author.

13. Forno, E.*, Wang, T.*, Qi, C.*, **Yan, Q.**, Xu, C.J., Boutaoui, N., Han, Y.Y., Weeks, D.E., Jiang, Y., Rosser, F., et al. (2019). DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. *Lancet Respir Med* 7, 336-346.

14. **Yan, Q.**, Nho, K., Del-Aguila, J.L., Wang, X., Risacher, S.L., Fan, K.H., Snitz, B.E., Aizenstein, H.J., Mathis, C.A., Lopez, O.L., et al. (2018). Genome-wide association study of brain amyloid deposition as measured by Pittsburgh Compound-B (PiB)-PET imaging. *Mol Psychiatry*.

15. **Yan, Q.**, Ding, Y., Liu, Y., Sun, T., Fritsche, L.G., Clemons, T., Ratnapriya, R., Klein, M.L., Cook, R.J., Liu, Y., et al. (2018). Genome-wide analysis of disease progression in age-related macular degeneration. *Hum Mol Genet* 27, 929-940.

16. **Yan, Q.**, Fang, Z., and Chen, W. (2018). KMgene: a unified R package for gene-based association analysis for complex traits. *Bioinformatics* 34, 2144-2146.

17. Wen, X.*, Liu, Y.*, **Yan, Q.***, Liang, M., Tang, M., Liu, R., Pan, J., Liu, Q., Chen, T., Guo, S., et al. (2018). Association of IGFN1 variant with polypoidal choroidal vasculopathy. *J Gene Med* 20, e3007. *co-first-author.

18. Fang, Z., Ma, T., Tang, G., Zhu, L., **Yan, Q.**, Wang, T., Celedon, J.C., Chen, W., and Tseng, G.C. (2018). Bayesian integrative model for multi-omics data with missingness. *Bioinformatics* 34, 3801-3808.

19. Burkart, K.M., Sofer, T., London, S.J., Manichaikul, A., Hartwig, F.P., **Yan, Q.**, Soler Artigas, M., Avila, L., Chen, W., Davis Thomas, S., et al. (2018). 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* 198, 208-219.

20. Forno, E., Wang, T., **Yan, Q.**, Brehm, J., Acosta-Perez, E., Colon-Semidey, A., Alvarez, M., Boutaoui, N., Cloutier, M.M., Alcorn, J.F., et al. (2017). A Multiomics Approach to Identify Genes Associated with Childhood Asthma Risk and Morbidity. *Am J Respir Cell Mol Biol* 57, 439-447.

21. Ding, Y., Liu, Y., **Yan, Q.**, Fritsche, L.G., Cook, R.J., Clemons, T., Ratnapriya, R., Klein, M.L., Abecasis, G.R., Swaroop, A., et al. (2017). Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. *Genetics* 206, 119-133.

22. **Yan, Q.**, Brehm, J., Pino-Yanes, M., Forno, E., Lin, J., Oh, S.S., Acosta-Perez, E., Laurie, C.C., Cloutier, M.M., Raby, B.A., et al. (2017). A meta-analysis of genome-wide association studies of asthma in Puerto Ricans. *Eur Respir J* 49. **With an accompanying Editorial.**

23. Forno, E., Sordillo, J., Brehm, J., Chen, W., Benos, T., **Yan, Q.**, Avila, L., Soto-Quiros, M., Cloutier, M.M., Colon-Semidey, A., et al. (2017). Genome-wide interaction study of dust mite allergen on lung function in children with asthma. *J Allergy Clin Immunol* 140, 996-1003 e1007.

24. Danila, M.I., Laufer, V.A., Reynolds, R.J., **Yan, Q.**, Liu, N., Gregersen, P.K., Lee, A., Kern, M., Langefeld, C.D., Arnett, D.K., et al. (2017). Dense Genotyping of Immune-Related Regions Identifies Loci for Rheumatoid Arthritis Risk and Damage in African Americans. *Mol Med* 23, 177-187.

25. Wang, L., Pan, D., **Yan, Q.**, and Song, Y. (2017). Activation mechanisms of alphaVbeta3 integrin by binding to fibronectin: A computational study. *Protein Sci* 26, 1124-1137.

26. Chen, W., Wang, T., Pino-Yanes, M., Forno, E., Liang, L., **Yan, Q.**, Hu, D., Weeks, D.E., Baccarelli, A., Acosta-Perez, E., et al. (2017). An epigenome-wide association study of total serum IgE in Hispanic children. *J Allergy Clin Immunol* 140, 571-577.

27. **Yan, Q.**, Chen, R., Sutcliffe, J.S., Cook, E.H., Weeks, D.E., Li, B., and Chen, W. (2016). The impact of genotype calling errors on family-based studies. *Sci Rep* 6, 28323.

28. **Yan, Q.**, Weeks, D.E., Tiwari, H.K., Yi, N., Zhang, K., Gao, G., Lin, W.Y., Lou, X.Y., Chen, W., and Liu, N. (2015). Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. *Hum Hered* 80, 126-138.

29. **Yan, Q.**, Weeks, D.E., Celedon, J.C., Tiwari, H.K., Li, B., Wang, X., Lin, W.Y., Lou, X.Y., Gao, G., Chen, W., et al. (2015). Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. *Genetics* 201, 1329-1339. **Chosen by the GENETICS Editors as one of the December 2015 Highlights.**

30. Fan, R.*, Wang, Y.*, **Yan, Q.***, Ding, Y., Weeks, D.E., Lu, Z., Ren, H., Cook, R.J., Xiong, M., Swaroop, A., et al. (2016). Gene-Based Association Analysis for Censored Traits Via Fixed Effect Functional Regressions. *Genet Epidemiol* 40, 133-143. *co-first-author.

31. Brehm, J.M., Man Tse, S., Croteau-Chonka, D.C., Forno, E., Litonjua, A.A., Raby, B.A., Chen, W., **Yan, Q.**, Boutaoui, N., Acosta-Perez, E., et al. (2015). A Genome-Wide Association Study of Post-bronchodilator Lung Function in Children with Asthma. *Am J Respir Crit Care Med* 192, 634-637.

32. Limdi, N.A., Brown, T.M., **Yan, Q.**, Thigpen, J.L., Shendre, A., Liu, N., Hill, C.E., Arnett, D.K., and Beasley, T.M. (2015). Race influences warfarin dose changes associated with genetic factors. *Blood* 126, 539-545. **With an accompanying Editorial.**

33. **Yan, Q.**, Tiwari, H.K., Yi, N., Gao, G., Zhang, K., Lin, W.Y., Lou, X.Y., Cui, X., and Liu, N. (2015). A Sequence Kernel Association Test for Dichotomous Traits in Family Samples under a Generalized Linear Mixed Model. *Hum Hered* 79, 60-68.

34. Chen, W., Brehm, J.M., Manichaikul, A., Cho, M.H., Boutaoui, N., **Yan, Q.**, Burkart, K.M., Enright, P.L., Rotter, J.I., Petersen, H., et al. (2015). A genome-wide association study of chronic obstructive pulmonary disease in Hispanics. *Ann Am Thorac Soc* 12, 340-348.

35. **Yan, Q.**, Tiwari, H.K., Yi, N., Lin, W.Y., Gao, G., Lou, X.Y., Cui, X., and Liu, N. (2014). Kernel-machine testing coupled with a rank-truncation method for genetic pathway analysis. *Genet Epidemiol* 38, 447-456. **2014 Best Paper Award - UAB from the Science Unbound Foundation.**

36. Shrestha, S., **Yan, Q.**, Joseph, G., Arnett, D.K., Martinson, J.J., and Kingsley, L.A. (2012). Replication of RYR3 gene polymorphism association with cIMT among HIV-infected whites. *AIDS* 26, 1571-1573.

37. Makowsky, R., **Yan, Q.**, Wiener, H.W., Sandel, M., Aissani, B., Tiwari, H.K., and Shrestha, S. (2012). The utility of mitochondrial and y chromosome phylogenetic data to improve correction for population stratification. *Front Genet* 3, 301.

38. **Yan, Q.**, McDonald, J.M., Zhou, T., and Song, Y. (2013). 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* 81, 377-385.

39. Pan, D., **Yan, Q.**, Chen, Y., McDonald, J.M., and Song, Y. (2011). Trifluoperazine regulation of calmodulin binding to Fas: a computational study. *Proteins* 79, 2543-2556.

40. **Yan, Q.**, Murphy-Ullrich, J.E., and Song, Y. (2011). Molecular and structural insight into the role of key residues of thrombospondin-1 and calreticulin in thrombospondin-1-calreticulin binding. *Biochemistry* 50, 566-573.

41. **Yan, Q.**, Murphy-Ullrich, J.E., and Song, Y. (2010). Structural insight into the role of thrombospondin-1 binding to calreticulin in calreticulin-induced focal adhesion disassembly. *Biochemistry* 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, Ge Yang, Esther Herrera-Luis, Maria Pino-Yanes, Sam Oh, Edna Acosta-Pérez, Donglei Hu, Celeste Eng, Scott Huntsman, José R. Rodriguez-Santana, Michelle M. Cloutier, Glorisa Canino, Esteban G. Burchard, Wei Chen, Juan C. Celedón. "A genome-wide association study of asthma hospitalizations in adults" Under revision in *J Allergy Clin Immunol*.

2. **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 *J Allergy Clin Immunol*.

3. **Qi Yan**, Erick Forno, Esther Herrera-Luis, Maria Pino-Yanes, Cancan Qi, Raimon Rios, Yueh-Ying Han, Soyeon Kim, Sam Oh, Edna Acosta-Pérez, Rong Zhang, Donglei Hu, Celeste Eng, Scott Huntsman, Lydiana Avila, Nadia Boutaoui, Michelle M. Cloutier, Manuel E. Soto-Quiros, Cheng-jian Xu, Scott T. Weiss, Jessica Lasky-Su, Megan R. Kiedrowski, Camila Figueiredo, Jennifer Bomberger, Mauricio L. Barreto, Glorisa Canino, Wei Chen, Gerard H. Koppelman, Esteban G. Burchard, Juan C. Celedón. "A genome-wide association study of severe asthma exacerbations in Latino children and youth". Under review in *Eur Respir J*.

4. **Qi Yan**, Yale Jiang, Heng Huang, Anand Swaroop, Emily Y. Chew, Daniel E. Weeks, Wei Chen, Ying Ding. "GWAS-based Machine Learning for Prediction of Age-Related Macular Degeneration Risk". Under review in *TVST*. Preprint is available

at medRxiv (doi: https://doi.org/10.1101/19006155)

5. Yueh-Ying Han, **Qi Yan**, Wei Chen, Erick Forno, Juan C. Celedón. "Serum insulin-like growth factor-1, asthma, and lung function among British adults in the United Kingdom Biobank". Under review in *CHEST*.

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".

2. **Qi Yan**, Erick Forno, Edna Acosta-Perez, Glorisa Canino, Juan C. Celedón and Wei Chen. "A causal mediation method with DNA methylated region as the mediator".

PRESENTATIONS

1. **Yan Q.** "Deep-learning-based Prediction of Late Age Related Macular Degeneration Progression" ASHG Conference. Poster. October 17, 2019

2. **Yan Q.** "KMgene: a unified R package for gene-based association analysis for complex traits" ASHG Conference. Poster. October 19, 2018

3. **Yan Q.** "Genome-wide analysis of age-related macular degeneration progression" ASHG Conference. Poster. October 19, 2017

4. **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

5. **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

6. **Yan Q.** "Set-based Methods for DNA Methylation Analysis" ASHG Conference. Poster. October 8, 2015

7. **Yan Q.** "Rare-Variant Kernel Machine Test for Longitudinal Data for Population and Family Samples" JSM Conference. Platform talk. August 12, 2015

8. **Yan Q.** "Sequence kernel association test for multivariate quantitative phenotype in family samples" ASHG Conference. Platform talk. October 19, 2014

9. **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
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*

Novel Methods for Analysis of Genetic and Epigenetic Studies of Childhood Asthma
Total cost: $714,630

RAC UPMC/University of Pittsburgh	*Principal Investigator*	*01/01/2016 – 12/31/2016*

Novel Methods for Analysis of Genetic and Epigenetic Studies of Childhood Asthma
Total cost: $45,100

TECHNICAL SKILLS

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

SOFTWARE

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.