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## Education and Training

**Ph.D.**, Department of Statistics, University of Florida. 1998 – 2002.

- Dissertation title: *A Statistical Method for Identifying Informative Genes in Microarrays*.
- Advisor: Dr. Mark C. K. Yang, American Statistical Association (ASA) Fellow.

**M.S.**, Institute of Statistics, National Tsing Hua University. 1994-1996.

**B.A.**, Department of Physics, National Tsing Hua University. 1989-1993.

## Certification

- NSF Plant Microarray Short Course on Design and Analysis of Plant Microarray Experimentation. June 13-14, 2005.
- Basic Life Support (CPR and AED) Program, American Heart Association. October 2018.

## Professional Appointments

**Associate Professor**, Department of Biostatistics and Data Science, School of Public Health, The University of Texas Health Science Center at Houston (UTHealth). 2019 – present.

Webpage: <https://sph.uth.edu/divisions/biostatistics/>

**Associate Research Scientist**, Office of Research and Global Affairs, School of Nursing, University of Michigan. 2014 – 2019.

- Interim Lead for the Statistical Consulting Team (April 2015- June 2016).
- Conducted methodology research and collaborative research.
- Proposed study design, statistical analysis and sample size estimation for grant submission.

**Associate Scientist** (2012 – 2013) & **Assistant Scientist** (2007 – 2012), Public Health Sciences (former Biostatistics and Research Epidemiology), Henry Ford Health Sciences Center.

- Evaluated, applied, and developed statistical methodology for medical research.
- Developed study design, analysis plan, and protocol for NIH, CDC, and DoD grant applications.
- Established quality control procedures for genomic research.
- Conducted genome-wide association and admixture mapping studies.
- Analyzed and interpreted MRI biomarker and imaging data.
- Reviewed NIH grant applications for NCI Special Emphasis Panel ZCA1 SRLB-4 (J2) B R03 Small Grants Program for Cancer Epidemiology, October 16-17, 2012.

**Biostatistician**, Biostatistics and Research Epidemiology, Henry Ford Health Sciences Center. 2003 – 2007.

- Provided statistical consultation and data analysis service for research investigators.
- Reviewed research grant applications for internal funding.

**Research Assistant**, Diabetes Research Center, University of Florida. 1998 – 2002.

- Conducted linkage disequilibrium analysis on simplex and multiplex affected sib-pair families and verified several type 1 diabetes loci.
- Developed statistical models and computing programs for cDNA microarrays.

**Second Lieutenant**, Commanding Officer, Yilan City, Taiwan. 1996 – 1998.

**Research Assistant**, Department of Statistics, National Tsing Hua University. 1995 – 1996.

- Developed a new method of point estimation for the measurement error model.

## Research Interests

- Statistical genetics and genomics
- Bioinformatics
- Substance use and addiction
- Analysis of data from wearable devices
- Longitudinal & EMA data analysis
- Multivariate analysis
- Causal inference

## Grant Funding

### Ongoing Research Support

R01DA049154, NIH/NIDA

Buu, Anne

8/15/2019-6/30/2024

Project Title: *Methodology and measurement for examining short-term and long-term effects of e-cigarette and polysubstance use*

Role: Co-Investigator with 50% efforts

HHS000563200001, The Texas Health and Human Services Commission

Wilkerson, J. Michael

8/7/2020-8/31/2024

Project Title: *Expansion and Evaluation of Recovery Residences for Persons in Recovery for Opioid Use on Medication Assisted Therapy in Texas*

Role: Co-Investigator with 10% efforts

U48DP006408, CDC

Maria Fernandez

9/30/2020-9/29/2024

Project Title: *University of Texas Prevention Research Center*

Role: Co-Investigator with 5% efforts

## Completed Research Support

P20NR015331, NIH/NINR

Barton, Debra L. & Dinov, Ivaylo (Multiple PI's)

09/26/14-07/31/19

Project Title: *Center for Complexity and Self-management of Chronic Disease (CSCD)*

Role: Co-Investigator

1-R01-DC013885-01, NIH/NIDCD

McCullagh, Marjorie (PI)

12/01/14-11/30/18

Project Title: *Test of Hearing Health Education Programs for Farm and Rural Youth*

Role: Co-Investigator

1-R01-HS-022305-01-A1, AHRQ

Manojlovich, Milisa (PI)

09/30/14-09/29/18

Project Title: *The Effect of Health Information Technology on Healthcare Provider Communication*

Role: Co-Investigator

5-R01-OH-010582-02, CDC/NIOSH

Friese, Christopher (PI)

07/01/14-06/30/18

Project Title: *Randomized Controlled Trial to Improve Oncology Nurses' Protective Equipment Use*

Role: Co-Investigator

4-R01-NR-013861-05, NIH

Holden, Janean (PI)

09/11/12-06/30/17

Project Title: *Posterior Hypothalamic Modulation of Pain*

Role: Co-Investigator

1-R03-CA-186183-01-A1, NIH

Smith, Ellen (PI)

04/01/15-03/31/17

Project Title: *Chemotherapy-Induced Peripheral Neuropathy (CIPN) Measurement Validation*

Role: Co-Investigator

K01 TW008763-01A1, NIH

Lori, Jody R. (PI)

09/17/11-07/30/16

Project Title: *New Avenues to Increase the Use of Skilled Birth Attendants in Ghana*  
Role: Co-Investigator

5-R01-DC-010827-04, HHS  
McCullagh, Marjorie (PI)  
01/01/11-12/31/15

Project Title: *Effectiveness of an Intervention to Prevent Hearing Loss among Farmers*  
Role: Co-Investigator

R01-01AG038648, NIH/NIA  
Morris, Daniel (PI)  
08/01/11-05/01/15

Project Title: *Treatment of Stroke in Young and Aged Rats Using Thymosin Beta 4*  
Role: Co-Investigator

R01 CA140341-01A2, NIH/NCI  
Zhong, Hualiang (PI)  
07/01/10-05/01/15

Project Title: *To Quantify Deformable Image Registration Errors in IGRT*  
Role: Co-Investigator

CDC Foundation  
Gordon, Stuart (PI)  
11/01/09-10/01/14

Project Title: *Chronic Hepatitis C and B Cohort Study (CheCS)*  
Role: Co-Investigator

R01 CA135329, NIH/NCI  
Ewing, James (PI)  
04/01/09-03/01/14

Project Title: *MRI Biomarkers of Response in Cerebral Tumors*  
Role: Co-Investigator

R01 DK64695, NIDDK  
Williams, L. Keoki (PI)  
03/01/09-02/01/14

Project Title: *The Clinical Effectiveness of Pharmacy Adherence Information for Diabetes Control*  
Role: Co-Investigator

## **Teaching**

- PH 1700: *Intermediate Biostatistics* (3 credits). Department of Biostatistics and Data Science, School of Public Health, The University of Texas Health Science Center at Houston (UTHealth). From Spring 2020 to present (every semester).
- PH 1986: *Introduction to Statistical Genetics and Bioinformatics* (3 credits), Department of Biostatistics and Data Science, School of Public Health, The University of Texas Health Science Center at Houston (UTHealth). From Fall 2021 to present (every fall semester).
- HS 853: *Scientific Methods for Health Sciences: Special Topics* (4 credits). School of Nursing, University of Michigan. Winter 2018.
- HS 852: *Scientific Methods for Health Sciences: Linear Modeling* (4 credits). School of Nursing, University of Michigan. Winter 2015.
- *Data Synthesis Workshop (Meta Analysis: Effect Size and Precision)*. School of Nursing, University of Michigan. May 12<sup>th</sup> 2014.
- *Tutorial in biostatistics (Structural equation modeling, Propensity score methodology)*. Public Health Sciences, Henry Ford Health Sciences Center. Spring 2013.

## Committee Service

- Advisor of Master Student Thesis Committee:
  - Devanshi Mukeshkumar Majeethia, Department of Biostatistics and Data Science, University of Texas Health Science Center at Houston (UTHealth). August 2021-April 2023.
- Member of Doctoral Students Dissertation Committee:
  - Robert Knoerl (Advisor: Dr. Ellen Lavoie Smith), Department of Health Behavior and Biological Sciences, University of Michigan. March 2015 - April 2017.
  - Yang Li (Advisor: Dr. Julia S. Seng), Department of Systems, Populations and Leadership, University of Michigan. Oct 2015 - April 2018.
- Institutional Review Board, Henry Ford Health System. 2010 – 2013.
  - Reviewed experimental design, statistical methods and power of all research projects involving human subjects in the institution.
  - Protected the rights and welfare of the research subjects.

## Seminars and Conference Presentations

- *A statistical method for identifying parallel and sequential mediators with applications in mental health*.  
Division of Clinical and Translational Sciences, Department of Internal Medicine, University of Texas Health Science Center at Houston (UTHealth). July 2019.
- *Scalable Statistical Inference for Genome-Wide Association Studies*.  
Department of Biostatistics and Data Science, University of Texas Health Science Center at Houston (UTHealth). April 2019.
- *Questions on correlation-based inference*.  
Faculty Development Workshop. School of Nursing, University of Michigan. April 2019.
- *A hybrid method of the sequential Monte Carlo and the Edgeworth expansion for very small p-values*.

- 2018 Joint Statistical Meetings, Vancouver.
- *A hybrid method of the sequential Monte Carlo and the Edgeworth expansion for very small p-values.*  
2018 ICSA China Conference with the Focus on Data Science. July 2018.
  - *Identify pleiotropic genes in genome-wide association studies for multivariate phenotypes with mixed measurement scales.*  
2017 IMS-China International Conference on Statistics and probability. July 2017.
  - *Identify pleiotropic genes in genome-wide association studies for multivariate phenotypes with mixed measurement scales.*  
Department of Computational Medicine & Bioinformatics, University of Michigan.  
October 2016.
  - *An efficient genome-wide association test for mixed binary and continuous phenotypes with applications to substance abuse research.*  
2016 Joint Statistical Meetings, Chicago. August 2016.
  - *An efficient method for GWAS of multivariate phenotypes.*  
IMS-APRM: The 4th Institute of Mathematical Statistics Asia Pacific Rim Meeting, Hong Kong. July 2016.
  - *Efficient association testing method for analyzing multivariate phenotypes using Fisher combination function.*  
IMS-APRM: The 3rd Institute of Mathematical Statistics Asia Pacific Rim Meeting, Taipei, Taiwan. July 2014.
  - *A Statistical Approach for Local Ancestry Inference in Admixed Individuals.*  
IMS-SWUFE International Conference on Statistics and Probability, Chengdu, China. July 2013.
  - *Covariate Adjustment in Pretest-Posttest Research Designs: Lord's Paradox and other issues.*  
Public Health Sciences, Henry Ford Health Sciences Center, Detroit, Michigan. May 2012.
  - *Alternative Estimation Procedures for  $Pr(X < Y)$  in Categorized Data.*  
Public Health Sciences, Henry Ford Health Sciences Center, Detroit, Michigan.  
December 2011.
  - *Causal Inference.*  
Public Health Sciences, Henry Ford Health Sciences Center, Detroit, Michigan. June 2011.
  - *Generalization of the Familywise Error Rate.*  
Public Health Sciences, Henry Ford Health Sciences Center, Detroit, Michigan.  
December 2010.
  - *Cochran-Armitage Trend Test: Past, Current and Future.*  
Biostatistics and Research Epidemiology, Henry Ford Health Sciences Center, Detroit, Michigan. March 2009.
  - *Admixture Mapping.*  
Institute of Statistics, National Tsing-Hua University, Hsinchu, Taiwan. May 2008.
  - *Statistical Modeling: Tree-based Methods.*  
Biostatistics and Research Epidemiology, Henry Ford Health Sciences Center, Detroit, Michigan. August 2006.

- *What a Lazy SAS User.*  
Biostatistics and Research Epidemiology, Henry Ford Health Sciences Center, Detroit, Michigan. May 2006.
- *Exegeses on Regression Models between Linear and Nonlinear.*  
Biostatistics and Research Epidemiology, Henry Ford Health Sciences Center, Detroit, Michigan. March 2006.
- *Statistical Methods for Dose-effect Data Analysis: From Linear to Nonlinear.*  
Hypertension and Vascular Research Division, Henry Ford Health Sciences Center, Detroit, Michigan. October 2005.
- *Microarray Experimental Design: Power and Sample Size Considerations.*  
ASA Joint Statistical Meeting, Minneapolis, Minnesota. August 2005.
- *A Simple Survey of Multiple Comparison Procedures.*  
Biostatistics and Research Epidemiology, Henry Ford Health Sciences Center, Detroit, Michigan. July 2005.
- *Cell Cycle Analysis.*  
Biostatistics and Research Epidemiology, Henry Ford Health Sciences Center, Detroit, Michigan. April 2004.
- *A Statistical Method for Identifying Informative Genes in Microarrays.*  
Department of Statistics, University of Florida, Gainesville, Florida. August 2002.
- *Class Discovery and Prediction Using Gene Expression Data.*  
Diabetes Research Center, University of Florida, Gainesville, Florida. June 2000.
- *Markov Chain Monte Carlo in Statistical Genetics.*  
Department of Statistics, University of Florida, Gainesville, Florida. April 2000.

## Bibliography

### Statistical Methodology Papers

1. **Yang, J. J., & Buu, A.** (2024). Adaptive Sequential Singular Spectrum Analysis: Effective Signal Extraction with Application to Heart Rate Signals Related to E-Cigarette Use. *Data Science in Science*, 3(1), 2383770.
2. **Yang, J. J., Piper, M. E., Indic, P., & Buu, A.** (2024). Statistical methods for predicting e-cigarette use events based on beat-to-beat interval (BBI) data collected from wearable devices. *Statistics in Medicine*.
3. **Yang, J. J., & Buu, A.** (2024). Efficient matrix profile computation with Euclidean distance using Eigen transformation: Performance evaluation based on beat-to-beat interval (BBI) data. *Statistics in Medicine*.
4. **Yang, J. J., Luo, X., Trucco, E. M., & Buu, A.** (2022). Polygenic risk prediction based on singular value decomposition with applications to alcohol use disorder. *BMC Bioinformatics*, 23: 28. PMID: PMC8744290
5. **Yang, J.J., Kuo, J., Su, W. C., Jorenby, D. E., Piper, M. E., & Buu, A.** (2022). A new statistical model for longitudinal ecological momentary assessment data on dual use of electronic and combustible cigarettes. *The American Journal of Drug and Alcohol Abuse*, 48, 529-537
6. **Yang, J. J., Trucco, E. M., Buu, A.** (2019) A hybrid method of the sequential Monte Carlo and the Edgeworth expansion for computation of very small  $p$ -values in permutation tests.

- Statistical Method in Medical Research*. 28(10-11):2937-2951. PMID: 30073912; PMCID: PMC6360137. DOI: <https://doi.org/10.1177/0962280218791918>
7. **Yang, J.J.**, Williams, L., Buu, A. (2017) Identify pleiotropic genes in genome-wide association studies from related subjects using the linear mixed model and Fisher combination function. *BMC Bioinformatics*. 18:376. PMID: 28836938; PMCID: PMC5571642. DOI: <https://doi.org/10.1186/s12859-017-1791-9>
  8. **Yang, J.J.**, Williams, L., Buu, A. (2017) Identify pleiotropic genes in genome-wide association studies for multivariate phenotypes with mixed measurement scales. *PLoS One*. 12(1): e0169893. PMID: 28081206; PMCID: PMC5231271. DOI: <https://doi.org/10.1371/journal.pone.0169893>
  9. Buu, A., Williams, L. K., **Yang, J. J.** (2018) An efficient genome-wide association test for mixed binary and continuous phenotypes with applications to substance abuse research. *Statistical Methods in Medical Research*. 27 (3):905-919. PMID: 27215414; PMCID: PMC6812509. DOI: <https://doi.org/10.1177/0962280216647422>
  10. **Yang, J. J.**, Li, J., Williams, L. K., and Buu, A. (2016) An efficient genome-wide association test for multivariate phenotypes based on the Fisher combination function. *BMC Bioinformatics*. 17 (1):19. PMID: 26729364; PMCID: PMC4704475. DOI: <https://doi.org/10.1186/s12859-015-0868-6>
  11. Li, J., **Yang, J. J.**, Levin, A. M., Montgomery, C. G., Datta, I., Trudeau, S., Adrianto, I., McKeigue, P., Iannuzzi, M. C., Rybicki, B. A. (2014) Efficient generalized least squares method for mixed population and family-based samples in genome-wide association studies. *Genetic Epidemiology*, 38 (5): 430-438. PMID: 24845555; PMCID: PMC4112407. DOI: <https://doi.org/10.1186/s12859-015-0868-6>
  12. **Yang, J. J.**, Li, J., Buu, A., and Williams, L. K. (2013) Efficient inference of local ancestry. *Bioinformatics*, 29 (21): 2750-2756. PMCID: PMC3799480. DOI: <https://doi.org/10.1093/bioinformatics/btt488>
  13. **Yang, J. J.** (2010) Distribution of Fisher's combination statistic when the tests are dependent. *Journal of Statistical Computation and Simulation*, 80 (1), 1-12. DOI: <https://doi.org/10.1080/00949650802412607>
  14. **Yang, J. J.** and Yang, M. C. K. (2006) An improved procedure for gene selection from microarray experiments using false discovery rate criterion. *BMC Bioinformatics*, 7, 15. PMCID: PMC1388243. DOI: <http://doi.org/10.1186/1471-2105-7-15>
  15. Yang, M. C. K., **Yang, J. J.**, McIndoe, R. A., and She, J. X. (2003) Microarray experimental design: power and sample size considerations. *Physiological Genomics*, 16 (1), 24-28. DOI: <https://doi.org/10.1152/physiolgenomics.00037.2003>
  16. Yang M. C. K., Ruan Q. G., **Yang J. J.**, Eckenrode S., Wu S., McIndoe R. A., She J. X. (2001) A statistical method for flagging weak spots improves normalization and ratio estimates in microarrays. *Physiological Genomics*, 7 (1), 45-53. PMID: 11595791. DOI: <https://doi.org/10.1152/physiolgenomics.00020.2001>
  17. Huwang, L. C. and **Yang, J.** (2000) Trimmed estimation in the measurement error model when the covariate has replicated observations. *Proceedings of the National Science Council, Part A: Physical Science and Engineering*, 24, 405-412.

### Genetic/Genomic Papers

1. **Yang, J.J.**, Wang, Z., Trucco, E.M., Buu, A., Lin, H.C. (2022). Chronic pain and delinquency partially explain the effect of the DRD4 gene polymorphism on adult substance use. *American Journal of Drug and Alcohol Abuse*, 48, 235-244.

2. Trucco, E. M., Yang, S., **Yang, J. J.**, Zucker, R. A., Li, R. and Buu, A. (2020) Time-varying effects of GABRG1 and maladaptive peer behavior on externalizing behavior from childhood to adulthood: Testing gene x environment x development effects. *Journal of Youth and Adolescence*. 49(7):1351-1364. doi: 10.1007/s10964-019-01171-3. Epub 2019 Nov 30. PMID: 31786770; PMCID: PMC7260088.
3. Levin, A. M., Gui, H., Hernandez-Pacheco, N., Yang, M., Xiao, S., **Yang, J. J.**, Hochstadt, S., Rynkowski, D., Kwok, P. Y., Pino-Yanes, M., Erle, D. J., Lanfear, D. E., Burchard, E. G., Williams, L. K. (2018) Integrative approach identifies corticosteroid response variant in diverse populations with asthma. *Journal of Allergy and Clinical Immunology*. pii: S0091-6749(18)31486-6. PMID: 30367910. DOI: <https://doi:10.1016/j.jaci.2018.09.034>
4. Demenais, F.,..., **Yang, J. J.**, ..., Nicolae, D. L. (2018) Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. *Nature Genetics*. 50(1): 42–53. PMCID: PMC5901974; NIHMSID: NIHMS919076; PMID: 29273806. DOI: <https://doi.org/10.1038/s41588-017-0014-7>
5. Paternoster, L.,..., **Yang, J. J.**, ..., Weidinger, S. (2015) Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis: EARly Genetics and Lifecourse Epidemiology (EAGLE) Eczema Consortium; Australian Asthma Genetics Consortium (AAGC); Australian Asthma Genetics Consortium (AAGC). *Nature Genetics*. 47(12):1449-1456. PMID: 26482879; PMCID: PMC4753676. DOI: <https://doi.org/10.1038/ng.3424>
6. Igartua, C.,..., **Yang, J. J.**,..., and Ober, C. (2015) Ethnic-specific associations of rare and low frequency DNA sequence variants with asthma. *Nature Communications*, 6: 5965. PMID: 25591454; PMCID: PMC4309441. DOI: <https://doi.org/10.1038/ncomms6965>
7. Bunyavanich, S., Schadt, E. E., Himes, B. E., Lasky-Su, J., Qiu, W., Lazarus, R., Ziniti, J. P., Cohain, A., Linderman, M., Torgerson, D. G., Eng, C. S., Pino-Yanes, M. Padhukasahasram, B., **Yang, J. J.**, Mathias, R. A., Beaty, T. H., Li, X., Graves, P., Romieu, I., del Rio Navarro, B. Salam, M. T., Vora, H., Nicolae, D. L., Ober, C., Martinez, F. D., Bleecker, E. R., Meyers, D. A., Gauderman, W. J., Gilliland, F., Burchard, E. G., Barnes, K. C., Williams, L. K., London, S. J., Zhang, B., Raby, B. A., Weiss, S. T. (2014) Integrated GWAS, coexpression network, and expression single nucleotide polymorphism analysis identifies novel pathways in allergic rhinitis. *BMC Medical Genomics*, 7:48. PMID: 25085501; PMCID: PMC4127082. DOI: <https://doi.org/10.1186/1755-8794-7-48>
8. Levin A.M., Wang Y., Wells K.E., Padhukasahasram B., **Yang J.J.**, Burchard E.G., Williams L.K. (2014) Nocturnal asthma and the importance of race-ethnicity and genetic ancestry. *American Journal of Respiratory and Critical Care Medicine*, 190(3):266-73. PMID: 24937318; PMCID: PMC4226040. DOI: <https://doi.org/10.1164/rccm.201402-0204OC>
9. Padhukasahasram, B. K., **Yang, J. J.**, Levin, A. M., Yang, M., Burchard, E. G., Kumar, R., Kwok, P., Lanfear, D. E., Williams, L. K. (2014) Gene-based association identifies SPATA13-AS1 as a pharmacogenomic predictor of inhaled short-acting beta-agonist response in multiple population groups. *The Pharmacogenomics Journal*, 14(4):365-71. PMID: 24418963; PMCID: PMC4098013. DOI: <https://doi.org/10.1038/tpj.2013.49>
10. Yao, T. C., Du, G., Han, L., Sun, Y., Hu, D., **Yang, J. J.**, Mathias, R., Roth, L. A., Rafaels, N., Thompson, E. E., Loisel, D. A., Anderson, R., Eng, C., Orbegozo, M. A., Young, M., Klocksieben, J. M., Anderson, E., Shanovich, K., Lester, L. A., Williams, L. K., Barnes, K. C., Burchard, E. G., Nicolae, D. L., Abney, M. & Ober, C. (2014) Genome-wide association study of lung function phenotypes in a founder population. *Journal of Allergy and Clinical*

*Immunology*, 133(1):248-255.e10. PMID: 23932459. DOI:  
<https://doi.org/10.1016/j.jaci.2013.06.018>

11. Himes, B. E., ..., **Yang, J. J.**, ..., Weiss, S. T. (2013) Integration of mouse and human genome-wide association data identifies *KCNIP4* as an asthma gene. *PLoS One*, 8 (2): e56179. PMID: PMC3572953. DOI: <https://doi.org/10.1371/journal.pone.0056179>
12. Rumpel, J. A., Ahmedani, B. K., Peterson, E. L., Wells, K. E., Yang, M., Levin, A. M., **Yang, J. J.**, Kumar, R., Burchard, E. G., Williams, L. K. (2012) Genetic ancestry and its association with asthma exacerbations among African American patients with asthma. *Journal of Allergy and Clinical Immunology*, 130 (6): 1302-1306. PMID: PMC3511609. DOI: <https://doi.org/10.1016/j.jaci.2012.09.001>
13. Myers, R. A., Himes, B. E., Gignoux, C. R., **Yang, J. J.**, Gauderman, W. J., Rebordosa, C., Xie, J., Torgerson, D. G., Levin, A. M., Baurley, J., Graves, P. E., Mathias, R. A., Romieu, I., Roth, L. A., Conti, D., Avila, L., Eng, C., Vora, H., LeNoir, M. A., Soto-Quiros, M., Liu, J., Celedón, J. C., Farber, H. J., Kumar, R., Avila, P. C., Meade, K., Serebrisky, D., Thyne, S., Rodriguez-Cintron, W., Rodriguez-Santana, J. R., Borrell, L. N., Lemanske, R. F., Bleeker, E. R., Meyers, D. A., London, S. J., Barnes, K. C., Raby, B. A., Martinez, F. D., Gilliland, F. D., Williams, L. K., Burchard, E. G., Weiss, S. T., Nicolae, D. L., Ober, C. (2012) Further replication studies of the EVE Consortium meta-analysis identifies 2 asthma risk loci in European Americans. *Journal of Allergy and Clinical Immunology*, 130(6):1294-301. PMID: PMC3666859. DOI: <https://doi.org/10.1016/j.jaci.2012.07.054>
14. Kumar, R., Williams, L. K., Kato, A., Peterson, E. L., Favoreto, S. Jr., Hulse, K., Wang, D., Beckman, K., Thyne, S., Lenoir, M., Meade, K., Lanfear, D. E., Levin, A. M., Favro, D., **Yang, J. J.**, Weiss, K., Boushey, H. A., Grammer, L., Avila, P. C., Burchard, E. G., Schleimer, R. (2012) Genetic variation in B cell-activating factor of the TNF family (BAFF) and asthma exacerbations among African American subjects. *Journal of Allergy and Clinical Immunology*. 130 (4): 996-999. PMID: PMC3520130. DOI: <https://doi.org/10.1016/j.jaci.2012.04.047>
15. Lanfear, D. E., **Yang, J. J.**, Mishra, S., and Sabbah, H. N. (2011) Genome-wide approach to identify novel candidate genes for beta blocker response in heart failure using an experimental model. *Discovery Medicine*, 11 (59): 359-366. PMID: 21524389; PMID: PMC3725612. DOI: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3725612/>
16. Harding, P., Yang, X. P., **Yang, J.**, Shesely, E, He, Q., and LaPointe, M. C. (2010) Gene expression profiling of dilated cardiomyopathy in older male EP4 knockout mice. *American Journal of Physiology – Heart and Circulatory Physiology*, 298: H623-H632. PMID: 20008274; PMID: PMC2822585. DOI: <https://doi.org/10.1152/ajpheart.00746.2009>
17. **Yang, J. J.**, Burchard, E. G., Choudhry, S., Johnson, C. C., Ownby, D. R., Favro, D., Chen, J., Akana, M., Ha, C., Kwok, P. Y., Krajenta, R., Havstad, S. L., Joseph, C. L., Seibold, M. A., Shriver, M. D., and Williams, L. K. (2008) Differences in allergic sensitization by self-reported race and genetic ancestry. *Journal of Allergy and Clinical Immunology*, 122 (4): 820-827. PMID: 19014772; PMID: PMC2951327. DOI: <https://doi.org/10.1016/j.jaci.2008.07.044>
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### Book Chapter

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### Development of Statistical Software

1. R: FisherCombinationStat package (Multivariate Test using Fisher Combination Statistic)  
URL: <https://github.com/jyangstat/FisherCombinationStat>
2. R: EILA package (efficient inference of local ancestry) URL: <http://cran.r-project.org/web/packages/EILA/index.html>
3. Globe-p (Program for proportion of nulls estimation).
4. SAS macro for microarray sample size calculation.

## Computer Experiences and Skills

### *Statistical Software*

- R: A Language and Environment for Statistical Computing
- The Julia programming language
- SAS (Statistical Analysis System): Base, Stat, and Macro
- MATLAB
- GNU Octave

### *Genetic Analysis Software*

- Genome-wide association study: PLINK
- Relationship inference: KING
- Admixture mapping: Eigenstrat, LAMP, Hapmix
- Genotyping: Affymetrix Power Tool

### *Computational Software*

- Perl 5
- Fortran 90/95, FORTRAN 77

### *Operating Systems*

- UNIX/Linux
- Windows 10