

CURRICULUM VITA

Qing Lu, Ph.D.

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Department of Biostatistics
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EDUCATION AND TRAINING

- 01/2004-08/2008 ***Doctoral Training – Statistical Genetics***
Department of Epidemiology and Biostatistics,
Case Western Reserve University
Degree Awarded: August 2008
- 07/2001-08/2003 ***Masters Training – Statistics***
Department of Statistics, University of Florida
Degree Awarded: August 2003
- 07/1994-08/1999 ***Undergraduate Training – Double Major***
Applied Mathematics, Department of Mathematics, Shanghai University
Industrial Foreign Trade, Department of Industrial Trade, Shanghai University
Degree Awarded: August 1999

POSITION

- 06/2019-present ***Professor***, Department of Biostatistics, University of Florida
- 01/2016-08/2016 ***Visiting faculty***, Department of Biostatistics, University of Michigan School
of Public Health
- 07/2014-05/2019 ***Associate Professor***, Department of Epidemiology and Biostatistics,
Michigan State University
- 02/2009-05/2019 ***Faculty Member***, BioMolecular Science, Michigan State University
Faculty Member, Quantitative Biology & Modeling Initiative, Michigan
State University
- 08/2008-07/2014 ***Assistant Professor***, Department of Epidemiology and Biostatistics,
Michigan State University
- 08/1999-07/2001 ***Software Engineer***, Industrial & Commercial Bank of China (ICBC) Data
Center

HONORS AND AWARDS

2014 Academic Competitiveness Award, College of Human Medicine, Michigan State University
2013 NIH K01 Career Development Awardee
2008 Jane M. Olson Memorial Award, Department of Epidemiology and Biostatistics, Case Western Reserve University

RESEARCH SUPPORT

Ongoing Research Support

1R01DA043501-01(Q. Lu, PI) 09/2017-05/2022

NIH/NIDA

Computational Efficient Statistical Tools for Analyzing Substance Dependence Sequencing Data

Role: PI

1R01LM012848-01 (Q. Lu, PI) 07/2018-05/2022

NIH/NLM

Methods and Software for High-dimensional Risk Prediction Research

Role: PI

GF13666 (S. Burt, PI) 09/2016-08/2019

John Templeton Foundation

Understanding “what could be”: Heritability in a randomized twin design

Role: Co-investigator

R25HL140319-01A1 (H. Neighbors, PI) 07/2018-06/2023

NIH/NHLBI

The Research to reduce disparities in disease (R2D2)

Role: Co-investigator

Completed Research Support

RG100930 (Q. Lu, PI) 05/2017–11/2018

Michigan State University

Discretionary Funding Initiative

Role: PI

1K01DA033346-01 (Q. Lu, PI) 02/2013-01/2018

NIH/NIDA

Gene-Gene/Gene-Environment Interactions Associated with Nicotine Dependence

Role: PI

1R03DE022379-01 (Q. Lu, PI) 05/2012-04/2015

NIH/NIDCR

A High-dimensional Statistical Genetic Approach for Family-based Orofacial Clefts research

Role: PI

1R01CA136861-01 (Ellen Velie, PI) 08/2010-07/2015

NIH/NCI

Life Course Energy Balance and Breast Cancer Risk in Black/White Women under 50
Role: Co-Investigator

RG070103 (Wenjiang Fu, PI) 09/2013-09/2014
Hunt for a Cure
A Comprehensive Search of Genetic Markers Promising for Gene Therapies of PA Infection in Cystic Fibrosis Patients
Role: Co-Investigator

08-IRGP-1519 (Q. Lu, PI) 12/2008-06/2010
MSU/Intramural Research Grants Program (IRGP)
Investigating New Predictive Genetic Tests for Type 1 and Type 2 Diabetes Based on Recent Genome-Wide Association Discoveries
Role: PI

5P41RR003655 sub-project ID: 5675, 6729, 7635 (Q. Lu, Sub-Project PI) 08/2008-07/2011
NIH/NCRR
Using the Optimal Receive Operating Characteristic Curve
Role: Sub-Project PI

SPG Award (Brian Schutte, PI) 06/2009-05/2012
MSU Strategic Partnership Grants (SPG)
Community-based cooperative for Studies Across Generations (CoSAGE)
Role: Co-Investigator

FACT Award (Debra Schutte, PI) 06/2009-05/2011
MSU/Families and Communities Together Coalition (FACT)
CoSAGE: Cooperative Study Across Generations
Role: Co-Investigator

SELECTED PEER REVIEWED PUBLICATIONS (current/former trainees)

1. Li M, He Z, Tong X, Witte JS and **Lu Q**. Detecting Rare Mutations with Heterogeneous Effects Using a Family-Based Genetic Random Field Method. *Genetics*. 2018; 210(2):463-476.
2. Jadhav S, Koul H, **Lu Q**. Dependent Generalized Functional Linear Models. *Biometrika* 2017;104(4):987-994
3. Wen Y, Burt A, **Lu Q**. Risk Prediction Modeling on Family-Based Sequencing Data Using a Random Field Method. *Genetics*. 2017; 207(1):63-73. PMID: 28679544
4. Wei C and **Lu Q**. A generalized association test based on U statistics. *Bioinformatics*. 2017; 33(13):1963-1971. PMID: 28334117
5. Tielbeek JJ, Johansson A, Polderman TJC, Rautiainen MR, Jansen P, Taylor M, Tong X, **Lu Q**, Burt AS, Tiemeier H, Viding E, Plomin R, Martin NG, Heath AC, Madden PAF, Montgomery G, Beaver KM, Waldman I, Gelernter J, Kranzler HR, Farrer LA, Perry JRB, Munafò M, LoParo D,

- Paunio T, Tiihonen J, Mous SE, Pappa I, de Leeuw C, Watanabe K, Hammerschlag AR, Salvatore JE, Aliev F, Bigdeli TB, Dick D, Faraone SV, Popma A, Medland SE, Posthuma D; Broad Antisocial Behavior Consortium collaborators. Genome-Wide Association Studies of a Broad Spectrum of Antisocial Behavior. *JAMA Psychiatry*. 2017; 74(12):1242-1250. PMID: 28979981
6. Wei C, Elston RC, and **Lu Q**. A weighted U statistic for association analyses considering genetic heterogeneity. *Statistics in Medicine*. 2016; 35(16):2802-14. PMID: 26833871
 7. Li M, He Z, Schaid DJ, Cleves MA, Nick TG, **Lu Q**. A Powerful Non-Parametric Statistical Framework for Family-Based Association Analyses. *Genetics*. 2015;200(1):69-78. PMID: 25745024
 8. He Z, Zhang M, Zhan X and **Lu Q**. Modeling and Testing for Joint Association Using a Genetic Random Field Model. *Biometrics*. 2014;70(3):471-9 PMID: 24628067
 9. **Lu Q**, Obuchowski N, Won S, Zhu X, Elston RC. Using the robust optimal receiver operating characteristic curve for predictive genetic tests. *Biometrics*. 2010; 66(2):586-93. PMID: 19508241
 10. **Lu Q**, Elston RC. Using the optimal receiver operating characteristic (ROC) curve to design a predictive genetic test exemplified with Type 2 Diabetes. *Am J Hum Genet*. 2008; 82(3):641-51. PMID: 18319073

COMPLETE LIST OF PUBLICATIONS

Peer Reviewed Publications (current/former trainees)

1. Zhang X, Lan T, Wang T, Xue W, Tong X, Ma T, Liu G, **Lu Q**. Considering Genetic Heterogeneity in the Association Analysis Finds Genes Associated With Nicotine Dependence. *Front Genet*. 2019 May 17;10:448. doi: 10.3389/fgene.2019.00448.
2. Geng P, Tong X, **Lu Q**. An integrative U method for joint analysis of multi-level omic data. *BMC Genet*. 2019 Apr 10;20(1):40. doi: 10.1186/s12863-019-0742-z.
3. Jing L, Cui Y, **Lu Q**, Yu H. Multiplier method estimates of the population of men who have sex with men: the effect of privacy protection. *J Public Health (Oxf)*. 2019 Feb 26. doi: 10.1093/pubmed/fdz019.
4. Wei C, Li M, Wen Y, Ye C, and **Lu Q**. A multi-locus predictiveness curve and its summary assessment for genetic risk prediction. *Stat Methods Med Res*. 2019. doi: 10.1177/0962280218819202.
5. Ma KL, Wang H, Gao X, Huang JJ, Sun CM, Qiao N, Zhang HX, **Lu Q**, Que XM, Li L, Wang T. Sleep quality mediating the association of personality traits and quality of life among underground workers and surface workers of Chinese coal mine: A multi-group SEM with latent response variable mediation analysis. *Psychiatry Res*. 2018 7;272:196-205.

6. An H, Wei CS, Wang O, Wang DH, Xu LW, **Lu Q**, Ye CY. An ensemble-based likelihood ratio approach for family-based genomic risk prediction. *J Zhejiang Univ Sci B*. 2018 Dec.;19(12):935-947.
7. Li M, He Z, Tong X, Witte JS and **Lu Q**. Detecting Rare Mutations with Heterogeneous Effects Using a Family-Based Genetic Random Field Method. *Genetics*. 2018; 210(2):463-476.
8. Wen Y, Shen X and **Lu Q**. Genetic Risk Prediction Using a Spatial Autoregressive Model with Adaptive Lasso. *Statistics in Medicine*. 2018 Nov 20; 37(26):3764-3775.
9. Shen X and **Lu Q**. Joint analysis of genetic and epigenetic data using a conditional autoregressive model. *BMC Genet*. 2018;19(Suppl 1):71.
10. Carlson J, Locke AE, Flickinger M, Zawistowski M, Levy S, Myers RM, Boehnke M, Kang HM, Scott LJ, Li JZ, Zöllner S and BRIDGES Consortium. Extremely rare variants reveal patterns of germline mutation rate heterogeneity in humans. *Nat Commun*. 2018; 9(1):3753.
11. Jadhav S, Koul H, **Lu Q**. Dependent Generalized Functional Linear Models. *Biometrika* 2017;104(4):987-994
12. Jadhav S, Tong X, **Lu Q**. A functional U-statistic method for association analysis of sequencing data. *Genet Epidemiol*. 2017;41(7):636-643. PMID: 28850771
13. Tielbeek JJ, Johansson A, Polderman TJC, Rautiainen MR, Jansen P, Taylor M, Tong X, **Lu Q**, Burt AS, Tiemeier H, Viding E, Plomin R, Martin NG, Heath AC, Madden PAF, Montgomery G, Beaver KM, Waldman I, Gelernter J, Kranzler HR, Farrer LA, Perry JRB, Munafò M, LoParo D, Paunio T, Tiihonen J, Mous SE, Pappa I, de Leeuw C, Watanabe K, Hammerschlag AR, Salvatore JE, Aliev F, Bigdeli TB, Dick D, Faraone SV, Popma A, Medland SE, Posthuma D; Broad Antisocial Behavior Consortium collaborators. Genome-Wide Association Studies of a Broad Spectrum of Antisocial Behavior. *JAMA Psychiatry*. *JAMA Psychiatry*. 2017; 74(12):1242-1250. PMID: 28979981
14. Shen YN, Yu MX, Gao Q, Li YY, Huang JJ, Sun CM, Qiao N, Zhang HX, Wang H, **Lu Q**, Wang T. External validation of non-invasive prediction models for identifying ultrasonography-diagnosed fatty liver disease in a Chinese population. *Medicine (Baltimore)*. 2017; 96(30):e7610. PMID: 28746214
15. Wen Y, Burt A, **Lu Q**. Risk Prediction Modeling on Family-Based Sequencing Data Using a Random Field Method. *Genetics*. 2017; 207(1):63-73. PMID: 28679544
16. Wei C and **Lu Q**. A generalized association test based on U statistics. *Bioinformatics*. 2017; 33(13):1963-1971. PMID: 28334117
17. Xu SH, Qiao N, Huang JJ, Sun CM, Cui Y, Tian SS, Wang C, Liu XM, Zhang HX, Wang H, Liang J, **Lu Q**, Wang T.(2016) Gender Differences in Dietary Patterns and Their Association with the Prevalence of Metabolic Syndrome among Chinese: A Cross-Sectional Study. *Nutrients*. 2016 25;8(4):180. PMID: 27023599

18. **Lu Q.** Novel Statistical Approaches for High-dimensional Gene-gene and Gene-environment Interaction Analyses. *Current Genomics* 17(5): 387 (Editorial) 2016; 17(5):387. *PMID: 28479866*
19. **Li M, Wei C, Wen Y, Tong W and Lu Q** Detecting Gene-Gene Interactions Associated with Multiple Complex Traits with U-Statistics. *Current Genomics.* 2016 17 (5) 403-415 2016; 17(5):403-415. *PMID: 28479869*
20. **Wen Y, Lu Q.** A Clustered Multiclass Likelihood-Ratio Ensemble Method for Family-Based Association Analysis Accounting for Phenotypic Heterogeneity. *Genet Epidemiol.* 2016; 40(6):512-9. *PMID: 27321816*
21. **Li M, Li J, He Z, Lu Q, Witte JS, Macleod SL, Hobbs CA, Cleves MA;** National Birth Defects Prevention Study. Testing Allele Transmission of an SNP Set Using a Family-Based Generalized Genetic Random Field Method. *Genet Epidemiol.* 2016; 40(4):341-51. *PMID: 27061818*
22. **Vsevolozhskaya OA, Zaykin DV, Barondess DA, Tong X, Jadhav S, Lu Q.** Uncovering local trends in genetic effects of multiple phenotypes via functional linear models. *Genet Epidemiol.* 2016;40(3):210-21. *PMID: 27027515*
23. **Wen Y, He Z, Li M, Lu Q.** Risk Prediction Modeling of Sequencing Data Using a Forward Random Field Method. *Sci Rep.* 2016; 6:21120. *PMID: 26892725*
24. **Wei C, Elston RC, and Lu Q.** A weighted U statistic for association analyses considering genetic heterogeneity. *Statistics in medicine.* 2016; 35(16):2802-14. *PMID: 26833871*
25. **Li M, Li J, Wei C, Lu Q, Tang X, Erickson SW, MacLeod SL, Hobbs CA.** A Three-Way Interaction among Maternal and Fetal Variants Contributing to Congenital Heart Defects. *Ann Hum Genet.* 2016;80(1):20-31. *PMID: 26612412*
26. **Wen Y and Lu Q.** A Clustered Multiclass Likelihood-Ratio Ensemble Method for Family-Based Association Analysis Accounting for Phenotypic Heterogeneity. *Genetic epidemiology.* 2016; 40(6):512-9. *PMID: 23934726*
27. **Jadhav S, Vsevolozhskaya OA, Tong X, and Lu Q.** The Impact of Genetic Structure on Sequencing Analysis *BMC Proceedings* 2016; 10(Suppl 7): 171–174
28. **Tong X, Wei C, Lu Q.** Genome-wide joint analysis of SNV sets and gene expression of hypertension and related phenotypes. *BMC Proceedings* 2016; 10(Suppl 7): 125–129.
29. **Wen Y, Lu Q.** Risk Prediction Models for Oral Clefts allowing for Phenotypic Heterogeneity. *Front Genet.* 2015; 6:264. *PMID: 26322076*
30. **Li M, He Z, Schaid DJ, Cleves MA, Nick TG, Lu Q.** A Powerful Non-Parametric Statistical Framework for Family-Based Association Analyses. *Genetics.* 2015;200(1):69-78. *PMID: 25745024*

31. Wei C and **Lu Q**. software for genome-wide gene-gene interaction analysis *BMC Genetics* 2014;15(1):101. PMID: 25318532
32. Wei C, Li M, He Z, Vsevolozhskaya O, Schaid DJ and **Lu Q**. A Weighted U Statistic for Genetic Association Analyses of Sequencing Data", *Genet Epidemiol.* 2014;38(8):699-708. PMID: 25331574
33. Vsevolozhskaya OA, Zaykin DV, Greenwood MC, Wei C, **Lu Q**. Functional Analysis of Variance for Association Studies. *PLoS One.* 2014;9(9):e105074. PMID: 25244256
34. Li M, Gardiner JC, Breslau N, Anthony J and **Lu Q**. A Non-parametric Approach for Detecting Gene-Gene Interactions Associated with Age-at-onset outcomes. *BMC Genetics* 2014;15:79. PMID: 24986733
35. Sun X, **Lu Q**, Mukheerjee S, Crane P, Elston RC, Ritchie MD. Analysis pipeline for the epistasis search – statistical versus biological filtering. *Frontiers in Applied Genetic Epidemiology*;5:106. PMID: 24817878
36. Wen Y, **Lu Q**. Analysis of gene-gene interactions underlying human disease. *eLS* 2014 DOI: 10.1002/9780470015902.a0022498
37. He Z, Zhang M, Zhan X and **Lu Q**. Modeling and Testing for Joint Association Using a Genetic Random Field Model. *Biometrics.* 2014;70(3):471-9 PMID: 24628067
38. Bonner JD, Fisher R, Klein J, **Lu Q**, Wilch E, Friderici KH, Elfenbein JL, Schutte DL, and Schutte BC. Pedigree structure and kinship measurements of a mid-Michigan community: A new North American Population Isolate Identified. *Human Biology* 86(1):59-68. 2014
39. Li M, He Z, Zhang M, Zhan X, Wei C, Elston RC, and **Lu Q**. A Generalized Genetic Random Field Method for the Genetic Association Analysis of Sequencing Data. *Genet Epidemiol.* 2014;38(3):242-53. PMID: 24482034
40. Ye C and **Lu Q**. Bridge: a GUI Software for Genetic Risk Prediction. *BMC Genet.* 2013;14:122 PMID: 24359333
41. Wei C, **Lu Q**, Khoo SK, Lenski M, Fichorova R, Leviton A, Paneth N*. Comparison of Frozen and Unfrozen Blood Spots for Gene Expression Studies. *Journal of Pediatrics* 2013 PMID: 24209717
42. Slaughter J, Wei C, Korzeniewski SJ, **Lu Q**, Beck JS, Khoo SK, Brovont A, Maurer J, Martin D, Lenski M, and Paneth N* High correlations in gene expression between paired umbilical cord blood and neonatal blood of healthy newborns on Guthrie cards. *J Matern Fetal Neonatal Med.* 2013. PMID: 23668672
43. Li M, Wen Y, **Lu Q**, and Fu WJ An Imputation Approach for Oligonucleotide Microarray. *PLoS One.* 2013;8(3):e58677. PMID: 23505547

44. Wen Y, Schaid DJ and **Lu Q** A Bivariate Mann-Whitney Approach for Unraveling Genetic Variants and Interactions Contributing to Comorbidity. *Genet Epidemiol.* 2013;37(3):248-55. PMID: 23334941
45. Wei C, Schaid DJ, **Lu Q**. Trees Assembling Mann-Whitney Approach for Detecting Genome-wide Joint Association among Low-Marginal-Effect loci. *Genet Epidemiol.* 2013;37(1):84-91. PMID: 23135745
46. Ho NT, Furge K, Fu W, Busik J, Khoo SK, **Lu Q**, Lenski M, Wirth J, Hurwitz E, Dodge N, Resau J, Paneth N*. Gene expression in archived newborn blood spots distinguishes infants who will later develop cerebral palsy from matched controls. *Pediatr Res.* 2012. PMID: 23269123
47. Li M, Lou X, **Lu Q**. On Epistasis: a Methodological Review for Detecting Gene-Gene Interactions Underlying Various Types of Phenotypic Traits. *Recent Patents on Biotechnology* 2012;6(3):230-6. PMID: 23003010
48. **Lu Q**, Wei C, Ye C, Li M, Elston RC. A Likelihood Ratio based Mann-Whitney Approach Finds Novel Replicable Joint Gene Action for Type 2 Diabetes. *Genetic Epidemiology* 2012; 36(6):583-93. PMID: 22760990
49. Wei C, Anthony JC, **Lu Q**. Genome-environmental risk assessment of cocaine dependence. *Front Genet.* 2012;3:83. PMID: 22629285
50. Li M, Peng R, Wei C, **Lu Q**, A U-Statistic-based random forest approach for genetic association study with quantitative traits. *Front Biosci (Elite Ed).* 2012;4:2707-17. PMID: 22652671
51. Won S, **Lu Q**, Bertram L, Tanzi RE, Lange C. On the meta-analysis of genome-wide association studies: A robust and efficient approach to combine population and family-based studies. *Human Heredity* 2012; 18;73(1):35-46. PMID: 22261799
52. Namkung J, Raska P, Kang J, Liu Y, **Lu Q**, Zhu X. Analysis of Exome Sequences With and Without Incorporating Prior Biological Knowledge. *Genetic Epidemiology* 2011;35 Suppl 1:S48-55
53. Li M, Ye C, Fu W, Elston RC, **Lu Q** Detecting the Joint Action of Genes for Quantitative Traits with U-Statistics. *Genetic Epidemiology* 2011; 35(6):457-68. PMID: 21618602
54. Ye C, Cui Y, Wei C, Elston RC, Zhu J, **Lu Q**. A non-parametric method for building predictive genetic tests on high-dimensional data. *Hum Hered.* 2011; 71(3):161-70. PMID: 21778735
55. Ye C, Zhu J, **Lu Q**. A Clustered Optimal ROC Curve Method for Family-based Genetic Risk Prediction. *Statistics and its interface* 2011; 4(3):373-380
56. Li M, Fu W, **Lu Q** A Selective Aggregating U-Test for the Genetic Association Study of Quantitative Traits. *BMC Proceedings* 2011, 5(Suppl 9):S23. PMID: 22373246
57. Wei C, **Lu Q** A Collapsing ROC approach for risk prediction research on both common and rare variants. *BMC Proceedings* 2011, 5(Suppl 9):S42. PMID: 22373267

58. Lillvis JH, Kyo Y, Tromp G, Lenk GM, Li M, Lu Q, Igo RP Jr, Sakalihasan N, Ferrell RE, Schworer CM, Gatalica Z, Land S, Kuivaniemi H. Analysis of positional candidate genes in the AAA1 susceptibility locus for abdominal aortic aneurysms on chromosome 19. *BMC Med Genet.* 2011; 12(1):14. PMID: 21247474
59. Stein CM, **Lu Q**, Elston RC, Freebairn LA, Hansen AJ, Shriberg L, Taylor HG, Lewis BA, Iyengar SK. Heritability Estimation for Speech-Sound Traits with Developmental Trajectories. *Behavior Genetics* 2011; 41(2):184-91. PMID: 20623172
60. **Lu Q**, Cui YH, Ye C, Wei C and Elston RC. A bagging optimal roc curve method for predictive genetic tests with an application to rheumatoid arthritis. *Journal of Biopharmaceutical Statistics* 2010; 20(2):401-14. PMID: 20309765
61. **Lu Q**, Obuchowski N, Won S, Zhu X, Elston RC. Using the robust optimal receiver operating characteristic curve for predictive genetic tests. *Biometrics.* 2010; 66(2):586-93. PMID: 19508241
62. Zhu X, Feng T, Li Y, **Lu Q**, Elston R.C. Detecting rare variants for complex traits using family and unrelated data. *Genet Epidemiology* 2010; 34(2):171-87. PMID: 19847924
63. Li SY, **Lu Q** and Cui YH. A systems biology approach for identifying novel pathway regulators in eQTL mapping. *Journal of Biopharmaceutical Statistics* 2010;20(2):373-400. PMID: 20309764
64. Won S, Morris N, **Lu Q**, Elston RC, An optimal method for combining p-values. *Statistics in Medicine* 2009; 28(11):1537-1553. PMID: 19266501
65. Li SY, **Lu Q**, Fu W, Romero R and Cui YH. A regularized regression approach for dissecting genetic conflicts that increase disease risk in pregnancy. *Statistical Applications in Genetics and Molecular Biology* 2009; 8(1):Article 45. PMID: 19883371
66. **Lu Q**, Wang X, Song Y, Won S, Cui Y, Elston R.C. The effect of multiple genetic variants in predicting the risk of Type 2 Diabetes. *BMC Proceedings* 2009 3 (Suppl 7):S49. PMID: 20018041
67. **Lu Q**, Elston RC. Using the optimal receiver operating characteristic (ROC) curve to design a predictive genetic test exemplified with Type 2 Diabetes. *Am J Hum Genet.* 2008; 82(3):641-51. PMID: 18319073
68. Goddard KA, Tromp G, Romero R, Olson JM, **Lu Q**, Xu Z, Parimi N, Nien JK, Gomez R, Behnke E, Solari M, Espinoza J, Santolaya J, Chaiworapongsa T, Lenk GM, Volkenant K, Anant MK, Salisbury BA, Carr J, Lee MS, Vovis GF, Kuivaniemi H. Candidate-gene association study of mothers with pre-eclampsia, and their infants, analyzing 775 SNPs in 190 genes. *Hum Hered.* 2007; 63(1):1-16. PMID: 17179726
69. Weinsheimer S, Goddard KA, Parrado AR, **Lu Q**, Sinha M, Lebedeva E, Ronkainen A, Niemelä M, Khusnutdinova E, Khusainova RI, Helin K, Jääskeläinen JE, Sakovich V, Land S, Kuivaniemi H,

- and Tromp G. Association of Kallikrein Gene Polymorphisms with Intracranial Aneurysms. *Stroke*. 2007; 38(10):2670-6. PMID: 17761919
70. Xing G, Xing C, **Lu Q**, Elston RC. A logistic mixture model for a family-based association study. *BMC Proc*. 2007;1 Suppl 1:S44. Epub 2007. PMID: 18466543
 71. Xing C, Torres-Caban M, Wang T, **Lu Q**, Xing G, Elston RC. Linkage studies of catechol-O-methyltransferase (COMT) and dopamine-beta-hydroxylase (DBH) cDNA expression levels. *BMC Proc*. 2007;1 Suppl 1:S95. Epub 2007. PMID: 18466599
 72. Wang T, **Lu Q**, Caban MT, Elston RC. Two-stage Analysis Strategy for Identifying the IgM Quantitative Trait Locus. *BMC Proc*. 2007;1 Suppl 1:S139. Epub 2007. PMID: 18466482
 73. Song K, **Lu Q**, Lin X, Waterworth D, Elston RC. Genome-wide association studies using adaptive two-stage analysis for a case-control design. *BMC Proc*. 2007;1 Suppl 1:S147. Epub 2007. PMID: 18466491
 74. Ogata T, Gregoire L, Goddard KA, Skunca M, Tromp G, Lancaster WD, Parrado AR, **Lu Q**, Shibamura H, Sakalihan N, Limet R, MacKean GL, Arthur C, Sueda T, Kuivaniemi H. Evidence for association between the HLA-DQA locus and abdominal aortic aneurysms in the Belgian population: a case control study. *BMC Med Genet*. 2006; 7:67. PMID: 16879749
 75. Cui Y, **Lu Q**, Cheverud JM, Littell RC, Wu R. Model for mapping imprinted quantitative trait loci in an inbred F2 design. *Genomics*. 2006. 87(4):543-51. PMID: 16413163
 76. Xing C, Sinha R, Xing G, **Lu Q**, Elston RC. The affected-/discordant-sib-pair design can guarantee validity of multipoint model-free linkage analysis of incomplete pedigrees when there is marker-marker disequilibrium. *Am J Hum Genet*. 2006; 79(2):396-401. PMID: 16826532
 77. Liu T, Todhunter R, **Lu Q**, Schoettinger L, Li H, Littell R, Burton-Wurster N, Acland G, Lust G, Wu R. Modelling Extent and Distribution of Zygotic Disequilibrium: Implications for a Multigenerational Canine Pedigree. *Genetics*. 2006; 174(1):439-53. PMID: 16849601
 78. Tromp G, Ogata T, Gregoire L, Goddard KA, Skunca M, Lancaster WD, Parrado AR, Lu Q, Shibamura H, Sakalihan N, Limet R, Mackean GL, Arthur C, Sueda T, Kuivaniemi H. HLA-DQA is associated with abdominal aortic aneurysms in the Belgian population. *Ann N Y Acad Sci*. 2006; 1085:392-5. PMID: 17182961
 79. Song K, Orloff MS, **Lu Q**, Elston RC. Fine-mapping using the weighted average method for a case-control study. *BMC Genetics*. 2005; 6(Suppl 1):S67. PMID: 18466491
 80. Xing C, Schumacher FR, Xing G, **Lu Q**, Wang T, Elston RC. Comparison of microsatellites, single-nucleotide polymorphisms (SNPs) and composite markers derived from SNPs in linkage analysis. *BMC Genetics*. 2005; 6(Suppl 1):S29. PMID: 18466543
 81. Thompson CL, Baechle D, **Lu Q**, Mathew G, Song Y, Iyengar SK, Gray-McGuire C, Goddard KA. Effect of genotyping error in model-free linkage analysis using microsatellite or single-nucleotide polymorphism marker maps. *BMC Genet*. 2005;6 Suppl 1:S153. PMID: 16451614

82. **Lu Q**, Cui Y, Wu RL. A Multilocus Likelihood Approach to Joint Modeling of Linkage, Parental Diplotype and Gene Order in a Full-sib Family. *BMC Genetics*. 2004; 5:20. PMID: 15274749
83. Olson JM, Song YJ, **Lu Q**, Wedig GC, Goddard KA. Using Overall Allele-sharing to Detect the Presence of Large-Scale Data Errors and Parameter Misspecification in Sib-pair Linkage Studies. *Human Heredity*. 2004; 58 (1):49-54. PMID: 15604564
84. Lou XY, Todhunter RJ, Lin M, **Lu Q**, Liu T, Wang Z, Bliss SP, Casella G, Acland GM, Lust G, Wu RL The extent and distribution of linkage disequilibrium in a multi-hierarchic outbred canine pedigree. *Mammalian Genome*.2003;14(8):555-64. PMID: 12925888

Book Chapter

85. **Lu Q**, Yeunjoo Song, Gray-McGuire C. Software for Genetics/Genomics. A chapter written for “*Wiley Encyclopedia of Clinical Trials*”. John Wiley & Sons. 2008 Sep; DOI: 10.1002/9780471462422.eoct401
86. Zeng YR, Zhao W, **Lu Q** and Wu RL. A systems biology approach for integrating allometry, ontogeny and plasticity through functional mapping. A chapter written for “*Floriculture, Ornamental and Plant Biotechnology: Advances and Topical Issues*”. Global Science Books. 2006 Jun

INVITED PRESENTATIONS

1. “A conditional autoregressive model for genetic association analysis of sequencing data”, ICOSA meeting, Qingdao, China (2018)
2. “A New Artificial Intelligence Tool for Substance Use and Dependence Research”, NIDA Genetics Consortium Meeting, Bethesda, Maryland (2018)
3. “A generalized association test based on U statistics”, Institute of Mathematical Statistics meeting, Nanning, China (2017)
4. “A Generalized Similarity U Test for Multivariate Analysis of Sequencing Data” ENAR Conference, Austin, Texas (2016).
5. “A Generalized Similarity U Test for Multivariate Analysis of Sequencing Data” Department of Biostatistics, University of Michigan, Michigan (2016)
6. “Statistical Approaches for High-Dimensional Family-Based Genetic Association Studies” (March, 2012) Statistical Colloquium, Michigan State University, East Lansing, MI.
7. “A non-parametric method for whole genome-wide risk prediction” (July, 2010) Inauguration Symposium of the Center for Computational Biology at Beijing Forestry University, Beijing, China.
8. “Predictive Genetic Testing in the Age of Genome-Wide Association Studies”(July, 2010), First Joint Biostatistics Symposium, Beijing, China.
9. “Predictive Genetic Testing in the Age of GWAS”(Dec, 2009), MGI seminar, Michigan State University, East Lansing, MI.
10. “Designing and Forming Predictive Genetic Tests Using Optimal Receiver Operating Characteristic Curve”(Jan, 2008), Washington University, St. Louis, Missouri.

11. “Designing and Forming Predictive Genetic Tests Using Optimal Receiver Operating Characteristic Curve”(Jan, 2008), Boston University, Boston, Massachusetts
12. “Designing and Forming Predictive Genetic Tests Using Optimal Receiver Operating Characteristic Curve”(Jan, 2008), Wake Forest, Winston-Salem, North Carolina
13. “Designing and Forming Predictive Genetic Tests Using Optimal Receiver Operating Characteristic Curve”(Feb, 2008), Mayo Clinic, Rochester, Minnesota.
14. “Using the Robust Optimal Receiver Operating Characteristic Curve for Predictive Genetic Tests”(June, 2009), BMB seminar, Michigan State University, East Lansing, MI.

SELECTED POSTER AND PLATFORM PRESENTATIONS

1. Zhang S, Geng Pei, Shen X, Tong X and **Lu Q**. A Functional Deep Neural Network for Genetic Data Analysis Involving High-dimensional Multivariate Outcomes. JSM conference (2018)
2. Tong X, Shen X and **Lu Q**. Kernel based genetic meta-analysis using batch training. JSM conference (2018)
3. Shen X, Tong X and **Lu Q**. A Kernel-Based Neural Network for High-dimensional Genetic Risk Prediction Analysis. JSM conference (2018)
4. Geng P, Zhang S and **Lu Q**. Neural network with functional smoothing and its application to genetic analysis. JSM conference (2018)
5. Shen X and **Lu Q**. A Conditional Autoregressive Model for Genetic Association Analysis of Sequencing Data. JSM conference (2016)
6. Li M, He Z and **Lu Q**. A random field based method for association analysis of family-based sequencing data. ICSA conference (2016)
7. Geng P and **Lu Q**. Functional U Test for Joint Effect of SNPs and Gene Expression in Association Study. ENAR Conference (2016)
8. Jadhav S, Koul H, **Lu Q**. Dependent Generalized Functional Linear Models. ENAR Conference (2016)
9. Wei C, Vsevolozhskaya OA, Elston RC, and **Lu Q**. A non-parametric method finds genetic etiology of nicotine dependence differs in males and females. 78th Annual CPDD Meeting (2015)
10. Wei C, Elston RC, and **Lu Q**. Detecting Association with Consideration of Genetic Heterogeneity. International Genetic Epidemiology Society Meeting (2015)
11. Wei C and **Lu Q**. A Generalized Similarity U Test for Multivariate Analysis of Sequencing Data. 64th American Society of Human Genetics Meeting (2014)
12. Li M, Gardiner JC, Breslau N, Anthony JC and **Lu Q**. Non-parametric Approach Identifies a New Gene-Gene Interaction Associated with Progression of Nicotine Dependence. 77th Annual CPDD Meeting (2014)
13. Wei C, Elston RC, and **Lu Q**. Detecting genetic heterogeneity in complex diseases with a weighted U statistic. 63th American Society of Human Genetics Meeting (2013)
14. Wei C, Li M, He Z, Vsevolozhskaya O, Schaid DJ and **Lu Q**. A Weighted U Statistic for Genetic Association Analyses of Sequencing Data. 22th International Genetic Epidemiology Society Meeting (2013)
15. **Lu Q**. A Clustered Mann-Whitney Approach for High-dimensional Family-based Genetic Association Studies 21th International Genetic Epidemiology Society Meeting (2012)
16. **Lu Q**, Wei C, Ye C, Elston R.C. A Mann-Whitney based whole genome-wide association study finds significant gene-gene interaction for Type 2 diabetes 60th American Society of Human Genetics Meeting (2010)
17. Li M, Fu W, and **Lu Q**. Mapping Multilocus Associations for Quantitative Traits with U-Statistics. 19th International Genetic Epidemiology Society Meeting (2010)

18. Wei C and **Lu Q**. Software for whole genome-wide gene-gene interactions analysis. 19th International Genetic Epidemiology Society Meeting (2010)
19. Ye C, Zhu J, **Lu Q**. A Clustered Optimal ROC Curve Method for Family-based Genetic Risk Prediction. 19th International Genetic Epidemiology Society Meeting (2010)
20. Schutte DL, Rivard J, Fisher RA, JD Bonner, C Wei, **Lu Q**, Friderici KH, Elfenbein JL, Wilch E, Schutte BC Linking gene discovery and translation in a large founder population in rural mid-Michigan using community-based participatory research methods. The International Society of Nurses Annual Conference (2010)
21. Ye C, Cui Y, Wei C, Elston R.C., Zhu J, and **Lu Q**. A non-parametric method for building predictive genetic tests on high-dimensional data, with an application to rheumatoid arthritis. ENAR Conference (2010)
22. Wei C and **Lu Q**. Trees assembling based Mann–Whitney test for large-scale genetic association study. ENAR Conference (2010)
23. **Lu Q**, Ye C, Zhu J, Elston R.C. Software for designing and forming predictive genetic tests. 59th American Society of Human Genetics Meeting (2009)
24. **Lu Q**, Cui Y, Ye C, Wei C, Elston R.C. A Bagging optimal ROC curve method for predictive genetic tests. 18th International Genetic Epidemiology Society Meeting (2009)
25. Bonner JD, Fisher RA, **Lu Q**, Friderici KH, Elfenbein JL, Schutte DL, Schutte BC. Isonymic analysis of an immigrant founder population in rural mid-michigan. 4th interanal meeting on genetics of complex diseases and isolated populations (2009)
26. Schutte BC, Fisher RA, Bonner JD, Wei C, **Lu Q**, Friderici KH, Elfenbein JL, Wilch E, Schutte DL. Pedigree and kinship analysis of a large founder population in rural mid-Michigan. 59th American Society of Human Genetics Meeting (2009)
27. **Lu Q**, Wang X, Song Y, Won S, Cui Y and Elston R.C. Using multiple genetic variants to predict an individual’s risk of Type 2 Diabetes. 16th Genetic Analysis Workshop (2008)
28. **Lu Q**, Obuchowski N, Won S, Zhu X, Elston R.C. Using the robust optimal receiver operating characteristic curve for predictive genetic tests. Competition for Roger W. Williams Award, 17th International Genetic Epidemiology Society meeting (2008)
29. **Lu Q**, Elston RC. Using the optimal ROC curve to design a predictive genetic test . 57th American Society of Human Genetics Meeting (2007)
30. Gray-McGuire C, Elston RC, **Lu Q**. Impact of data synthesis on the power and stability of association analysis: joint analysis of family and case-control data with a moving window approach. 57th American Society of Human Genetics Meeting (2007)
31. Parrado A, Weinsheimer S, **Lu Q**, Sinha M, Goddard KA, Ronkainen A, Niemela M, Jaaskelainen JE, Land S, Kuivaniemi H, Tromp G. Single Nucleotide Polymorphisms in the Kallikrein Genes Are Associated with Intracranial. 47th Annual Conference on Cardiovascular Disease Epidemiology and Prevention (2007)
32. **Lu Q**, Sinha R, Xing C, Elston RC. Mantel-Haenszel Approach to Case-Parents Triad Data. 15th International Genetic Epidemiology Society meeting (2006)
33. **Lu Q**, Song K, Xing C, Wang T, Xu Z, Elston RC. Detecting associated variants versus prediction from case-control data. 14th Genetic Analysis Workshop (2006)
34. Friel L, Kuivaniemi H, Gomez R, Goddard K, Nien JK, Tromp G, **Lu Q**, Xu Z, Behnke E, Solari M, Espinoza J, Kim CJ, Chaiworapongsa T, Kim YM, Lenk G, Volkenant K and Romero R. Genetic Predisposition for Preterm PROM: Results Of A Large Candidate-Gene Association Study of Mothers and Their Offspring. SMFM 26th Annual Scientific Meeting (2006)
35. Goddard KA, Tromp G, Romero R, Olson JM, **Lu Q**, Xu Z, Nien JK, Gomez R, Behnke E, Solari M, Espinoza J, Kim CJ, Santolaya J, Chaiworapongsa T, Kim YM, Lenk GM, Volkenant K and

Kuivaniemi H. Candidate-Gene Association Study of Mothers with Pre-Eclampsia and Their Offspring, Analyzing 758 SNPs in 187 Genes. 55th American Society of Human Genetics Meeting (2005)

36. Lu Q, Wang T, Xing C, Xu Z, Goddard KA. Generalized Multi-locus Score Statistics for the Case-control Association Studies. ENAR Conference (2005)
37. Xu Z, Lu Q, Elston RC, Iyengar S. Using locally weighted regression models to estimate familial correlations. ENAR Conference (2005)

TEACHING EXPERIENCE

Spring 2019	Introduction to Biostatistics II (EPI 809), 3 credits
Fall 2018	Biostatistical Modeling in Genomic Data Analysis (EPI 855), 3 credits
Spring 2018	Introduction to Biostatistics II (EPI 809), 3 credits
Fall 2017	Introduction to Statistical Genetics (STT855), Guest Lecture
Spring 2017	Introduction to Biostatistics II (EPI 809), 3 credits
Spring 2015	Biostatistical Modeling in Genomic Data Analysis (EPI 855), 3 credits
Spring 2015	Cancer Epidemiology (EPI 823), Guest Lecture
Spring 2014	Introduction to Biostatistics II (EPI 809), 3 credits
Spring 2013	Introduction to Biostatistics II (EPI 809), 3 credits
Spring 2013	Cancer Epidemiology (EPI 823), Guest Lecture
Spring 2012	Introduction to Biostatistics II (EPI 809), 3 credits
Fall 2011	Human Molecular Genetics (MMG 890), Guest Lecture
Fall 2011	Statistical Genetics (STT 855), Guest Lecture
Spring 2011	Introduction to Biostatistics II (EPI 809), 3 credits
Spring 2010	Introduction to Biostatistics II (EPI 809), 3 credits
Fall 2009	Epidemiology Exercise and Applications (EPI 811), Guest Lecturer
Fall 2009	Human Molecular Genetics (MMG 890), Guest Lecture
Fall 2008	Epidemiology Exercise and Applications (EPI 811), Guest Lecturer

REFEREEING FOR JOURNALS AND BOOK PROPOSAL

Journal of the American Statistical Association, Biometrics, Statistics and Probability Letters, Communications in Statistics – Theory and Methods, Statistics in Medicine, Journal of Biopharmaceutical Statistics, Biometrical Journal, Computational Statistics and Data Analysis, Statistica Neerlandica

Bioinformatics, BMC Bioinformatics, Briefings in Bioinformatics, Genetics, Genetic Epidemiology, Genomics, Journal of Computer Science and System Biology, Algorithms, international conference on Biomedical Engineering and Informatics, Theoretical and Applied Genetics, Journal of Theoretical Biology,

Trend in Genetics, Trends in Plant Science, PLoS Genetics, Human Genetics, Annals of Human Genetics, Current Genomics, PLoS One, Biological Procedures Online, Journal of Biomedicine and Biotechnology, Journal of Neurochemistry, Science China, European Neuropsychopharmacology, CRC Press, Psychiatry Research, Scientific Report, European Neuropsychopharmacology, The plant journal

SERVICE

Society and Funding Agency

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|---------|--|
| 06/2019 | Reviewer, NIH ZDA1 IXR-Q (07) S |
| 05/2019 | Reviewer, Rutherford Discovery Fellowship, New Zealand |
| 01/2019 | Reviewer, Unite Kingdom Medical Research Council |

10/2018 – Member, IGES communication committee
 03/2018 Reviewer, Pennsylvania Department of Health Formula Grants Final Performance Review – 17-18 Cycle B
 11/2017 Reviewer, Nazarbayev University Research Council in Astana, Kazakhstan
 10/2017 Reviewer, NIH ZRG1 PSE-W (55) R
 06/2017 Breakout group chair, NIDA Genetics Consortium Meeting
 03/2017 Reviewer, NIH ZRG1 PSE-P (55) R
 12/2016 – Associate Editor, BMC Genetics
 06/2016 Session Chair, 2016 ICSA China Statistics Conference
 1/2016 Guest Editor, Current Genomics
 11/2014 Reviewer, NIH ZRG1 PSE-R 80 A, Population Sciences and Epidemiology Area Review
 07/2014 Reviewer, National Research Foundation of Korea
 04/2013 Reviewer, NIH/CSR Early Career Reviewer Program
 04/2013 Reviewer, Pennsylvania Department of Health Final Performance Review
 03/2010 – Editorial Board, Frontiers in Applied Genetic Epidemiology
 03/2009 Board Member of the Program Committee for the 3rd International Conference on BioMedical Engineering and Informatics

Department, College, and University

03/2018 – 05/2019 Member, College Student Grievance/Complaint Hearing Panel
 11/2017 – 05/2019 Mentor, College Tenure System Mentor Program
 10/2017 – 05/2019 Member, Graduate Admissions and Performance Committee, Department of Epidemiology and Biostatistics, Michigan State University
 09/2014 – 08/2018 Member, Reappointment, Promotion and Tenure (RPT) Committee, Department of Epidemiology and Biostatistics, Michigan State University
 12/2016 – 12/2017 Neurodegenerative Faculty Search Committee, Department of Epidemiology and Biostatistics, Michigan State University
 09/2014 – 10/2017 Member, Student Recruitment Committee, Department of Epidemiology and Biostatistics, Michigan State University
 01/2015 – 10/2017 Member, AWARD Committee, Department of Epidemiology and Biostatistics, Michigan State University
 09/2014 – 12/2014 Member, Computational Biology Initiative Search Committee
 01/2012 – 03/2014 Member, Graduate Admissions and Performance Committee, Department of Epidemiology and Biostatistics, Michigan State University
 08/2009 – 08/2011 Member, Reappointment, Promotion and Tenure (RPT) Committee, College of Human Medicine, Michigan State University

STUDENTS/POSTDOC ADVISING

Advisor or Co-advisor

Postdoc Fellow

Yalu Wen	Ph.D.	Senior Lecturer, Department of Statistics, University of Auckland
Olga Vsevolozhskaya	Ph.D.	Assistant Professor, University of Kentucky (Co-advise with Jim Anthony)
Xiaoxi Shen	Ph.D.	Ongoing

Ph.D. Students

Changshuai Wei	Ph.D.	Machine Learning Scientist, Amazon
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Li Ming	Ph.D.	Associate Professor, Indiana University (Co-advise with Wenjiang Fu)
Chengyin Ye	Ph.D.	Assistant Professor, Hongzhou Normal University in China (Co-advise with Jun Zhu)
Sneha Jadhav	Ph.D.	Assistant Professor, Wake Forest University (Co-advise with Hira L. Koul)
Maria Parker	Ph.D.	Postdoc Fellow, University of Vermont (Co-advise with Jim Anthony)
Xiaoran Tong	Ph.D.	Ongoing
Shan Zhang	Ph.D.	Ongoing
Jinghang Lin	Ph.D.	Ongoing
Chang Jiang	Ph.D.	Ongoing
Di Wu	Ph.D.	Ongoing (Co-advise with Chenxi Li)

Master Students

Yuan Zhou	M.S.	Ongoing
Tengfei Ma	M.S.	Defended
Junjie Han	M.S.	Defended

Rotation Students

Melanie Noell Bernard	Ph.D.	2/16/2018-5/8/2018
Scott Funkhouser	Ph.D.	9/3/2013-11/8/2013
Yi Liang	Master	1/1/2019-05/31/2019
Rongzi Liu	Master	5/1/2019-

Committee Member for Other MSU Students

Ph.D. Students

Kipling Bohnert	Ph.D.	Department of Epidemiology and Biostatistics (Defended)
Yalu Wen	Ph.D.	Department of Epidemiology and Biostatistics (Defended)
John Troost	Ph.D.	Department of Epidemiology and Biostatistics (Defended)
Nhan Thi Ho	Ph.D.	Department of Epidemiology and Biostatistics (Defended)
Cen Wu	Ph.D.	Department of Statistics and Probability (Defended)
Fabian Fiestas	Ph.D.	Department of Epidemiology and Biostatistics (Defended)
Gao Bin	Ph.D.	Department of Statistics and Probability (Defended)
WenZhao Yang	Ph.D.	Department of Animal Science (Defended)
Chunyu Chen	Ph.D.	Department of Animal Science (Defended)
Hsueh-Han Yeh	Ph.D.	Department of Epidemiology and Biostatistics (Defended)
Pei Geng	Ph.D.	Department of Statistics and Probability (Defended)
Jingyi Zhang	Ph.D.	Department of Statistics and Probability (Defended)
Karl Alcover	Ph.D.	Department of Epidemiology and Biostatistics (Defended)
Thien Minh Le	Ph.D.	Department of Statistics and Probability (Ongoing)

Master Students

Victor Cruz	M.S.	Department of Epidemiology and Biostatistics (Defended)
Mallory Doan	M.S.	Department of Epidemiology and Biostatistics (Defended)
Manuel Catacora	M.S.	Department of Epidemiology and Biostatistics (Defended)
Sebastian Casiro	M.S.	Department of Animal Science (Defended)

Alyssa Vanderziel M.S. Department of Epidemiology and Biostatistics (Defended)

Training Faculty on the T32 Programs

T32DA021129 (J. Anthony, PI) 07/2012-06/2017
NIH/NIDA

Training Program in Drug Dependence Epidemiology

T32OD011127 (Vilma Yuzbasiyan-Gurkan, PI) 07/2011-04/2014
NIH/OD

Building Researchers on the Diverse Foundation of a Veterinary Medical Education

T32 OD011167 (Vilma Yuzbasiyan-Gurkan, PI) 07/2011-04/2016
NIH/OD

Veterinary Research Student Training Program: Building Capacity

Training Faculty on the F31 NRSA Program

Elizabeth Shewark Ph.D. Department of Psychology, Pennsylvania State University

PROFESSIONAL MEMBERSHIP

American Society of Human Genetics
International Genetic Epidemiology Society
American Statistical Association