

CURRICULUM VITA

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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
Member, Center for Addiction Research & Education
Member, University of Florida Health Cancer Center
Member, Center for Genetic Epidemiology and Bioinformatics
- 04/2021- present Co-chair, University of Florida Cancer AI Working Group
- 01/2020-present Adjunct ***Professor***, Department of Epidemiology and Biostatistics, Michigan State University
- 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

- 2022 Outstanding Teacher Award, Department of Biostatistics, University of Florida
- 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

PATENT

1. **Qing Lu**, Shan Zhang, and Tingting Hou. Functional Deep Neural Network for High-dimensional Data Analysis. United States Patent Application Publication US-2021-0313065-A1; Oct 7th, 2021.
2. **Qing Lu**, Xiaoxi Shen, and Tingting Hou. High Dimensional and Ultrahigh Dimensional Data Analysis with Kernel Neural Networks (PCT Patent Application PCT/US2021/072811; Dec 8th, 2021).

SELECTED PEER REVIEWED PUBLICATIONS (current/former trainees)

1. Liu R, Li C, **Lu Q**. Neural-network transformation models for counting processes. *Stat. Anal. Data Min.: ASA Data Sci. J.*15 (2022), 322– 338.
2. Shen X, Jiang C, Sakhanenkob L, **Lu Q**. A goodness-of-fit test based on neural network sieve estimators. *Statistics & Probability Letters*. 2021; 174: 109100.
3. Wen Y and **Lu Q**. An optimal kernel-based multivariate U-statistic to test for associations with multiple phenotypes. *Biostatistics*. 2020 Oct 26; kxaa049.
4. Jadhav S, Koul H, **Lu Q**. Dependent Generalized Functional Linear Models. *Biometrika* 2017;104(4):987-994
5. 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
6. Wei C and **Lu Q**. A generalized association test based on U statistics. *Bioinformatics*. 2017; 33(13):1963-1971. PMID: 28334117
7. 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

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. Liu L, Meng Q, Weng C, **Lu Q**, Wang T, Wen Y. Explainable deep transfer learning model for disease risk prediction using high-dimensional genomic data. *PLoS Comput Biol*. 2022 Jul 15;18(7):e1010328. doi: 10.1371/journal.pcbi.1010328. eCollection 2022 Jul.
2. Wen Y and **Lu Q**. An optimal kernel-based multivariate U-statistic to test for associations with multiple phenotypes. *Biostatistics*. 2022 Jul 18;23(3):705-720.
3. Tang M, Hou T, Tong X, Shen X, Zhang X, Wang T, **Lu Q**. Fast heritability estimation based on MINQUE and batch training. *Brief Bioinform*. 2022 May 13;23(3):bbac115.
4. Jami ES, Hammerschlag AR, Ip HF, Allegrini AG, Benyamin B, Border R, Diemer EW, Jiang C, Karhunen V, Lu Y, **Lu Q**, Mallard TT, Mishra PP, Nolte IM, Palviainen T, Peterson RE, Sallis HM, Shabalin AA, Tate AE, Thiering E, Vilor-Tejedor N, Wang C, Zhou A, Adkins DE, Alemany S, Ask H, Chen Q, Corley RP, Ehli EA, Evans LM, Havdahl A, Hagenbeek FA, Hakulinen C, Henders AK, Hottenga JJ, Korhonen T, Mamun A, Marrington S, Neumann A, Rimfeld K, Rivadeneira F, Silberg JL, van Beijsterveldt CE, Vuoksima E, Whipp AM, Tong X, Andreassen OA, Boomsma DI, Brown SA, Burt SA, Copeland W, Dick DM, Harden KP, Harris KM, Hartman CA, Heinrich J, Hewitt JK, Hopfer C, Hypponen E, Jarvelin MR, Kaprio J, Keltikangas-Järvinen L, Klump KL, Krauter K, Kujala R, Larsson H, Lehtimäki T, Lichtenstein P, Lundström S, Maes HH, Magnus P, Munafò MR, Najman JM, Njølstad PR, Oldehinkel AJ, Pennell CE, Plomin R, Reichborn-Kjennerud T, Reynolds C, Rose RJ, Smolen A, Snieder H, Stallings M, Standl M, Sunyer J, Tiemeier H, Wadsworth SJ, Wall TL, Whitehouse AJO, Williams GM, Ystrøm E, Nivard MG, Bartels M, Middeldorp CM. Genome-wide Association Meta-analysis of Childhood and Adolescent Internalizing Symptoms. *J Am Acad Child Adolesc Psychiatry*. 2022 Jul;61(7):934-945.
5. Lin, J, Tong, X, Li, C, and **Lu, Q**. Expectile Neural Networks for Genetic Data Analysis of Complex Diseases. *IEEE/ACM Trans Comput Biol Bioinform* 2022 Jan 27;PP
6. Liu R, Li C, **Lu Q**. Neural-network transformation models for counting processes. *Anal. Data Min.: ASA Data Sci. J.*15 (2022), 322– 338.
7. Wu D, Li C, **Lu Q**. Multi-marker genetic association and interaction tests with interval-censored survival outcomes. *Genet Epidemiol*. 2021 Dec;45(8):860-873.

8. Shen X, Wen Y, Cui Y, **Lu Q**. A conditional autoregressive model for genetic association analysis accounting for genetic heterogeneity. *Stat Med.* 2022 Feb 10;41(3):517-542.
9. Shen X, Jiang C, Sakhanenkob L, **Lu Q**. A goodness-of-fit test based on neural network sieve estimators. *Statistics & Probability Letters. Stat Probab Lett.* 2021 Jul;174:109100.
10. Wu C, Zhu J, King A, Tong X, **Lu Q**, Park JY, Wang L, Gao G, Deng HW, Yang Y, Knudsen KE, Rebbeck TR, Long J, Zheng W, Pan W, Conti DV, Haiman CA, Wu L. Novel strategy for disease risk prediction incorporating predicted gene expression and DNA methylation data: a multi-phased study of prostate cancer. *Cancer Commun (Lond).* 2021 Dec;41(12):1387-1397.
11. Fan S, Zhao Z, Zhang Y, Yu H, Zheng C, Huang X, Yang Z, Xing M, **Lu Q**, Luo Y. Probability calibration-based prediction of recurrence rate in patients with diffuse large B-cell lymphoma. *BioData Min.* 2021 Aug 13;14(1):38.
12. Ip HF, van der Laan CM, Krapohl EML, Brikell I, Sánchez-Mora C, Nolte IM, St Pourcain B, Bolhuis K, Palviainen T, Zafarmand H, Colodro-Conde L, Gordon S, Zayats T, Aliev F, Jiang C, Wang CA, Saunders G, Karhunen V, Hammerschlag AR, Adkins DE, Border R, Peterson RE, Prinz JA, Thiering E, Seppälä I, Vilor-Tejedor N, Ahluwalia TS, Day FR, Hottenga J-J, Allegrini AG, Rimfeld K, Chen Q, Lu Y, Martin J, Soler Artigas M, Rovira P, Bosch R, Español G, Ramos Quiroga JA, Neumann A, Ensink J, Grasby K, Morosoli JJ, Tong X, Marrington S, Middeldorp C, Scott JG, Vinkhuyzen A, Shabalin AA, Corley R, Evans LM, Sugden K, Alemany S, Sass L, Vinding R, Ruth K, Tyrrell J, Davies GE, Ehli EA, Hagenbeek FA, De Zeeuw E, Van Beijsterveldt TCEM, Larsson H, Snieder H, Verhulst FC, Amin N, Whipp AM, Korhonen T, Vuoksima E, Rose RJ, Uitterlinden AG, Heath AC, Madden P, Haavik J, Harris JR, Helgeland Ø, Johansson S, Knudsen GPS, Njolstad PR, **Lu Q**, Rodriguez A, Henders AK, Mamun A, Najman JM, Brown S, Hopfer C, Krauter K, Reynolds C, Smolen A, Stallings M, Wadsworth S, Wall T, Silberg JL, Miller A, Keltikangas-Järvinen L, Hakulinen C, Pulkki-Råback L, Havdahl A, Magnus P, Raitakari OT, Perry JRB, Llop S, Lopez-Espinosa M-J, Bønnelykke K, Bisgaard H, Sunyer J, Lehtimäki T, Arseneault L, Standl M, Heinrich J, Boden J, Pearson J, Horwood J, Kennedy M, Poulton R, Eaves LJ, Maes HH, Hewitt J, Copeland WE, Costello EJ, Williams GM, Wray N, Järvelin M-R, McGue M, Iacono W, Caspi A, Moffitt TE, Whitehouse A, Pennell CE, Klump KL, Burt SA, Dick DM, Reichborn-Kjennerud T, Martin NG, Medland SE, Vrijkkotte T, Kaprio J, Tiemeier H, Davey Smith G, Hartman CA, Oldehinkel AJ, Casas M, Ribasés M, Lichtenstein P, Lundström S, Plomin R, Bartels M, Nivard MG and Boomsma DI. Genetic Association Study of Childhood Aggression across raters, instruments and age. *Translational Psychiatry* 2021 Jul 30;11(1):413.
13. Palmer RHC, Johnson EC, Won H, Polimanti R, Kapoor M, Chitre A, Bogue MA, Benca-Bachman CE, Parker CC, Verma A, Reynolds T, Ernst J, Bray M, Kwon SB, Lai D, Quach BC, Gaddis NC, Saba L, Chen H, Hawrylycz M, Zhang S, Zhou Y, Mahaffey S, Fischer C, Sanchez-Roige S, Bandrowski A, **Lu Q**, Shen L, Philip V, Gelernter J, Bierut LJ, Hancock DB, Edenberg HJ, Johnson EO, Nestler EJ, Barr PB, Prins P, Smith DJ, Akbarian S, Thorgeirsson T, Walton D, Baker E, Jacobson D, Palmer AA, Miles M, Chesler EJ, Emerson J, Agrawal A, Martone M, Williams RW. Integration of evidence across human and model organism studies: A meeting report. *Genes Brain Behav.* 2021 Apr 23;20(6):e12738.
14. Fan S, Zhao Z, Yu H, Wang L, Zheng C, Huang X, Yang Z, Xing M, **Lu Q**, Luo Y. Applying probability calibration to ensemble methods to predict 2-year mortality in patients with DLBCL.

BMC Med Inform Decis Mak. 2021 Jan 7;21(1):14.

15. Ma T, Chen H, **Lu Q**, Tong X. Polygenic Risk for Insomnia in Adolescents of Diverse Ancestry. *Front Genet*. 2021 May 10;12:654717.
16. Wu C, Wu L, Wang J, Lin L, Li Y, **Lu Q**, Deng HW. Systematic identification of risk factors and drug repurposing options for Alzheimer's disease. *Alzheimers Dement (N Y)*. 2021 Mar 3;7(1):e12148.
17. Li C, Wu D, **Lu Q**. Set-based genetic association and interaction tests for survival outcomes based on weighted V statistics. *Genet Epidemiol*. 2021 Feb;45(1):46-63.
18. TZ Movsas, IH Gewolb, N Paneth, **Q Lu**, A Muthusamy. The association between high levels of luteinizing hormone and proliferative retinopathy of prematurity in female preterm infants. *Journal of American Association for Pediatric Ophthalmology and Strabismus* 2020; S1091-8531(20) 30106-3.
19. Wen Y and **Lu Q**. Multi-kernel linear mixed model with adaptive lasso for complex phenotype prediction. *Stat Med*. 2020; 39(9):1311-1327.
20. Li J, **Lu Q**, Wen Y Multi-kernel linear mixed model with adaptive lasso for prediction analysis on high-dimensional multi-omics data. *Bioinformatics*. 2020; 36(6):1785-1794.
21. Movsas TZ, Paneth N, Gewolb IH, **Lu Q**, Cavey G, Muthusamy A. The postnatal presence of human chorionic gonadotropin in preterm infants and its potential inverse association with retinopathy of prematurity. *Pediatr Res*. 2020; 87(3):558-563.
22. 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*. 2020; 29 (1), 44-56
23. Schwartz L, **Lu Q**, Liu R, Kornreich R, Edelman L, et al. Estimating the Prevalence of the Adult Polyglucosan Body Disease at the Gene Level for Ashkenazi Jews in the United States. *American J Rare Dis Diagn Ther*. 2020;3(1): 004-008
24. 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)*. 2020 May 26;42(2):429-434.
25. Geng P, Tong X, **Lu Q**. An integrative U method for joint analysis of multi-level omic data. *BMC genetics*. 2019; 20(1):40.
26. 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;10:448.
27. Lan T, Yang B, Zhang X, Wang T, **Lu Q**. Statistical Methods and Software for Substance Use and Dependence Genetic Research. *Curr Genomics*. 2019;20(3):172-183.
28. 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.
29. 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;19(12):935-947.
 30. 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.
 31. 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.
 32. Shen X and **Lu Q**. Joint analysis of genetic and epigenetic data using a conditional autoregressive model. *BMC Genet.* 2018;19(Suppl 1):71.
 33. 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.
 34. Jadhav S, Koul H, **Lu Q**. Dependent Generalized Functional Linear Models. *Biometrika* 2017;104(4):987-994
 35. 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
 36. 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
 37. 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
 38. 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
 39. Wei C and **Lu Q**. A generalized association test based on U statistics. *Bioinformatics.* 2017; 33(13):1963-1971. PMID: 28334117
 40. 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
41. **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
 42. **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
 43. **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
 44. **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
 45. **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
 46. **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
 47. **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
 48. **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
 49. **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
 50. **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
 51. **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.
 52. **Wen Y, Lu Q**. Risk Prediction Models for Oral Clefts allowing for Phenotypic Heterogeneity. *Front Genet*. 2015; 6:264. PMID: 26322076
 53. **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

54. Wei C and Lu Q. software for genome-wide gene-gene interaction analysis *BMC Genetics* 2014;15(1):101. PMID: 25318532
55. 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
56. 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
57. 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
58. 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
59. Wen Y, Lu Q. Analysis of gene-gene interactions underlying human disease. *eLS* 2014 DOI: 10.1002/9780470015902.a0022498
60. 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
61. 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
62. 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
63. Ye C and Lu Q. Bridge: a GUI Software for Genetic Risk Prediction. *BMC Genet.* 2013;14:122 PMID: 24359333
64. 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
65. 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
66. Li M, Wen Y, Lu Q, and Fu WJ An Imputation Approach for Oligonucleotide Microarray. *PLoS One.* 2013;8(3):e58677. PMID: 23505547
67. 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

68. 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
69. 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
70. 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
71. **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
72. Wei C, Anthony JC, **Lu Q**. Genome-environmental risk assessment of cocaine dependence. *Front Genet.* 2012;3:83. PMID: 22629285
73. 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
74. 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
75. 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
76. 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
77. 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
78. 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
79. 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
80. 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
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- AAA1 susceptibility locus for abdominal aortic aneurysms on chromosome 19. *BMC Med Genet.* 2011; 12(1):14. PMID: 21247474
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83. **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
84. **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
85. 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
86. 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
87. 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
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90. **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
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93. 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

94. 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
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96. 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
97. Ogata T, Gregoire L, Goddard KA, Skunca M, Tromp G, Lancaster WD, Parrado AR, **Lu Q**, Shibamura H, Sakalihasan 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
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102. 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
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104. 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
105. **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

106. 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
107. 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

108. **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
109. 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

RESEARCH SUPPORT

Ongoing Research Support

1R01DA043501-01(Q. Lu, PI) 09/2017-05/2023 (NCE)

NIH/NIDA

Computational Efficient Statistical Tools for Analyzing Substance Dependence Sequencing Data

Role: PI

R56AG075803 (C. Li, PI) 09/2022 – 09/2023

NIH/NIA

Survival genetics methods for detecting sex-dependent genetic effects on Alzheimer’s disease

Role: Subcontract PI

R03DE032357 (C. Li, PI) 09/2022 – 09/2024

NIH/NIDCR

Efficient methods for genome-wide survival analysis of early childhood caries

Role: Subcontract PI

R01HL151659 (Y.Gong, PI) 08/2021 – 08/2025

NIH/NHLBI/NCI

A multi-omics evaluation of carfilzomib-related cardiotoxicity in multiple myeloma patients.

Role: Co-investigator

W81XWH-21-SCIRP-CTA (E. Fox, PI) 09/2022 – 09/2026

DOD

Genetic biomarkers of intermittent hypoxia-induced respiratory motor plasticity in chronic SCI

Role: Co-investigator

Completed Research Support

1R01LM012848-01 (Q. Lu, PI) 07/2018-06/2022

NIH/NLM
Methods and Software for High-dimensional Risk Prediction Research
Role: PI

OR_DRD_AI2020 (Q. Lu, PI) 12/2020-12/2021
UF/Artificial Intelligence Research Catalyst Fund
A Kernel Neural Network for High-dimensional Genomic Risk Prediction
Role: PI

R56DE030437 (C. Li, PI) 08/2021-08/2022
NIH/NIDCR
Survival genetics methods for genetic association studies of early childhood caries
Role: Subcontract PI

R56DE030538 (Y.Gong, PI) 09/2021 – 08/2022
NIH/NIDCR
Toward a Precision Medicine Approach to Medication-related Osteonecrosis of the Jaw.
Role: Co-investigator

2020 CTSI Rapid-Response Translational Research Projects 06/2020-12/2020
Genomics and Pharmacogenomics of susceptibility and severity of COVID-19 in the UK Biobank
Role: Co-investigator

GF13666 (S. Burt, PI) 09/2016-08/2019
John Templeton Foundation
Understanding “what could be”: Heritability in a randomized twin design
Role: Co-investigator

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) Hunt for a Cure A Comprehensive Search of Genetic Markers Promising for Gene Therapies of PA Infection in Cystic Fibrosis Patients Role: Co-Investigator | 09/2013-09/2014 |
| 08-IRGP-1519 (Q. Lu, PI) 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 | 12/2008-06/2010 |
| 5P41RR003655 sub-project ID: 5675, 6729, 7635 (Q. Lu, Sub-Project PI) NIH/NCRR Using the Optimal Receive Operating Characteristic Curve Role: Sub-Project PI | 08/2008-07/2011 |
| SPG Award (Brian Schutte, PI) MSU Strategic Partnership Grants (SPG) Community-based cooperative for Studies Across Generations (CoSAGE) Role: Co-Investigator | 06/2009-05/2012 |
| FACT Award (Debra Schutte, PI) MSU/Families and Communities Together Coalition (FACT) CoSAGE: Cooperative Study Across GEnerations Role: Co-Investigator | 06/2009-05/2011 |

INVITED PRESENTATIONS

1. "A Kernel-Based Neural Network for High-dimensional Risk Prediction on Massive Genetic Data, 2021 Statistics colloquium at Florida State University
2. "A Kernel Neural Network for High-dimensional Genomic Risk Prediction", The Spring 2021 HiPerGator Symposium
3. "A Kernel-Based Neural Network for High-dimensional Genetic Data Analysis", 2020 ICSA meeting (2020)
4. "A Kernel-Based Neural Network for High-dimensional Genetic Risk Prediction Analysis" The University of Auckland (2019)
5. "A Kernel-Based Neural Network for High-dimensional Genetic Risk Prediction Analysis" the University of Tennessee Health Science Center (2019)
6. "A Kernel-Based Neural Network for High-dimensional Risk Prediction on Massive Genetic Data" Rutgers University (2018)
7. "A Kernel-Based Neural Network for High-dimensional Risk Prediction on Massive Genetic Data" University of Florida (2018)
8. "A conditional autoregressive model for genetic association analysis of sequencing data", ICSA meeting, Qingdao, China (2018)
9. "A New Artificial Intelligence Tool for Substance Use and Dependence Research", NIDA Genetics Consortium Meeting, Bethesda, Maryland (2018)

10. "A generalized association test based on U statistics", Institute of Mathematical Statistics meeting, Nanning, China (2017)
11. "A Generalized Similarity U Test for Multivariate Analysis of Sequencing Data" ENAR Conference, Austin, Texas (2016).
12. "A Generalized Similarity U Test for Multivariate Analysis of Sequencing Data" Department of Biostatistics, University of Michigan, Michigan (2016)
13. "Statistical Approaches for High-Dimensional Family-Based Genetic Association Studies" (March, 2012) Statistical Colloquium, Michigan State University, East Lansing, MI.
14. "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.
15. "Predictive Genetic Testing in the Age of Genome-Wide Association Studies"(July, 2010), First Joint Biostatistics Symposium, Beijing, China.
16. "Predictive Genetic Testing in the Age of GWAS"(Dec, 2009), MGI seminar, Michigan State University, East Lansing, MI.
17. "Designing and Forming Predictive Genetic Tests Using Optimal Receiver Operating Characteristic Curve"(Jan, 2008), Washington University, St. Louis, Missouri.
18. "Designing and Forming Predictive Genetic Tests Using Optimal Receiver Operating Characteristic Curve"(Jan, 2008), Boston University, Boston, Massachusetts
19. "Designing and Forming Predictive Genetic Tests Using Optimal Receiver Operating Characteristic Curve"(Jan, 2008), Wake Forest, Winston-Salem, North Carolina
20. "Designing and Forming Predictive Genetic Tests Using Optimal Receiver Operating Characteristic Curve"(Feb, 2008), Mayo Clinic, Rochester, Minnesota.
21. "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, Zhou Yu, Chen H, Chitre AS, Trey I, Palmer AA, and **Lu Q**. "Transferring the Knowledge between Different Populations by Using a Functional Deep Neural Network". NIDA genetic consortium meeting (2020)
2. 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)
3. Tong X, Shen X and **Lu Q**. Kernel based genetic meta-analysis using batch training. JSM conference (2018)
4. Shen X, Tong X and **Lu Q**. A Kernel-Based Neural Network for High-dimensional Genetic Risk Prediction Analysis. JSM conference (2018)
5. Geng P, Zhang S and **Lu Q**. Neural network with functional smoothing and its application to genetic analysis. JSM conference (2018)
6. Shen X and **Lu Q**. A Conditional Autoregressive Model for Genetic Association Analysis of Sequencing Data. JSM conference (2016)
7. Li M, He Z and **Lu Q**. A random field based method for association analysis of family-based sequencing data. ICSA conference (2016)
8. Geng P and **Lu Q**. Functional U Test for Joint Effect of SNPs and Gene Expression in Association Study. ENAR Conference (2016)
9. Jadhav S, Koul H, **Lu Q**. Dependent Generalized Functional Linear Models. ENAR Conference (2016)
10. 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)

11. Wei C, Elston RC, and **Lu Q** Detecting Association with Consideration of Genetic Heterogeneity. International Genetic Epidemiology Society Meeting (2015)
12. Wei C and **Lu Q**. A Generalized Similarity U Test for Multivariate Analysis of Sequencing Data. 64th American Society of Human Genetics Meeting (2014)
13. 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)
14. 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)
15. Wei C, Li M, He Z, Vsevolzhskaya O, Schaid DJ and **Lu Q**. A Weighted U Statistic for Genetic Association Analyses of Sequencing Data. 22th International Genetic Epidemiology Society Meeting (2013)
16. **Lu Q**. A Clustered Mann-Whitney Approach for High-dimensional Family-based Genetic Association Studies 21th International Genetic Epidemiology Society Meeting (2012)
17. **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)
18. Li M, Fu W, and **Lu Q**. Mapping Multilocus Associations for Quantitative Traits with U-Statistics. 19th International Genetic Epidemiology Society Meeting (2010)
19. Wei C and **Lu Q**. Software for whole genome-wide gene-gene interactions analysis. 19th International Genetic Epidemiology Society Meeting (2010)
20. 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)
21. 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)
22. 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)
23. Wei C and **Lu Q**. Trees assembling based Mann–Whitney test for large-scale genetic association study. ENAR Conference (2010)
24. **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)
25. **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)
26. 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)
27. 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)
28. **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)
29. **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)

30. **Lu Q**, Elston RC. Using the optimal ROC curve to design a predictive genetic test . 57th American Society of Human Genetics Meeting (2007)
31. 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)
32. 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)
33. **Lu Q**, Sinha R, Xing C, Elston RC. Mantel-Haenszel Approach to Case-Parents Triad Data. 15th International Genetic Epidemiology Society meeting (2006)
34. **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)
35. 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)
36. 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)
37. **Lu Q**, Wang T, Xing C, Xu Z, Goddard KA. Generalized Multi-locus Score Statistics for the Case-control Association Studies. ENAR Conference (2005)
38. Xu Z, **Lu Q**, Elston RC, Iyengar S. Using locally weighted regression models to estimate familial correlations. ENAR Conference (2005)

TEACHING EXPERIENCE

| | |
|-------------|---|
| Fall 2022 | Introduction to Statistical Learning, 3 credits |
| Spring 2022 | Statistical Learning with Applications in Health Sciences, 3 credits |
| Fall 2021 | Introduction to Statistical Learning, 3 credits |
| Spring 2021 | Statistical Learning with Applications in Health Sciences, 3 credits |
| Summer 2020 | Introduction to Applied Survival Analysis, 3 credits |
| Spring 2020 | Statistical Learning with Applications in Health Sciences, 3 credits |
| 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

07/2022 Reviewer, NIH IRAP study section
 03/2022 Reviewer, NIH ZRG1 PSE-B (02)
 05/2021 Reviewer, Rutherford Discovery Fellowship, New Zealand
 03/2021 Reviewer, NIH BGES study section
 2021 – Associate Editor, BMC Genomics
 2020 – Scientific Advisory Board member, Adult Polyglucosan Body Disease Research Foundation
 2020 Reviewer, NIH ZDA1 TXT-V (16) R
 2020 Reviewer, NIH BMRD study section
 11/2019 Reviewer, NIH ZDA1 IXR-Q (19)S
 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
 03/2017 Reviewer, NIH ZRG1 PSE-P (55) R
 2016–2020 Associate Editor, BMC Genetics
 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 (University of Florida)

- 01/2020 – Member, Admission Committee, Department of Biostatistics
07/2020 Member, Bioinformatics Faculty Search Committee, Division of Quantitative Sciences, University of Florida Health Cancer Center
10/2020 Member, Health Data Science program committee
03/2011 – Member, AI Determinants of Health Search Committee
03/2011 – Member, AI Corporate and Foundation Programs Committee
04/2011 – Co-Chair, Cancer AI Workgroup

Department, College, and University (Michigan State 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
09/2014 – 08/2018 Member, Reappointment, Promotion and Tenure (RPT) Committee, Department of Epidemiology and Biostatistics
12/2016 – 12/2017 Neurodegenerative Faculty Search Committee, Department of Epidemiology and Biostatistics
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. | Assistant Professor, Texas State University |

Ph.D. Students

- | | | |
|----------------|-------|---|
| Li Ming | Ph.D. | Associate Professor, Indiana University (Co-advise with Wenjiang Fu) |
| Changshuai Wei | Ph.D. | Principal Applied Researcher, Expedia |
| 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) |
| Xiaoran Tong | Ph.D. | Research Assistant Professor, University of Kentucky |
| Shan Zhang | Ph.D. | Staff Fellow, FDA |

| | | |
|--------------|-------|------------------------|
| Jinghang Lin | Ph.D. | Postdoc Fellow at Yale |
| Chang Jiang | Ph.D. | Ongoing |
| Tingting Hou | Ph.D. | Ongoing |
| Rongzi Liu | Ph.D. | Ongoing |
| Yuan Zhou | Ph.D. | Ongoing |

Master Students

| | | |
|------------|------|----------|
| 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 |

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

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|--|-----------------|
| T32DA021129 (J. Anthony, PI) | 07/2012-06/2017 |
| NIH/NIDA | |
| Training Program in Drug Dependence Epidemiology | |
| T32OD011127 (Wilma 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)
NIH/OD

07/2011-04/2016

Veterinary Research Student Training Program: Building Capacity

T32 (Julie Johnson, PI)
NIH/NIGRI

07/2020-

Program for Applied Research and Development in Genomic Medicine

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