

Curriculum Vitae

Qiongshi Lu

Department of Biostatistics and Medical Informatics
University of Wisconsin-Madison
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Education

2012-2017 **Ph.D. in Biostatistics**, Yale University, New Haven, CT
2008-2012 **B.S. in Mathematics**, Tsinghua University, Beijing, China

Positions and Employment

2017- **Assistant Professor**
Department of Biostatistics and Medical Informatics
University of Wisconsin-Madison, Madison, WI

2014-2017 **Research Assistant**
Center for Statistical Genomics and Proteomics, Yale University, New Haven, CT
Mentor: Dr. Hongyu Zhao

2013-2016 **Teaching Assistant**
Yale School of Public Health, New Haven, CT

2011-2012 **Research Assistant**
Peking University Health Science Center, Beijing, China
Mentor: Dr. Tingting Li

2011-2012 **Research Assistant**
MOE Key Laboratory of Bioinformatics, Tsinghua University, Beijing, China
Mentor: Dr. Xuegong Zhang

Fellowships and Awards

Honors and Awards

2017 Liberty Mutual Insurance Student Poster Award, the 31st New England Statistics Symposium
2016 ACGA Trainee Award - Predoctoral Basic Sciences
2016 Best Student Poster Award, the 30th New England Statistics Symposium
2015 ASHG/Charles J. Epstein Trainee Award for Excellence in Human Genetics Research - Finalist
2012 Outstanding Graduate of Tsinghua University
2011 Top Ten Outstanding Student, Tsinghua University Student Art Troupe
2011 Torchbearer, The 26th Summer Universiade, Shenzhen, China

Fellowships

2012-2014 China Scholarship Council-Yale World Scholarship
2010-2012 Tsinghua Xuetang Mathematics Program
2010 National Scholarship, Ministry of Education of the People's Republic of China
2010 Tsinghua Scholarship for Excellence in Academic Performance

2009, 2011 Tsinghua Scholarship for Excellence in Extracurricular Work

2009, 2010 Tsinghua Scholarship for Excellence in Literature and Art

Travel Awards

2016 Travel Fellowship, Alzheimer's Association International Conference 2016

2016 Conference Travel Fellowship, Yale Graduate Student Assembly

Publications

* junior author with equal contribution

† senior author with equal contribution

Submitted Papers

[15] **Lu Q.***, Powles R.*, Abdallah S., Ou D., Wang Q., Hu Y., Lu Y., Liu W., Mukherjee S., Crane P., Zhao H. **Systematic tissue-specific functional annotation of the human genome highlights immune-related DNA elements for late-onset Alzheimer's disease.** (manuscript available on *bioRxiv*)

Winner of 2016 ACGA Trainee Award - Predoctoral Basic Sciences

[14] **Lu Q.**, Li B., Ou D., Erlendsdottir M., Powles R., Jiang T., Hu Y., Chang D., Jin C., Dai W., He Q., Liu Z., Mukherjee S., Crane P., Zhao H. **A powerful approach to estimating annotation-stratified genetic covariance using GWAS summary statistics.** (manuscript available on *bioRxiv*)

Winner of Liberty Mutual Insurance Student Poster Award, the 31st New England Statistics Symposium

[13] Jin S.*, Homsy J.*, Zaidi S.*, **Lu Q.**, Morton S., DePalma S., Zeng X., Qi H., Chang W., Hung W., Sierant M., Haider S., Zhang J., Knight J., Bjornson R., Castaldi C., Tikhonova I., Bilguvar K., Mane S., Sanders S., Mital S., Russell M., Gaynor W., Deanfield J., Giardini A., Porter G., Srivastava D., Lo C., Shen Y., Watkins S., Yandell M., Yost J., Tristani-Firouzi M., Newburger J., Roberts A., Kim R., Zhao H., Kaltman J., Goldmuntz E., Chung W., Seidman J., Gelb B., Seidman C.†, Lifton R.†, Brueckner M.† **Contribution of rare transmitted and *de novo* variants among 2,871 congenital heart disease probands.**

[12] Zhao B., Than M., Schulman V., Bai Y., **Lu Q.**, Zhang J., Arroyo J., Choi M., Igelman A., Thakral D., Bi M., Stiegler A., Nelson-Williams C., Boffa D., Boggon T., Gassaway B., Rinehart J., Zhao H., Overton J., Mane S., Schlessinger J., Rimm D., Lifton R. **Recurrent somatic mutations in *PCBP1* in colorectal cancer metastasis.**

Published Papers

[11] Hu Y., **Lu Q.**, Liu W., Zhang Y., Li M., Zhao H. (2017). **Joint modeling of genetically correlated diseases and functional annotations increases accuracy of polygenic risk prediction.** *PLOS Genetics*, in press.

[10] Hu Y.*, **Lu Q.***, Powles R., Yao X., Yang C., Fang F., Xu X., Zhao H. (2017). **Leveraging functional annotations in genetic risk prediction for human complex diseases.** *PLOS Computational Biology*, in press.

[9] Zhao B., **Lu Q.**, Cheng Y., Belcher J., Siew E., Leaf D., Body S., Fox A., Waikar S., Collard C., Thiessen-Philbrook H., Ikizler T., Ware L., Edelstein C., Garg A., Choi M., Schaub J., Zhao H., Lifton R., Parikh C. for the TRIBE-AKI Consortium. (2017). **A genome-wide association study to identify single nucleotide polymorphisms for acute kidney injury.** *American Journal of Respiratory and Critical Care Medicine*, 195(4), 482-490.

[8] Li M., Foli Y., Liu Z., Wang G., Hu Y., **Lu Q.**, Selvaraj S., Lam W., Paintsil E. (2017). **High frequency of mitochondrial DNA mutations in HIV-infected treatment-experienced individuals.** *HIV Medicine*, 18(1), 45-55.

[7] **Lu Q.**, Jin C., Sun J., Bowler R., Kechris K., Kaminski N., Zhao H. (2017). **Post-GWAS prioritization through data integration provides novel insights on chronic obstructive pulmonary disease.** *Statistics in Biosciences*, in press.

[6] Timberlake A., Choi J., Zaidi S., **Lu Q.**, Nelson-Williams C., Brooks E., Bilguvar K., Tikhonova I., Mane S., Yang J., Sawh-Martinez R., Persing S., Zellner E., Loring E., Chuang C., Galm A., Hashim P., Steinbacher D., DiLuna M., Duncan

C., Pelphey K., Zhao H., Persing J., Lifton R. (2016). **Two locus inheritance of non-syndromic midline craniosynostosis via rare *SMAD6* and common *BMP2* alleles.** *eLife*, 5: e20125.

[5] **Lu Q.***, Powles R.* , Wang Q., He B., Zhao H. (2016). **Integrative tissue-specific functional annotations in the human genome provide novel insights on many complex traits and improve signal prioritization in genome wide association studies.** *PLOS Genetics*, 12(4): e1005947.

*Pre-doctoral Finalist of 2015 ASHG/Charles Epstein Trainee Award for Excellence in Human Genetics Research
Winner of Best Student Poster Award, the 30th New England Statistics Symposium*

[4] **Lu Q.**, Yao X., Hu Y., Zhao H. (2016). **GenoWAP: GWAS signal prioritization through integrated analysis of genomic functional annotation.** *Bioinformatics*, 32(4), 542-548.

[3] **Lu Q.**, Hu Y., Sun J., Cheng Y., Cheung K., Zhao H. (2015). **A statistical framework to predict functional non-coding regions in the human genome through integrated analysis of annotation data.** *Scientific Reports*, 5, 10576.

[2] Wang Q.* , **Lu Q.***, Zhao H. (2015). **A review of study designs and statistical methods for genomic epidemiology studies using next generation sequencing.** *Frontiers in Genetics*, 6:149.

[1] **Lu Q.**, Ren S., Lu M., Zhang Y., Zhu D., Zhang X., Li T. (2013). **Computational prediction of associations between long non-coding RNAs and proteins.** *BMC Genomics*, 14(1), 651.

Published Conference Abstracts

[3] Timberlake A., Choi J., Zaidi S., **Lu Q.**, Nelson-Williams C., Brooks E., Bilguvar K., Tikhonova I., Mane S., Yang J., Sawh-Martinez R., Persing S., Zellner E., Loring E., Chuang C., Galm A., Hashim P., Steinbacher D., DiLuna M., Duncan C., Pelphey K., Zhao H., Persing J., Lifton R. (2017). **Two locus inheritance of non-syndromic midline craniosynostosis via rare *SMAD6* and common *BMP2* alleles.** *Plastic and Reconstructive Surgery-Global Open*, 5(4S), 19-20.

[2] **Lu Q.**, Mukherjee S., Kunkle B., Crane P., Zhao H. (2016). **Integrative analysis of GWAS summary data and functional annotations identifies additional loci for late-onset Alzheimer's disease.** *Alzheimer's & Dementia: The Journal of the Alzheimer's Association*, 12(7), P854.

[1] **Lu Q.**, Mukherjee S., Crane P., Zhao H. (2016). **Integrative analysis of GWAS summary data and functional annotations highlights signal enrichment in immune-related DNA elements for late-onset Alzheimer's disease.** *Alzheimer's & Dementia: The Journal of the Alzheimer's Association*, 12(7), P176-177.

Presentations

Talks and Seminars

- 09/2017 Advanced Psychometrics Methods in Cognitive Aging Research 2017, University of Washington - Friday Harbour Laboratories, Friday Harbour, WA
- 08/2017 JSM 2017, Baltimore, MD
- 07/2017 AAIC 2017, London, UK
- 06/2017 The 14th Graybill Conference on Statistical Genomics and Genetics, Colorado State University, Fort Collins, CO
- 03/2017 Department of Biostatistics, Yale University, New Haven, CT
- 03/2017 Cushing/Whitney Medical Library, Yale University, New Haven, CT
- 02/2017 Department of Biostatistics and Department of Genetics, UNC-CH, Chapel Hill, NC
- 01/2017 Department of Biostatistics and Medical Informatics, UW-Madison, Madison, WI
- 12/2016 The 10th ICSA International Conference, SJTU, Shanghai, China
- 12/2016 SJTU-Yale Joint Center for Biostatistics, Shanghai, China
- 08/2016 JSM 2016, Chicago, IL
- 07/2016 AAIC 2016, Toronto, Canada

10/2015 ASHG 2015, Baltimore, MD
 07/2015 Workshop on Data Science in Biomedicine, HKBU, Hong Kong, China
 05/2015 Bioinformatics Transition Workshop, SAMSI, Research Triangle Park, NC
 02/2015 Workshop on Statistical and Computational Challenges in Omics Data Integration, SAMSI, Research Triangle Park, NC

Poster Presentations

04/2017 The 31st New England Statistics Symposium, University of Connecticut, Storrs, CT
 10/2016 ASHG 2016, Vancouver, Canada
 07/2016 AAIC 2016, Toronto, Canada
 04/2016 The 30th New England Statistics Symposium, Yale University, New Haven, CT
 06/2015 ENCODE 2015: Research Applications and Users Meeting, Potomac, MD
 04/2015 The 29th New England Statistics Symposium, University of Connecticut, Storrs, CT

Teaching and Mentorship

Instructor

Spring 2017

Cushing/Whitney Medical Library Bioinformatics Training Workshop, Yale University, New Haven, CT

Teaching Assistant

Spring 2015, Spring 2016

Nonparametric Statistical Methods and Their Applications, Yale University, New Haven, CT

Fall 2013, Fall 2014

Applied Regression Analysis, Yale University, New Haven, CT

Guest Lecturer

Spring 2017

High School Biology, Academy of Our Lady of Mercy - Luralton Hall, Milford, CT

Spring 2016

Statistical Methods for Human Genetics, Yale University, New Haven, CT

Fall 2013, Fall 2014

Applied Regression Analysis, Yale University, New Haven, CT

Doctoral Dissertation Committee Member

2017- Kathryn Hatchell, population health sciences, UW-Madison

Other Mentoring Activities

2016-2017 Wei (David) Dai, biostatistics MPH research, Yale School of Public Health
 2016-2017 Yu Shi, biostatistics MS research, Yale School of Public Health
 2016-2017 Jiawei Wang, computational biology student rotation, Yale University
 2016-2017 Yuhua Zhang, visiting undergraduate student, Shanghai Jiao Tong University
 2016-2017 Boyang Li, biostatistics MS thesis research, Yale School of Public Health
 2016-2017 Tony Jiang, undergraduate research, Yale College
 2015-2017 Chentian (Lionel) Jin, undergraduate research, Yale College
 2016 Sydney Muchnik, genetics student rotation, Yale University
 2016 Wei Liu, visiting undergraduate student, Peking University
 2016 David Chang, computational biology student rotation, Yale University

2016 Zefeng Liu, visiting undergraduate student, Shanghai Jiao Tong University
 2016 Qidu He, visiting undergraduate student, Shanghai Jiao Tong University
 2016 Sarah Abdallah, MD student summer research, Yale School of Medicine
 2016 Derek Ou, MD student summer research, Yale School of Medicine
 2015-2016 Fang Fang, biostatistics MS thesis research, Yale School of Public Health
 2015-2016 Xinran Xu, biostatistics MS thesis research, Yale School of Public Health
 2015 Ryan Powles, computational biology student rotation, Yale University

Professional Activities

Professional Membership

2016-present Member, American Statistical Association (ASA)
 2016-present Member, Association of Chinese Geneticists in America (ACGA)
 2015-present Member, American Society of Human Genetics (ASHG)

Journal Referee

American Journal of Human Genetics, Bioinformatics, BMC Bioinformatics, Genetic Epidemiology, Genome Biology, Human Genomics, Human Heredity, Nucleic Acids Research, PLOS Genetics, PLOS One, Science, Statistical Applications in Genetics and Molecular Biology, Statistics in Biosciences

Conference Referee

Asia Pacific Bioinformatics Conference

References

Dr. Hongyu Zhao

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Dr. Richard Lifton

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Head of Laboratory of Human Genetics and Genomics

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