

Xing Qiu

Curriculum Vitae

Current Position and Contact Information

Title: Associate Professor of Biostatistics and Computational Biology

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Positions and Employment

2007 - 2013 Assistant Professor, University of Rochester, Department of Biostatistics and Computational Biology, Rochester, NY

2013-2015 Bioinformatics Unit Leader of Center for Biodefense Immune Modeling, Rochester, NY

2013 - Associate Professor, University of Rochester, Department of Biostatistics and Computational Biology, Rochester, NY

2013 - Bioinformatics and Computational Biology Unit Leader, Center for AIDS Research at the University of Rochester, Rochester, NY

2015 - Data Management, Informatics and Computational Biology Core Leader, Respiratory Pathogens Research Center, Rochester, NY

Education

2000-2004 Ph.D., Mathematics, University of Rochester, Rochester, NY.

1998-2000 M.A., Mathematics, University of Rochester, Rochester, NY.

1996-1998 Two years of graduate training in the field of Applied Mathematics, South China University of Technology, Guangzhou, China.

1992-1996 B.E., Civil Engineering, South China University of Technology, Guangzhou, China.

Doctoral Research

2000-2004 Department of Mathematics, University of Rochester, Rochester, NY.
Research field: theory of probability and its applications.
Ph.D. thesis: "On Stochastic Flows and Backward Stochastic Differential Equations with Reflection".
Thesis advisor: Professor Michael Cranston, Department of Mathematics, University of Rochester.

Postdoctoral Research

2004-2007 Postdoctoral Fellow, Department of Biostatistics and Computational Biology, University of Rochester, Rochester, NY.
Research field: microarray data analysis, multiple testing adjustment, resampling techniques, and software development.

Honors

2018 GPU Grant, NVIDIA's Academic Programs.

2017 Best Mentor Award, Sixth Annual Conference of the Upstate Chapters of the American Statistical Association (UP-STAT) 2017, Buffalo, NY.

2016 Novel Biostatistical and Epidemiologic Methods (NBEM) Pilot Award, Clinical and Translational Science Institute at the University of Rochester

2015 Behrooz A. Akbarnia, MD Award for the Best Paper, the International Congress on Early Onset Scoliosis.

2014 The best Basic Science E-Poster at the 2014 Scoliosis Research Society Annual Meeting.

2013 Novel Biostatistical and Epidemiologic Methods (NBEM) Pilot Award, Clinical and Translational Science Institute at the University of Rochester

2011 Provost's Multidisciplinary Award, University of Rochester 2002-2003
Dean's Teaching Fellowship, University of Rochester

1999 Research Assistantship, supported by the National Security Agency

1998-2002 Teaching Assistantship, Department of Mathematics, University of Rochester

Professional Associations

Member of the American Statistical Association

Contribution to Science

1. In the past decade, I have made significant contributions to high-throughput transcriptome data pre-processing and statistical analysis, which include three comparative studies on gene expression data normalization, several differential expression analysis procedures for high-throughput data with substantial long-range correlation, and two gene prioritizing procedures based on differential association, which is defined as the significant phenotypic changes in correlation and covariance matrices instead of mean values. The overarching theme of my research in this area focuses on extracting rich information encoded in the covariance structure of high-dimensional data, and utilize this structure for better statistical inference.
 - a. Klebanov, L., **Qiu, X.**, Welle, S., and Yakovlev, A. (2007). Statistical methods and microarray data, *Nature Biotechnology*, **25**(1):25-26. PMID: [17211383](#)
 - b. Hu, R., **Qiu, X.**, and Glazko, G. (2010). A new gene selection procedure based on the covariance distance. *Bioinformatics*, **26**(3):348-354. PMID: [PMC2815661](#)
 - c. **Qiu, X.**, Hu, R., and Wu, H. (2013) The Impact of Quantile and Rank Normalization on the Testing Power of Gene Differential Expression Analysis, *BMC Bioinformatics*, **14**(1):124. PMID: [23578321](#)
 - d. Zhang, Y., Topham, J.D., Thakar*, J., and **Qiu***, **X.** (2017) FUNNEL-GSEA: FUNctioNal ELastic-net Regression in time-course Gene Set Enrichment Analysis. *Bioinformatics*, **33**(13): 1944-1952. [*Senior authorship shared] PMID: [28334094](#).

- e. Liu, Y., Zhang*, J., and **Qiu***, **X.** (2017) Super-delta: A new approach that combines gene expression data normalization and differential expression test. *BMC Bioinformatics*, *in press*. [*Senior authorship shared]
2. I have developed advanced computational biology methods beyond pre-processing and gene selection for transcriptome data. Specifically, I played critical role in developing a gene regulatory network reconstruction pipeline which involves five steps: 1. Gene selection based on functional principal component analysis test. 2. Cluster analysis based on either biologically defined features or a data-driven criterion based on Euclidean or geodesic distance. 3. Regulatory network structure identification based on a high-dimensional ordinary differential equation model and penalized regression (LASSO, elastic net, or SCAD). 4. Parameter refinement based on nonlinear least squares optimization procedures. 5. Gene set enrichment analyses. I also developed a hierarchical parallel computing framework based on message passing interface (MPI) and Pthreads so that time consuming computational biology procedures can utilize modern CPU architecture more efficiently.
 - a. Needham, M., Hu, R., Dwarkadas, S., and **Qiu**, **X.** (2011) Hierarchical parallelization of gene differential association analysis. *BMC Bioinformatics*, **12**(1):374. [PMID: 21936916](#), [PMCID: PMC3248234](#)
 - b. Wu, S., Liu, Z. P., **Qiu**, **X.**, and Wu, H. (2013). High-Dimensional Ordinary Differential Equation Models for Reconstructing Genome-Wide Dynamic Regulatory Networks. In *Topics in Applied Statistics* (pp. 173-190). Springer New York.
 - c. **Qiu**, **X.**, Wu, S., and Wu, H. (2015). A new information criterion based on Langevin mixture distribution for clustering circular data with application to time course genomic data. *Statistica Sinica*, **25**:1459-1476.
 - d. Chen, I., Kelkar, Y.D., Gu, Y, Zhou, J., **Qiu***, **X.**, and Wu, H*. (2017) High-Dimensional Linear State Space Models for Dynamic Microbial Interaction Networks. *PloS One*, *in press*. [*Senior authorship shared]
 - e. Wu*, L., **Qiu***, **X.**, Yuan, Y.X., and Wu, H. (2017) Parameter Estimation and Variable Selection for Big systems of High-Dimensional Linear ordinary Differential Equations: A Matrix-Based Approach. *Journal of American Statistical Association*, *in press*. [*First authorship shared]
 3. In recent years, I developed several medical imaging analysis tools together with researchers from the departments of radiology, imaging science, and neurology. Specifically, we developed a personalized medical image analysis pipeline that has the capability of making statistical inference at the subject-level with as few as only two longitudinal observations. This method is based on spatial regression model, Perona-Malik anisotropic diffusion equation, nonparametric resampling methods, and several multiple testing procedures that are optimized for resampling tests and spatio-temporally correlated hypotheses. I have also been involved in several application-oriented projects and provided imaging data analysis service to my collaborators.
 - a. Zhu, T., Hu, R., **Qiu**, **X.**, Taylor, M., Tso, Y., Yiannoutsos, C., Navia, B., Mori, S., Ekholm, S., Schifitto, G., and Zhong, J. (2011) Quantification of accuracy and precision of multi-center DTI measurements: A diffusion phantom and human brain study. *Neuroimage*, **56**(3):1398–1411. [PMID:21316471](#); [PMCID: PMC3085553](#)
 - b. Zhu, T., Hu, R., Tian, W., Ekholm, S., Schifitto, G., **Qiu***, **X.**, and Zhong*, J. (2013) Spatial regression analysis of diffusion tensor imaging (spread) for longitudinal progression of neurodegenerative disease in individual subjects. *Magnetic Resonance Imaging*, **31**(10), 1657-1667. [*Senior authorship shared] [PMID: 24099667](#)
 - c. Liu*, B., **Qiu***, **X.**, Zhu, T., Tian, W., Hu, R., Ekholm, S., Schifitto, G., Zhong, J. (2016) Spatial regression analysis of serial DTI for subject-specific longitudinal changes of neurodegenerative disease, *NeuroImage: Clinical* **11**: 291-301. [*First authorship shared] [PMID: 26977399](#), [PMCID: PMC4782002](#).

- d. Liu*, B., **Qiu***, X., Zhu, T., Tian, W., Hu, R., Ekholm, S., Schifitto, G., Zhong, J. (2016) Improved spatial regression analysis of diffusion tensor imaging for lesion detection during longitudinal progression of multiple sclerosis in individual subjects, *Physics in Medicine and Biology*, **61**(6): 2497. [*First authorship shared] [PMID: 26948513](#).
- e. Abidin, A.Z., Dsouza, A.M., Nagarajan, M.B., Lu, W., **Qiu, X.**, Schifitto, G., Wismüller, A. (2017) Alteration of Brain Network Topology in HIV Associated Neurocognitive Disorder: A Novel Functional Connectivity Perspective. *NeuroImage: Clinical*, *in press*.
4. I have participated in many immunology-related collaborative research projects in recent years. By using statistical analyses and advanced computational biology tools developed by our group, we were able to understand the extensive difference in transcriptome profiles between subpopulations of CpG-activated memory B cells, the role of inhibitory kappa B kinase complex in platelet activation induced by HIV and cocaine, and the molecular mechanisms underlying pulmonary capillary-alveolar leak syndrome during influenza infection, etc.
- a. Wu, S., Liu, Z. P., **Qiu, X.**, and Wu, H. (2014) Modeling genome-wide dynamic regulatory network in mouse lungs with influenza infection using high-dimensional ordinary differential equations. *PloS One*, **9**(5):e95276. [PMID: 24802016](#); [PMCID: PMC4011728](#)
- b. **Qiu***, X., Wu*, S., Hilchey, S. P., Thakar, J., Liu, Z. P., Welle, S. L., Henn, A.D., Wu, H., and Zand, M. S. (2015). Diversity in Compartmental Dynamics of Gene Regulatory Networks: The Immune Response in Primary Influenza A Infection in Mice. *PloS one*, **10**(9), e0138110. [*First authorship shared] [PMID: 26413862](#); [PMCID: PMC4586376](#)
- c. Chu*, C., **Qiu***, X., Wang, L., Bhattacharya, S., Lofthus, G., Corbett, A., Holden-Wiltse, J., Grier, A., Tesini, B., Gill, S.R., Falsey, A.R., Caserta, M.T., Walsh, E.E., and Mariani, T.J. (2016) The Healthy Infant Nasal Transcriptome: A Benchmark Study. *Scientific Reports* **6**. [*First authorship shared] [PMCID: PMC5034274](#)
- d. Mariani, T.J., **Qiu, X.**, Chu, C., Wang, L., Thakar, J., Holden-Wiltse, J., Corbett, A., Topham, D.J., Falsey, A.R., Caserta, M.T., Walsh, E.E. (2017) Dynamic changes in the CD4 T cell transcriptome are associated with disease severity during primary RSV infection in young infants. *Journal of Infectious Diseases*, *in press*.
- e. Grier, A., **Qiu, X.**, Bandyopadhyay, S., Holden-Wiltse, J., Kessler, H, Gill, A.L., Hamilton, B., Huyck, H., Misra, S., Mariani, T.J., Ryan, R., Scholar, L., Scheible, K., Lee, Y.H., Caserta, M., Pryhuber, G.S., and Gill, S.R. (2017+) Impact of Prematurity and Nutrition on the Developing Gut Microbiome and Preterm Infant Growth. *Microbiome*, *in press*.

Professional Services and Activities

2010-present	Associate editor, International Journal of Computers and Their Applications
2016	Session chair, Statistical Methods for High-Dimensional Correlated Data, the 10 th ICSC International Conference, Shanghai, China.
2016	<i>Ad hoc</i> grant reviewer for the University of Rochester Clinical and Translational Sciences Institute Mentored Career Development (KL2) Program.
2016	<i>Ad hoc</i> grant reviewer for NIH/NIEHS Hazardous Substance Research and Training Program (P42).
2014	Served as a member of the Admissions Committee for the Department of Biostatistics and Computational Biology.
2014	<i>Ad hoc</i> grant reviewer for the Clinical and Translational Science Award at the University of Cincinnati and Cincinnati Children's Hospital Medical Center.
2012	<i>Ad hoc</i> grant reviewer for the Clinical and Translational Science Award at the University of Cincinnati and Cincinnati Children's Hospital Medical Center.

- 2010 Served on the program committee of the Association for Computing Machinery international conference on bioinformatics and computational biology, Niagara Falls, NY
- 2005-present Served as a reviewer for
- *Annals of Applied Statistics*
 - *Biometrics*
 - *Bioinformatics*
 - *Computational Statistics*
 - *BMC Bioinformatics*
 - *BMC Genomics*
 - *Gene Regulation and Systems Biology*
 - *Genomics*
 - *IEEE/ACM Transactions on Computational Biology and Bioinformatics*
 - *Journal of Biology and Computational Biology*
 - *Neurobiology of Aging*
 - *PloS One*
 - *Statistical Advances in the Biomedical Sciences*
 - *Statistical Applications in Genetics and Molecular Biology*
 - *Statistics in Medicine*
- 2007-present Served as the Brown Bag Seminar organizer for the Department of Biostatistics and Computational Biology.
- 2009 Served as a member of the Admissions Committee for the Department of Biostatistics and Computational Biology.

Teaching Experiences

- 2017- Lecturing BST 401, Probability Theory
- 2017- Serving as Jiatong Sui's Ph.D. thesis advisor
- 2015- Serving as Yun Zhang's Ph.D. thesis advisor
- 2015-2016 Served as the advisor for postdoctoral trainees, Drs. Yogeshwar Kelka and Hongjun Li.
- 2016 Lectured BST 550, "Functional Data Analysis".
- 2016 Served as Hongyi Kang's M.A. thesis advisor.
- 2015 Lectured BST 411, "Statistical Inference", required course for Doctoral students in the Department of Biostatistics and Computational Biology.
- 2015 Served as Bilan Liu's Ph.D. thesis advisor (co-advising with Professor Jianhui Zhong).
- 2015 Served as Kyra Singh's Ph.D. dissertation proposal committee member.
- 2015 Lectured BST 550, "Functional Data Analysis".
- 2013 Served as Yao Yu's Ph.D. dissertation proposal committee member.
- 2013 Served as Tong Zhu's M.A. dissertation advisor.
- 2012-2014 Lectured BST 411, "Statistical Inference", a required course for Doctoral students in the

Department of Biostatistics and Computational Biology.

- 2012 Served as the advisor of BST 591, Reading Course at the Ph.D. Level, for Tian Chen.
- 2012 Served as Xiao Zhang's Ph.D. dissertation proposal committee member.
- 2011 Served as the advisor of BST 591, Reading Course at the Ph.D. Level, for Tian Chen.
- 2011 Served as Xiang Liu's Ph.D. dissertation committee member.
- 2011 Lectured BST 478, "Introduction to Statistical Software II". Required course for Doctoral students in the Department of Biostatistics and Computational Biology.
- 2010 Lectured BST 401, "Probability Theory". Required course for Doctoral students in the Department of Biostatistics and Computational Biology.
- 2010 Served as Xiang Liu's Ph.D. dissertation proposal committee member.
- 2009 Lectured BST 401, "Probability Theory". Required course for Doctoral students in the Department of Biostatistics and Computational Biology.
- 2009 Lectured BST 497, "Seminar in Statistical Literature". Required course for Doctoral students in the Department of Biostatistics and Computational Biology.
- 2008-2011 Served as the advisor for a postdoctoral trainee, Dr. Rui Hu.
- 2008 Served as Linlin Chen's Ph.D. dissertation committee
- 2007-2008 Lectured "Introduction to Biostatistics" for the Department of Radiation Oncology.
- 2000-2003 Served as an Instructor in the Department of Mathematics at the University of Rochester.
- Fall 2003, Math 141(Calculus I)
 - Summer 2003, Math 235(Linear Algebra with Proofs)
 - Spring 2003, Math 142(Calculus II)
 - Fall 2002, Math 141(Calculus I)
 - Summer 2001, Math 163(Ordinary Differential Equations I)
 - Summer 2000, Math 164(Multidimensional Calculus)
- 1999-2002 Served as a Teaching Assistant in the Department of Mathematics at the University of Rochester.
- Spring 2002, Math 163(Ordinary Differential Equations I)
 - Fall 2001, Math 165(Linear Algebra with Differential Equations)
 - Spring 2001, Math 174Q(Honors Calculus IV)
 - Fall 2000, Math 164(Multidimensional Calculus)
 - Spring 2000, Math 164(Multidimensional Calculus)
 - Fall 1999, Math 201(Introduction to Probability)
 - Spring 1999, Math 161(Calculus I)

Presentations

- 2017 "Toward the Era of "Large p^2 , medium n ", DBCB Colloquium, University of Rochester, Rochester, New York.
- 2017 "Multiple testing, spherical statistics, and random number generation on manifolds: A

- love story between mathematics and statistics”, **invited speaker**, Beijing Forestry University, Beijing, China.
- 2017 “Large-scale Network Reconstruction Based on Ordinary Differential Equation Systems”, **invited speaker**, South China University of Technology, Guangzhou, China.
- 2017 “Dimension reduction, spherical representation, and a more powerful way to control familywise error”, Respiratory Pathogens Research Center Research in Motion, Rochester, New York.
- 2017 “A novel FWER controlling procedure for data with reduced rank correlation structure”, the 10th International. Conference on Multiple Comparison Procedures, Riverside, California.
- 2016 “A Time Course Inferential Framework for Gene Set Enrichment Analysis Based on Functional Elastic-net Regression”, the 10th ICSA International Conference, Shanghai, China.
- 2015 “How Many Clusters Are There on a Circle? A New Information Criterion for Clustering Circular Data with Application to Time Course Genomic Data”, Gorgen Institute for Data Science Seminar, University of Rochester, Rochester, New York.
- 2015 “How Many Clusters Are There on a Circle? A New Information Criterion for Clustering Circular Data with Application to Time Course Genomic Data”, **invited speaker**, IMS-China International Conference on Statistics and Probability, Kunming, China.
- 2015 “A Powerful Longitudinal Medical Image Analysis Pipeline for Detecting Progression of Brain Abnormality in Individual Subject”, **invited speaker**, University of Xiamen, Xiamen, China.
- 2012 “From Data to Knowledge: an Introduction of Statistical Methods in Bioinformatics”, Jinan University, Guangzhou, China.
- 2012 “Biostatistical Applications in Genomic Research”, **invited speaker**, Southwest University, Chongqing, China.
- 2012 “A Geometric Illustration of Differential Gene Association Analysis for Microarray Data”, American Statistical Association Upstate Conference, Rochester, New York.
- 2012 “RINO: A Robust Interchangeable Normalization Method for Testing Differential Expressions”, Transcriptomics and Integrated Genomics Working Group, University of Rochester, Rochester, New York.
- 2011 “Demystify the pre-processing step for the NG-sequencing data: Why one size does not fit all in computational genomics”, Center for Biodefense Immune Modeling, University of Rochester, Rochester, New York.
- 2009 “Detecting Correlation Changes: A New Perspective on Gene Selection”, **invited speaker**, Statistical Modeling for Biological Systems, University of Rochester, Rochester, New York.
- 2008 “Is there an alternative to increasing the sample size in microarray studies?”, **invited speaker**, International Biometric Conference, Dublin, Ireland.
- 2008 “Overcoming Adverse Effects of Correlations in Microarray Data Analysis”, ENAR Spring Meeting, Arlington, Virginia
- 2006 “Adverse Effects of Inter-gene Correlations in Microarray Data Analysis”, Department

of Biostatistics and Computational Biology, University of Rochester, Rochester, New York.

- 2006 “Instability of False Discovery Rate Estimation from Microarray Gene Expression Data”, International Biometric Conference, Montreal, Canada.
- 2006 “Assessing Stability of Gene Selection in Microarray Data Analysis”, University of Rochester Bioinformatics Cluster, Rochester, New York.
- 2005 “The effects of normalization on the correlation structure of microarray data”, Joint Statistical Meeting, Minneapolis, Minnesota.

Inventions

- 2007 U.S. Patent No.: US 2007/0196851 A1 “System and Method for Selecting Differentially Dependent Genes from Gene Expression Data”, Yakovlev, A., Klebanov, L. and **Qiu, X.**

Consulting Experiences

I have been providing professional statistical consultation service for over 30 collaborative research projects since 2004. My collaborative research include projects that involves gene and protein expression analyses; Diffusion Tensor Imaging modeling and analysis; many infectious disease (human influenza, HIV/AIDS, RSV, etc) related projects, orthopaedics related projects; esophageal cancer related projects; radiation oncology related projects, etc.

I have extensive experience leading and contributing to the biostatistics/bioinformatics cores of large NIH-sponsored center grants. Currently, I am the Data Management, Informatics and Computational Biology Core Leader of Respiratory Pathogens Research Center (RPRC, Rochester, NY). RPRC is an NIAID sponsored center (contract number: HHSN272201200005C) that consists of a national network of scientists focusing on research that will lead to a better understanding of the complex interactions between respiratory pathogens, the immune system, and other genetic and environmental factors and how these interactions can cause complications, and developing new ways to treat or prevent these diseases. DMICBC provides statistics, bioinformatics, computation, and mathematical modeling service to all research Cores/Projects of RPRC. I am also the Bioinformatics and Computational Biology Unit Leader of the Center for AIDS Research at the University of Rochester (CFAR at UR, NIAID P30AI078498). I was Bioinformatics Unit Leader of Center for Biodefense Immune Modeling (NIAID HHSN272201000055C) between 2013 and 2015.

Publications

Peer-Reviewed Publications

1. **Qiu, X.**, Hong, Y. and Shen, Y. (2001). An Improvement on the concentration-compactness principle. *Acta Mathematicae Applicatae Sinica*, **17**:60-67.
2. **Qiu, X.**, Brooks, A. I., Klebanov, L. and Yakovlev, A. (2005). The effects of normalization on the correlation structure of microarray data, *BMC Bioinformatics* **6**:120. [PMID: 15904488](#), [PMCID: PMC 1156869](#).
3. **Qiu, X.**, Klebanov, L. and Yakovlev, A. (2005). Correlation Between Gene Expression Levels and Limitations of the Empirical Bayes Methodology for Finding Differentially Expressed Genes, *Statistical Applications in Genetics and Molecular Biology* **4** Article 34. [PMID: 16646853](#).
4. **Qiu, X.**, Xiao, Y., Gordon, A. and Yakovlev, A. (2006). Assessing Stability of Gene Selection in Microarray Data Analysis, *BMC Bioinformatics*, **7** Article 50. [PMID: 16451725](#), [PMCID: PMC1403808](#).
5. **Qiu, X.** and Yakovlev, A. (2006) Some comments on instability of false discovery rate estimation, *Journal of Bioinformatics and Computational Biology*, **4**(5):1057-1068, 2006. [PMID: 17099941](#).
6. Almudevar, A., Klebanov, L.B., **Qiu, X.**, Salzman, P., and Yakovlev, A.Y. (2006) Utility of correlation measures in analysis of gene expression, *NeuroRx*, **3**(3):384-395. [PMID: 16815221](#).
7. **Qiu, X.** and Yakovlev, A. (2006). Instability of false discovery rate estimation, *J. Bioinformatics and Computational Biology*, **4** Article 5.

8. Klebanov, L., **Qiu, X.**, Welle, S., and Yakovlev, A. (2007). Statistical methods and microarray data, *Nature Biotechnology*, **25**(1):25-26. PMID: [17211383](#)
9. **Qiu, X.** and Yakovlev, A. (2007). Comments on probabilistic models behind the concept of false discovery rate, *Journal of Bioinformatics and Computational Biology*, **5**(4):963-975. PMID: [17787065](#).
10. Gordon, A., Glazko, G., **Qiu, X.** and Yakovlev, A. (2007). Control of the Mean Number of False Discoveries, Bonferroni, and Stability of Multiple Testing, *Annals of Applied Statistics*, **1**(1):179-190.
11. Li, X., Nott, S.L., Huang, Y., Hilf, R., Bambara, R.A., **Qiu, X.**, Yakovlev, A., Welle, S., and Muyan, M. (2008). Gene expression profiling reveals that the regulation of estrogen-responsive element-independent genes by 17beta-estradiol/estrogen receptor beta is uncoupled from the induction of phenotypic changes in cell models. *J Mol Endocrinol*, **40**(5):211–229. PMID: [18434428](#).
12. Wuertzer, C., Sullivan, M., **Qiu, X.**, and Federoff, H. (2008). CNS Delivery of Vectored Prion-specific Single-chain Antibodies Delays Disease Onset, *Molecular Therapy*, **16**(3):481-486. PMID: [18180775](#).
13. Klebanov, L., **Qiu, X.** and Yakovlev, A. (2008). Testing differential expression in non-overlapping gene pairs: A new perspective for the empirical Bayes method, *J. Bioinfo and Comp Bio*, **60**(2):301-316. PMID: [18464324](#).
14. Hu, R., **Qiu, X.**, Glazko, G., Klebanov, L., and Yakovlev, A. (2009). Detecting intergene correlation changes in microarray analysis: A new approach to gene selection, *BMC Bioinformatics*, **10**(1):20 PMCID: [PMC2657217](#).
15. Nott, S., Huang, Y., Li, X., Fluharty, B., **Qiu, X.**, Welshons, W., Yeh, S., and Muyan, M. (2009). Genomic Responses from the Estrogen-responsive Elementdependent Signaling Pathway Mediated by Estrogen Receptor alpha Are Required to Elicit Cellular Alterations, *Journal of Biological Chemistry*, **284**(22):15277-15288. PMID: [19321454](#), PMCID: [PMC2685708](#).
16. Sepesi, B., Raymond, D.P., Polomsky, M., Watson, T.J., Litle, V.R., Jones, C.E., Hu, R., **Qiu, X.**, and Peters, J.H. (2009) Does the value of pet-ct extend beyond pretreatment staging? An analysis of survival in surgical patients with esophageal cancer. *J Gastrointest Surg*, **13**(12):2121-2127. PMID: [19795177](#).
17. Will, R.E., Stokes, I.A., **Qiu, X.**, Walker, M.R., and Sanders, J.O. (2009). Cobb angle progression in adolescent scoliosis begins at the intervertebral disc. *Spine*, **34**(25):2782–2786. PMID: [19940737](#), PMCID: [PMC2784923](#).
18. Hu, R., **Qiu, X.**, and Glazko, G. (2010). A new gene selection procedure based on the covariance distance. *Bioinformatics*, **26**(3):348-354. PMCID: [PMC2815661](#).
19. Polomsky, M., Hu, R., Sepesi, B., O'Connor, M., **Qiu, X.**, Raymond, D.P., Litle, V.R., Jones, C.E., Watson, T.J., and Peters, J.H. (2010) A population-based analysis of emergent vs. elective hospital admissions for an intrathoracic stomach, *Surgical Endoscopy*, **24**(6):1250-1255. PMID: [19957207](#).
20. Liu, X., Tian, W., Kolar, B., Yeane, G.A., **Qiu, X.**, Johnson, M.D., and Ekholm, S. (2011) MR diffusion tensor and perfusion-weighted imaging in preoperative grading of supratentorial nonenhancing gliomas. *Neuro Oncology*, **13**(4):447–455.
21. Zhu, T., Hu, R., **Qiu, X.**, Taylor, M., Tso, Y., Yiannoutsos, C., Navia, B., Mori, S., Ekholm, S., Schifitto, G., and Zhong, J. (2011) Quantification of accuracy and precision of multi-center DTI measurements: A diffusion phantom and human brain study. *Neuroimage*, **56**(3):1398–1411. PMID:[21316471](#); PMCID: [PMC3085553](#)
22. Liu, X., Tian, W., Li, L., Kolar, B., **Qiu, X.**, Chen, F., and Dogra, V.S. (2012) Hyperintensity on diffusion weighted image along ipsilateral cortical spinal tract after cerebral ischemic stroke: A diffusion tensor analysis. *European Journal of Radiology*, **81**(2):292-297.
23. Hu, Y., Bandla, S., Godfrey, T.E., Tan, D., Luketich, J.D., Pennathur, A., **Qiu, X.**, Hicks, D.G., Peters, J.H., and Zhou, Z. (2011) Her2 amplification, overexpression and score criteria in esophageal adenocarcinoma. *Mod Pathol*, **24**(7):899-907. PMID: [21460800](#).
24. Sanders, J., Howell, J., and **Qiu, X.** (2011) Comparison of the Paley method using chronological age with use of skeletal maturity for predicting mature limb length in children. *Journal of Bone and Joint Surgery*, **93**(11):1051–1056. PMID: [21655898](#).
25. Groom, L., Muldoon, S., Tang, Z., Brandom, B., Bayarsaikhan, M., Bina, S., Lee, H., **Qiu, X.**, Sambuughin, N. and Dirksen, R. (2011) Identical de novo Mutation in the Type 1 Ryanodine Receptor Gene Associated with Fatal, Stress-induced Malignant Hyperthermia in Two Unrelated Families *Anesthesiology*, **115**(5):938-945. PMID: [21918424](#), PMCID: [PMC3203251](#).

26. Needham, M., Hu, R., Dwarkadas, S., and **Qiu, X.** (2011) Hierarchical parallelization of gene differential association analysis. *BMC Bioinformatics*, **12**(1):374. PMID: 21936916, PMCID: PMC3248234.
27. **Qiu, X.** and Hu, R. (2012) Correlation between the true and false discoveries in a positively dependent multiple comparison problem. In IMS Andrei Yakovlev Collection. *Institute of Mathematical Statistics, in press.*
28. Liu, X., Tian, W., **Qiu, X.**, Li, J., Thomson, S., Li, L., and Wang, H. Z. (2012). Correlation analysis of quantitative diffusion parameters in ipsilateral cerebral peduncle during Wallerian degeneration with motor function outcome after cerebral ischemic stroke. *Journal of Neuroimaging*, **22**(3), 255-260. PMID: 21699612
29. Henn, A.D., Laski, M., Yang, H., Welle, S., **Qiu, X.**, Miao, H., Barry, C.T., Wu, H., and Zand, M.S. (2012) Functionally Distinct Subpopulations of CpG-Activated Memory B Cells. *Scientific Reports*, **2**:345. PMID: 22468229; PMCID: PMC3315693
30. Smolock, E.M., Korshunov, V.A., Glazko, G., **Qiu, X.**, Gerloff, J., and Berk, B.C. (2012) Ribosomal Protein L17, RPL17, Is an Inhibitor of Vascular Smooth Muscle Growth and Carotid Intima Formation. *Circulation*, **126**(20):2418-27. PMID: 23065385; PMCID: PMC3502943
31. **Qiu, X.**, Hu, R., and Wu, H. (2013) The Impact of Quantile and Rank Normalization on the Testing Power of Gene Differential Expression Analysis, *BMC Bioinformatics*, **14**(1):124. PMID: 23578321
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64. Abidin, A.Z., Dsouza, A.M., Nagarajan, M.B., Lu, W., **Qiu, X.**, Schifitto, G., Wismüller, A. (2017) Alteration of Brain Network Topology in HIV Associated Neurocognitive Disorder: A Novel Functional Connectivity Perspective. *NeuroImage: Clinical*, *in press*.
65. Wu*, L., **Qiu***, **X.**, Yuan, Y.X., and Wu, H. (2017) Parameter Estimation and Variable Selection for Big systems of High-Dimensional Linear ordinary Differential Equations: A Matrix-Based Approach. *Journal of American Statistical Association*, *in press*. [*First authorship shared]

OTHER PUBLICATIONS

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68. Hu, R. and **Qiu, X***. (2013) A Geometric Illustration of Differential Gene Association Analysis for Microarray Data. *Journal of Unified Statistical Techniques*, **1**(1).
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SUBMITTED MANUSCRIPTS

70. Li, H. and **Qiu***, **X.** (2017+) A fast algorithm for finding the intersection of two partitions of a finite set with applications to clustering evaluation. *Submitted*.
71. Zhang, Y., Topham, D.J., Falsey, A.R., **Qiu***, **X.** (2017+). Highly Efficient Two-Group Comparison Methods for Correlated Observations and Heterogeneous Variance Structure. *Submitted*.

72. Chen, G., Ramírez, J.C., Deng, N., **Qiu, X.**, Wu, C., Zheng, W.J., Wu, H. (2017+). Restructured GEO: Restructuring Gene Expression Omnibus metadata for genome dynamics analysis. *Submitted*.
73. Sanders, J.O., Karbach, L., Osinski, T., Liu, R., **Qiu, X.**, Lu, X., Cooperman, D. (2017+) Normal human spine growth and prediction of final spine height developed from a longitudinal cohort of children followed through their growth until completion. *Submitted*.
74. Caserta, M.T., Yang, H., Bandyopadhyay, S., **Qiu, X.**, Gill, S.R., Java, J., McDavid, A., Falsey, A.R., Topham, D.J., Holden-Wiltse, J., Scheible, K., Pryhuber, G. (2017+) Measuring the Severity of Respiratory Illness in the First Two Years of Life in Pre-Term and Term Infants in an Ambulatory Setting. *Submitted*.

Ongoing Research Support

1R01AG054328-01A1 Schifitto, Maggirwar (PI) NIH/NIA	07/01/2017 – 05/31/2022	
Role of Myeloid Cells in Cerebrovascular Permeability and Reactivity in Older HIV Infected Individuals The major goal of this study is to inform us on the preventive strategies for CSVD that can be developed in older HIV infected individuals.		
University of Rochester Center for AIDS Research – Biostats Core E The mission of the University of Rochester (UR) Center for AIDS Research (CFAR) is to raise the overall quality and quantity of HIV/AIDS research at the UR.		
5 R01 MH099921-03 Schifitto (PI) NIH	04/15/13 – 03/31/18	
Chronic Exposure to cART Predispose Older HIV Infected Individuals to CNS Injury The primary aim for this project is to determine whether chronic exposure to cART alters brain structure and function and whether this differs in young versus older HIV infected individuals.		
5 R01 HL123346-03 Schifitto (PI) NIH	09/15/14 – 05/31/19	
cART Accelerates Vascular Aging in HIV Infected Subjects To determine whether chronic exposure to cART in older HIV infected individuals alters inflammatory cellular functions that are consistent with atherosclerosis and whether these cellular changes correlate with clinical measures of atherosclerosis (CIMT and FMD).		
HHSN272201200005C Topham (PI) NIH	12/13/11 – 12/12/18	
Rochester Viral Respiratory Pathogens Research Centers – 13J – Mariani/Falsey The role of the RPRC is to provide the NIAID Division of Microbiology and Infectious Diseases (DMID) with the capability of conducting translational and clinical research focused on the development and optimization of control measures for viral and bacterial respiratory pathogens.		
2015098 Nayak (PI) Doris Duke Foundation	07/01/15 – 06/30/18	
Understanding How the Initial Encounter with Influenza Virus Poises Children for Protective Immunity The central hypothesis is that differences in the mode of influenza antigen exposure in early childhood will generate long lasting, detectable changes in memory CD4 cell specificity and function that influence the response to future influenza vaccinations and infections.		
1 R21 AI119646-01A1 Daiss (PI) NIH	02/15/16 – 01/31/18	

Diagnosis of Early Staphylococcus Aureus Infections using Circulating Plasmablasts

Completed Research Support

Yakovlev (PI) Johnson & Johnson	09/01/06 – 08/31/07	
<p>A New Type of Dependence Between Gene Expression Levels and its Biological Implications The aims were to: 1) Systematically study specific types of stochastic dependence between gene expression levels in an effort to decipher their biological context and 2) Develop methods for statistical inference of correlations between gene expression levels in the presence of a multiplicative random noise in the data. Role: Postdoctoral Fellow</p>		
HR0011-08-C-0041 Okunieff (PI) Defense Advanced Research Projects Agency	02/27/08 – 11/26/08	
<p>A Biosimulator Based on Radiation-Induced Release of DNA into Plasma Role: Biostatistician</p>		
Sanders (PI) Pediatric Orthopaedic Society of North America	01/01/09 – 12/31/09	
<p>Skeletal Maturity and Growth Relative to the Peak Height Velocity Using prospectively collected data and radiographs, the aims are: 1) The null hypothesis is that skeletal maturity relative to the PHV not better than chronological age in relating the various skeletal regions and the multipliers. 2) Identify the timing of each visit relative to the PHV in 100 subjects (50 boys and 50 girls). 3) Correlate skeletal maturity of the hand, elbow and pelvis with timing relative to the PHV. 4) Identify ratios of the physical parameters collected in the subjects of each skeletal maturity stage including the ranges, skews, and standard deviations relative to these same parameters at maturity. 5) Create both a high quality digital and paper atlas of the correlated radiographs and anthropometric measurements. Role: Biostatistician</p>		
5 R21 GM079259-02 Qiu (PI) NIH	07/01/07 – 06/30/10	
<p>Correlation Vectors in Gene Expression Profiling The specific aims of this project are 1) develop a new method of microarray gene expression data analysis designed to select candidate genes that change their relationships (correlations) with other genes across the conditions (phenotypes) under study; 2) develop a parallelizable algorithm and software to implement the proposed method of microarray data analysis; and 3) apply the proposed methodology to publicly available and “in-house” sets of microarray data and evaluate its performance. Role: Principle Investigator</p>		
3 RC1 AI078519-01S1 Zhang (PI) NIH	09/15/07 – 2/28/10	
<p>A Novel Mitigation Agent for Gastrointestinal Syndrome of Acute Radiation Injury The specific aims are 1) To measure the pharmacokinetics of FGF-P; 2) To define the optimal dose and schedule of FGF-P; and 3) To determine receptor binding affinity and activation by FGF-P in mouse and human cells. The results of these pre-clinical studies will provide the basis for eventual approval as a drug for mitigating AGS through the animal rule. Role: Biostatistician</p>		
1 RC1 AI081244-01 Williams (PI) BARDA/NIAID	09/10/08 – 04/30/11	
<p>Combined Target Therapy for the Pulmonary Syndrome and Supplement With the current state of heightened terrorism risk, rapidly accessible & easily distributed countermeasures are urgently required following a mass radiological or nuclear event. There is no single agent or strategy</p>		

<p>which is likely to be effective. We devised a systematic experimental design which will assess combination therapies that include a broad-based anti-inflammatory together with a number of alternative agents that will be assessed in terms of acute vs. chronic treatment approach. We hope to identify on or more combination therapies that could be developed for use in both immediate delayed periods following a radiological event. Role: Biostatistician</p>		
5 UL1 RR024160 Qiu (PI) UR CTSI	12/01/10 – 06/30/12	
<p>Gene Expression Profiles in Tumors: Distinguishing Two Phenomena with One Array Develop computational framework to disentangle gene expression differences into 2 parts: those related to chromosomal aberrations & those differentially expressed due to changes in <i>cys-</i> or <i>trans-</i>acting regulatory factors or other changes; using publicly available data repositories create a collection of comparative genomic hybridization & expression arrays taken from same samples; for tumors of different origins & grades, identify common signatures of chromosomal aberrations & expression profiles, to find common molecular mechanisms of cancer progressions & metastases; construct Tumors' Aberrations Network, study its structural properties & community structure. Find tumors of different histogenesis included in the same network module with aim to develop refined protocols for their therapy. Role: PI</p>		
5 R01 AI087135-03 Wu (PI) NIH	01/15/10 – 12/31/12	
<p>Estimation Methods for Nonlinear ODE Models in AIDS Research Integrate parameter identifiability techniques from different research disciplines to address Identifiability issues for ODE models; develop novel statistical estimation methods for ODE models & study asymptotic & finite-sample properties of estimators; evaluate new methods by comparing them to existing methods based on theoretical perspective, finite sample properties & computational efficiency, test & validate proposed methods using examples & data from studies of immune response to viral infections; develop efficient computational algorithms & user-friendly software packages to implement methods. Role: Biostatistician</p>		
Zhong, Blackman, Bazarian, Qiu (PIs) Provost's Multidisciplinary Award	07/01/11 – 10/31/12	
<p>New Interdisciplinary Approach to Improve Diagnosis of Traumatic Brain Injury: Combining Physics with Medical Imaging Identify mechanical measures from players' impact force history as measured by accelerometer sensors imbedded on helmet & general brain geometry. This model will be used to predict brain injury based on to-be-determined thresholds in acceleration & shear force, & will be correlated with brain injuries as predicted from DTI data. Work will be performed in collaboration with a Lawrence Livermore National Lab group; incorporate high-resolution MR DTI information into mechanical model to predict individual injury thresholds & correlate specific spatial locations of injury from imaging findings. This will allow improvement in brain mechanical model; use optimized model & football player data to inform changes in helmet design, & implement these changes in new helmets Role: Co-PI</p>		
UL1 RR024160 Hu (PI) UR-CTSI	07/01/12 – 06/30/13	
<p>Detecting Intergene Association Changes in Microarray Data Focus on gene pairs & search for most powerful statistical tests to detect differential associated genes. A permutation based testing approach will be developed. This study will contribute to a new direction in microarray analysis of using intergene dependence structure to uncover biological mechanisms which would be otherwise ignored by gene expression analysis. Role: Biostatistician</p>		

UL1 RR024160 Qiu (PI) UR-CTSI	07/01/13 – 06/30/14	
<p>A Unified Method for Differential Expression and Association Analyses The specific aims are: 1) Develop statistical & computational methods for proposed procedure; 2) Our method will be compared with several popular alternative procedures, such as how well each procedure controls type I error when sample size is large and/or effect size is large, will be studied in detail; 3) The proposed method will be used to study primary Glial precursor cells transduced by two cooperative oncogenes: DNp53 and EGFRvIII. Role: Biostatistician</p>		
5 R01 HL062826-12 Berk (PI) NIH	08/01/10 – 05/31/14	
<p>Genetics of Vascular Remodeling The work described in this project involves many labor intensive procedures including a great deal of tissue culture work, cell transfections, biochemistry, immunoprecipitation, enzyme assays, and analysis of transgenic mice. We have assembled a highly experienced team and will make extensive use of the Histopathology core. Role: Biostatistician</p>		
HHSN272201200005C Topham (PI) NIH	12/13/11 – 12/12/14	
<p>Respiratory Pathogens Research Centers (RPRC) The role of RPRC is to provide NIAID Division of Microbiology & Infectious Diseases (DMID) with capability of conducting translational & clinical research focused on development & optimization of control measures for viral & bacterial respiratory pathogens. Research conducted under RPRC shall focus primarily on development of information, tools, & strategies to decrease significant global health burden of diseases, such as bacterial pneumonia, influenza, bronchiolitis, & RSV. Activities include design, conduct, & analysis of translational, clinical, & innovation research projects. Role: Biostatistician</p>		
HHSN272201000055C Wu (PI) NIH/NIAID	09/30/10 - 09/29/15	
<p>University of Rochester Center for Biodefense Immune Modeling The objectives of this project are to 1) Develop mathematical/computational models to simulate immune responses to influenza A virus, both native and modified bioterror strains. 2) Design and conduct in vitro, ex vivo and in vivo experiments to identify, measure, and validate the immune response models. 3) Develop statistical methods and user-friendly computer packages for immunology data analysis, immunity model identifications and predictions. 4) Develop a deliverable web server-based software system for modeling and simulating immune responses to influenza A virus and other biopathogens. 5) Investigate the feasibility to extend and modify influenza mathematical/computational models to vaccinate virus for immune response simulations in the context of vaccination to induce protective immunity to smallpox. Role: Biostatistician</p>		
T32 AI083206-05 Liang, Wu, Qiu (PIs) NIH/NIAID	08/01/10 - 07/31/16	
<p>Training in Biostatistics for HIV/AIDS The goal of this program is to offer predoctoral and postdoctoral training to biostatisticians for work in HIV/AIDS biostatistics.</p>		
Schifitto, Doyley, Maggirwar, Benesch, Qiu , Dogra (PIs) University Research Awards	07/01/14 – 06/30/15	
<p>Carotid Disease, Elastography and Inflammatory Markers The aim is to develop a sensitive and non-invasive marker of atherosclerosis that can provide additional</p>		

information beyond the current available methods. The preliminary data obtained via this application will provide the necessary data that will justify the use of this methodology in future clinical trials and observational studies of cardiovascular and cerebrovascular disease.

UL1 TR002001 **Qiu, Thakar** (PIs)
NCATS

08/15/16 – 05/31/17

Weighted Functional Gene Set Enrichment Analysis for Time-course Transcriptome Studies
We propose a gene set enrichment analyses pipeline based on functional data analysis that can efficiently extract temporal trends from time-course expression data. The proposed method will be used to study strain-specific mechanism involved in immune cell and cytokine mediated response to influenza infections.

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