

Qike (Max) Li

Keating Building, BIO5, University of Arizona, Tucson, AZ
(520) 647-6973 qikeli@gmail.com <https://qikeli.github.io>

OVERVIEW

- Ph.D. in Statistics–Statistical Informatics track.
- 5+ years' experience in data analytics using R, shell, and high throughput computing.
- Author of *three* R packages and a Shiny App.
- Proficient in Python, SQL, Spark, Hadoop.
- Experience in text mining.
- 4+ years' experience working in interdisciplinary teams.
- Solid understanding of statistical machine learning.
- *Thirteen* scientific papers (*seven* as first author) in applied statistics.
- Effective communication of data and statistics.

EDUCATION

Ph.D in Statistics <i>University of Arizona, Tucson, AZ</i> Statistics Graduate Interdisciplinary Program (GIDP) Minor in Biostatistics Advisors: Hao Helen Zhang (Statistics) & Yves A. Lussier (Biomedical Informatics)	2012-2017
MS Molecular Biology <i>Guizhou University, Guiyang, China</i>	2006-2009
BS Biotechnology <i>Zhengzhou University, Zhengzhou, China</i>	2001-2005

TECHNICAL SKILLS

R, UNIX and BASH, Python, SQL, Spark, Hadoop, SAS, Git and GitHub, Cluster computing, HTML and CSS, Emacs and Elisp, LaTeX, Adobe Illustrator

RESEARCH AREAS

Large-scale inference, statistical machine learning, computing, high dimensional data, count data, multivariate statistics, big data, data visualization, high-throughput data, single-subject inference, Bayesian statistics.

APPOINTMENTS

Postdoctoral Fellow

2017.9-present

Center for Biomedical Informatics & Biostatistics, University of Arizona

Collaborating with Natural Language Processing (NLP) experts, computer scientists, and physicians to conduct research in case-based reasoning using data retrieved from the electronic medical record (EMR).

Research Assistant

2014-2017.8

Lussier Group, Center for Biomedical Informatics & Biostatistics, University of Arizona

Developed statistical informatics methodology for precision medicine. Engaged in interdisciplinary research: working with an expert team of statisticians, physicians, engineers, biologists, geneticists, and computer scientists. Responsibilities include original research, statistical support, grant writing, and software engineering.

Research Assistant

2013-2014

McCarthy Group, University of Arizona

Developed statistical informatics methodology for RNA-Seq analysis.

Research Technician

2010-2012

Michod Group, University of Arizona

Studied the evolution of multicellularity using bioinformatics, comparative genomics, phylogenetic analysis and molecular biology.

AWARDS

- Distinguished Written Paper Award, June 2017, WNAR
- HE Carter Travel Award, Summer 2017, University of Arizona
- Travel Award, Summer 2017, Statistics GIDP, University of Arizona
- HE Carter Travel Award, Fall 2016, University of Arizona

TALKS

- “The 7th Annual Translational Bioinformatics Conference”, Los Angeles, USA, 9/30/2017
- “Joint Statistical Meetings (JSM)”, Baltimore, USA, 7/30/2017
- “WNAR Annual Meeting”, Santa Fe, USA, 6/27/2017
- “The 6th Annual Translational Bioinformatics Conference”, Jeju, Korea, 10/16/2016
- “Short Course: Computational methods for precision medicine and single subject studies with genomes and transcriptomes”, Jeju, Korea, 10/15/2016

TEACHING

- Spring 2016 MATH 363: Introduction to Statistical Methods
Teaching Assistant
- Spring 2016 MCB 516A/416A: Statistical Bioinformatics and Genomic Analysis
Guest Lecturer
- Fall 2013 ABE 613: Applied Biostatistics
Guest Lecturer

SYNERGISTIC ACTIVITIES

- University of Arizona Graduate & Professional Student Council Travel Grant Judge (2017)
- Contributed to the University of Arizona Health Sciences' participation in the National Precision Medicine Initiative® (Feb 2016)
- Referee: the Journal of Biomedical Informatics (2016)
- Member: American Statistical Association (ASA), International Society for Computational Biology (ISCB)

PUBLICATIONS

8. Li, Qike, A. Grant Schissler, Vincent Gardeux, Ikbel Achour, Colleen Kenost, Joanne Berghout, Haiquan Li, Hao Helen Zhang, and Yves A. Lussier, "N-of-1-pathways MixEnrich: advancing precision medicine via single-subject analysis in discovering dynamic changes of transcriptomes", *BMC medical genomics* **10**, 1 (2017).
7. Li, Qike, A. Grant Schissler, Vincent Gardeux, Joanne Berghout, Ikbel Achour, Colleen Kenost, Haiquan Li, Hao Helen Zhang, and Yves A. Lussier, "kMEN: Analyzing noisy and bidirectional transcriptional pathway responses in single subjects", *Journal of biomedical informatics* **66**, (2017).
6. Schissler, A. Grant*, Qike Li*, James L. Chen, Colleen Kenost, Ikbel Achour, D. Dean Billheimer, Haiquan Li, Walter W. Piegorsch, and Yves A. Lussier, "Analysis of aggregated cell-cell statistical distances within pathways unveils therapeutic-resistance mechanisms in circulating tumor cells", *Bioinformatics* **32**, 12 (2016). (* joint first authorship)
5. Schissler, A. Grant*, Vincent Gardeux*, Qike Li*, Ikbel Achour, Haiquan Li, Walter W. Piegorsch, and Yves A. Lussier, "Dynamic changes of RNA-sequencing expression for precision medicine: N-of-1-pathways Mahalanobis distance within pathways of single subjects predicts breast cancer survival", *Bioinformatics* **31**, 12 (2015). (* joint first authorship)
4. Pookhao, Naruekamol, Michael B. Sohn, Qike Li, Isaac Jenkins, Ruofei Du, Hongmei Jiang, and Lingling An, "A two-stage statistical procedure for feature selection and comparison in functional analysis of metagenomes", *Bioinformatics* **31**, 2 (2015).

3. Li, Haiquan, Nima Pouladi, Ikbel Achour, Vincent Gardeux, Jianrong Li, Qike Li, Hao Helen Zhang, Fernando D. Martinez, Joe G N Skip Garcia, Yves A. Lussier, “eQTL networks unveil enriched mRNA master integrators downstream of complex disease-associated SNPs”, *Journal of Biomedical Informatics* **58**, (2015).
2. Lussier, Yves a, Haiquan Li, Nima Pouladi, and Qike Li, “Accelerating precision biology and medicine with computational biology and bioinformatics”, *Genome Biology* **15**, 9 (2014).
1. Sohn, Michael B, Lingling An, Naruekamol Pookhao, and Qike Li, “Accurate genome relative abundance estimation for closely related species in a metagenomic sample”, *BMC Bioinformatics* **15**, 1 (2014).

PAPERS UNDER REVIEW

5. Gardeux, Vincent, Joanne Berghout, Ikbel Achour, A. Grant Schissler, Qike Li, Colleen Kenost, Jianrong Li, Yuan Shang, Anthony Bosco, Saner Don, Marilyn J. Halonen, Daniel J. Jackson, Haiquan Li, Fernando D. Martinez, Yves A. Lussier, “A genome-by-environment interaction classifier for precision medicine: personal transcriptome response to rhinovirus identifies children prone to asthma exacerbations”, *Journal of the American Medical Informatics Association* (2017) (in press)
4. Vitali, Francesca, Qike Li, A. Grant Schissler, Joanne Berghout, Colleen Kenost, and Yves A. Lussier, “Developing a ‘personalome’ for precision medicine: emerging methods that unveil clinically-interpretable effect sizes from single-subject omics” (*submitted to Briefings of Bioinformatics*)
3. Li, Qike, Hao Helen Zhang, Yves A. Lussier, iDEG: a single-subject method for assessing gene differential expression from two transcriptomes of an individual (*submitted to Biometrics*)
2. Berghout, Joanne*, Qike Li*, Nima Pouladi, Yves Lussier. “Single subject transcriptome analysis applied to isogenic subjects reproduces cohort analysis of murine response to high fat diet” (*submitted to Pacific Symposium on Biocomputing*) (* joint first authorship)
1. Zaim, Samir *, Qike Li*, Grant Schissler*, Colleen Kenost, Yves Lussier. “Emergence of pathway biomarkers from converging heterogeneous Genome x Environment responses” (*submitted to Pacific Symposium on Biocomputing*) (* joint first authorship)

PAPERS IN PREPARATION

1. Li, Qike, Hao Helen Zhang, Joseph C. Watkins, Fiona M. McCarthy, “Identifying Differentially expressed genes: accounting for sampling bias”.