

# 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 of experience in data analytics using R, shell, and high throughput computing.
- Author of 3 R packages and a Shinny App.
- Proficient in Python, SQL, Spark.
- 4+ years of experience working in interdisciplinary teams.
- Solid understanding of statistical machine learning.
- 13 scientific papers (7 as first author) in applied statistics.
- Effective communication and visualization of data.

## EDUCATION

---

<b>Ph.D in Statistics</b>	2012-2017
<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)	

<b>MS Statistics</b>	2012-2014
<i>University of Arizona, Tucson, AZ</i>	

## TECHNICAL SKILLS

---

R, UNIX/Linux, Python, SQL, Spark, SAS, Git and GitHub, H2O, Cluster computing, distributed computing, HTML and CSS, Emacs and Elisp, LaTeX, Adobe Illustrator

## EXPERTISE

---

Large-scale inference, machine learning (linear and logistic regression, decision trees, GBM, SVM, KNN, k-means, random forest, dimensionality reduction, etc.), computing, data visualization, high-throughput data, high dimensional data, big data, multivariate statistics, single-subject inference, Bayesian statistics, time series, TensorFlow.

## 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*

Responsibilities include original methodology research, statistical support, grant writing, and software engineering.

- Developed statistical methods for advancing precision medicine. These methods were published in 3 peer-reviewed papers, implemented as R packages, used as a major component of an NIH grant, and being applied in more than 5 medical research projects.
- Engaged in interdisciplinary research: working with an expert team of statisticians, physicians, engineers, biologists, geneticists, and computer scientists.
- Served as an in-house statistical consultant to translate medical questions to data science problems, apply/develop machine learning/statistical algorithms to solve those problems, and communicate results through visualization, presentations, and reports.

### Research Assistant

2013-2014

*McCarthy Group, University of Arizona*

Developed statistical informatics methodology for RNA-Seq analysis.

## TALKS

---

- “The 2018 Pacific Symposium on Biocomputing”, The Big Island of Hawaii, USA, 1/5/2018
- “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

## AWARDS

---

- PSB 2018 Travel Award, Fall 2017, Pacific Symposium on Biocomputing
- 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

## 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

---

9. 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).
8. 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).
7. 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)
6. 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)
5. 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).

4. 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).
3. 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).
2. 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).
1. 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* **24**, 6 (2017).

## PAPERS UNDER REVIEW

---

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” (*accepted by 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” (*accepted by 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” (*accepted by Pacific Symposium on Biocomputing*) (\* joint first authorship)