

Qike Li

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EDUCATION

PhD Candidate in Statistics—Statistical Informatics track 2012-present
University of Arizona, Tucson, AZ
[Statistics Graduate Interdisciplinary Program \(GIDP\)](#)
Minor in Biostatistics
Advisors: Yves A. Lussier (Bioinformatics) & Hao Helen Zhang (Statistics)
Expected graduation date: August 2017

MS Molecular Biology 2006-2009
Guizhou University, Guiyang, China

BS Biotechnology 2001-2005
Zhengzhou University, Zhengzhou, China

RESEARCH AREAS

Statistical

Single-subject inference, large-scale inference, count data, multivariate statistics, computing, machine learning, high dimensional data, small-sample, paired-sample statistics, big data, data visualization, high-throughput data

Interdisciplinary

Biomedical informatics, bioinformatics, precision medicine, clinical translation, N-of-1, gene expression, gene set analysis, single-cell RNA-seq, cancer, systems biology, big clinical data

APPOINTMENT

Research Assistant 2014-current
Lussier Group, Center for Biomedical Informatics & Biostatistics, University of Arizona
Developing statistical informatics methodology for precision medicine. Engaging 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

Fionna McCarthy Group, University of Arizona

Developed statistical informatics methods for the analysis of high throughput sequencing data.

Research Technician

2010-2012

Rick Michod Group, University of Arizona

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

PUBLICATIONS [statistics]

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

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* (2017)(*in press*).

PAPERS IN PREPARATION

1. [Qike Li, Hao Helen Zhang, Yves A. Lussier, “iDEG: a single-subject method for assessing gene differential expression from two transcriptomes of an individual”](#).

TALKS

4. “Joint Statistical Meetings (JSM)”, Baltimore, USA, 7/30/2017
3. “[WNAR Annual Meeting](#)”, Santa Fe, USA, 6/27/2017
2. “The 6th Annual Translational Bioinformatics Conference”, Jeju, Korea, 10/16/2016
1. “Short Course: Computational methods for precision medicine and single subject studies with genomes and transcriptomes”, Jeju, Korea, 10/16/2016

POSTER SESSIONS AND SHOWCASES

2. University of Arizona Student Showcase, N-of-1-pathways for precision medicine, 2/22/2017
1. GIDP Student Research Showcase, N-of-1-pathways for precision medicine, 12/10/2015

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)

AWARDS

- [Fall 2016 HE Carter Travel Award](#), Graduate Interdisciplinary Programs, University of Arizona
- Summer 2017 HE Carter Travel Award, Graduate Interdisciplinary Programs, University of Arizona

TECHNICAL SKILLS

R (*advanced*), UNIX and BASH (*intermediate*), LaTeX (*intermediate*), Python (*basic*), HTML and CSS (*basic*), Adobe Illustrator, Emacs and Elisp, Cluster computing

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