

# Qike Li

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## EDUCATION

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**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

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### Statistical

*Single-subject 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

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**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]**

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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**

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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**

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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**

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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**

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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**

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- 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**

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- [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**

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

## **TEACHING**

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- 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*