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 Univeristy, Guiyang, China

BS Biotechnology 2001-2005
Zhengzhou Univeristy, Zhengzhou, China

RESEARCH AREAS

Statistical

Single-subject inference, large-scale inference, count data, multivariate statistics, computing, statistical machine learning, high dimensional data, Bayesian statistics, 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

5. "The 7th Annual Translational Bioinformatics Conference", Los Angeles, USA, 9/30/2017

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, 10/15/2016

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

- Distinguished Written Paper Award, June 2017, WNAR

- HE Carter Travel Award, Summer 2017, Graduate Interdisciplinary Programs, University of Arizona

- Travel Award, Summer 2017, Statistics GIDP, University of Arizona

- HE Carter Travel Award, Fall 2016, 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 Asisstant

- Spring 2016 **MCB 516A/416A: Statistical Bioinformatics and Genomic Analysis**
  Guest Lecturer

- Fall 2013 **ABE 613: Applied Biostatistics**
  Guest Lecturer