PROMOTION RECOMMENDATION
The University of Michigan
School of Public Health
Department of Biostatistics

Hui Jiang, assistant professor of biostatistics, Department of Biostatistics, School of Public Health, is recommended for promotion to associate professor of biostatistics, with tenure, Department of Biostatistics, School of Public Health.

Academic Degrees:

Ph.D.	2009	Stanford University (Computational and Mathematical Engineering)
M.S.	2004	Peking University (Computer Science)
B.S.	2001	Peking University (Computer Science)

Professional Record:

2011 - present	Assistant Professor, Department of Biostatistics, University of Michigan
2009 - 2011	Post-doctoral Scholar, Department of Statistics and Stanford Genome Technology Center, Stanford University

Summary of Evaluation:

Teaching: Professor Jiang is an outstanding and creative teacher who has taught some of the key and most challenging courses in our portfolio, with outstanding evaluations. Notably, he is currently teaching BIO 521 "Applied Biostatistics." This is one of the largest BIO core courses, a four credit class which teaches the fundamental statistical concepts related to the practice of public health to ~200 students. The course is highly heterogenous and challenging to teach, with many instructors scoring Q2 at 3.0 (or below) in their first attempts at teaching the course. Professor Jiang scored Q2 of 4.6 in the course. In a variety of other courses, he has always had outstanding evaluations, ranging from 4.13 to 5.0 overall. Highlights in his teaching portfolio include courses on analysis of modern DNA sequencing data (BIO 830, Q2: 4.5, 5.0, 4.8); on extensions of regression based analysis methods (BIO 651, the second course in our Masters level regression sequence Q2: 4.13 and 4.42); on statistical computing (BIO 615, 4.42 and 4.55); and an introduction to biocomputing (BIO 606).

Professor Jiang has also been active in doctoral student advising. He is also a highly sought-after member for doctoral thesis committees. He has served on fifteen doctoral committees since joining our faculty in the fall of 2011. Professor Jiang has been an active advisor for the university's Undergraduate Research Opportunity Program, advising six students between 2013-2015. Professor Jiang currently advises a Ph.D. student and two masters students and funds or has funded two biostatistics students.

Research: Professor Jiang works in the burgeoning field of statistics that seeks to develop and apply flexible and efficient computational methods for dealing with very large data, particularly the data that arises from modern biological experiments. He seeks to both develop generic computational strategies (such as improved methods for permutation based analyses) and better models for biology (such as improved methods for quantifying the expression of individual isoforms for each gene).

Professor Jiang is best known for two series of important contributions. In one line of work, he has developed methods for accurately quantifying gene expression levels using RNA-sequencing data and accounting for potential isoforms and batch effects and also developed methods for comparing these estimated expression levels between samples. In a second line of work, he has developed very efficient, generic methods for accurate assessment of p-values through permutation. Methods and ideas developed by Professor Jiang are used in the analysis of many modern studies and have also served as the foundation for further methods development by others.

Professor Jiang has 53 peer-reviewed articles (including those accepted for publication) including 14 as first and/or corresponding author. Among these, about one quarter are in absolutely top journals (*Nature Biotechnology, Bioinformatics x 7, Biometrika, Cancer Cell, Journal of the American Statistical Association, Genome Biology, Nature Communications, PNAS*). Thirty two of Professor Jiang's papers have already received >10 citations, including a combination of methodological papers and applied collaborations. His most cited paper, with 716 citations, describes software for analyzing CHIP-seq data (Ji, Jiang, Ma, Johnson, Myers and Wong, 2008, *Nature Biotechnology*). Among recent work, he has helped characterize diversity of the vaginal microbiome and its relationship with pre-term birth (Hyman et al, 2014, *Reproductive Sciences*, 94 citations), use RNA biomarkers to predict clinical outcomes (Mehra et al, 2014, *Neoplasia*; 38 citations), and evaluated gene expression patterns during the generation of induced pluripotent stem cells (Brady et al, 2013, *Nature Cell Biology*, 35 citations).

Recent and Significant Publications:
Segal B, Braun T, Elliott M, Jiang H. (2017) Fast approximation of small p-values in permutation tests by partitioning the permutations. *Biometrics* doi:10.1111/biom.12731.
Jiang H and Zhan T. (2017) Unit-free and robust detection of differential expression from RNA-Seq data. *Statistics in Biosciences*, 9(1): 178-199.
Jiang H, Mu JC, Yang K, Du C, Lu L, Wong WH. (2016) Computational aspects of optional polya tree. *Journal of Computational and Graphical Statistics*, 25(1): 301-320.
Shi Y, Chinnaiyan AM, Jiang H. (2015) rSeqNP: A non-parametric apaproach for detecting differential expression and splicing from RNA-Seq data. *Bioinformatics*, 31(13): 177-182.
Jiang H and Salzman J. (2012) Statistical properties of an early stopping rule for resampling-based multiple testing. *Biometrika*, 99(4): 973-980.
Salzman J, Jiang H, Wong WH. (2011) Statistical modeling of RNA-Seq Data. *Statistical Science*, 26(1): 62-83.

Service: Professor Jiang is a regular contributor to department life and committees. He is a thoughtful contributor to faculty meetings and discussion and has performed generously in a variety of key committees, including the seminar committee, where he co-managed our seminar program for 2011/12; the admissions committee, which reviews and prioritizes among hundreds of applicants for our highly selective doctoral and masters program, the candidacy committee, which manages and grades the annual qualifying exam; and the qualifying exam review committee. His service on the candidacy and admissions committee has been especially valuable to the department, since the two committees have substantial workloads.

Professor Jiang is a regular contributor beyond the department. He has chaired sessions for several national and international conferences, such as the Joint Statistical Meetings and the International Chinese Statistical Association International Conference. He has also organized sessions for both the Western and Eastern North American Region meetings of the International Biometric Society. Together, these are the three most important annual meetings for U.S.-based biostatisticians. In addition to these roles, he is a regular reviewer for several top journals both in the areas of biostatistics and statistical genetics and genomics and is currently serving on the editorial board of *Scientific Reports*.

External Reviewers:
Reviewer A: "This paper is a foundational contribution to RNA-Seq data analysis... The files for raw RNA-Seq counts can easily be hundreds of gigabytes. To handle dataset of this magnitude and provide efficient computation tools demands tremendous computational skills."

Reviewer B: "More importantly, his strong computer science background has given him a unique advantage in terms of building software tools based on the methods and algorithms he has developed. His publication list is excellent in both quality and quantity."

Reviewer C: "This represents a major advance over the aforementioned two papers [also published by Jiang] in that it presents a unified statistical model that allows joint detection of differential gene expression and between-sample normalization from RNA-seq data. This unified framework is highly desirable due to its simplicity, and I anticipate that it will be widely used in RNA-seq studies."

Reviewer D: "Hui has made fundamental contributions to high-through genomic data analysis."

Reviewer E: "Together with his collaborator, Dr. Jiang introduced a novel early stopping rule that can substantially reduce computing time for resampling-based multiple hypothesis testing procedures. The paper is published after he became independent and is published in one of the top four journals of the statistical field."

Reviewer F: "In this paper he presents a unit free method for detecting differential expression, using a unified model that also combines normalization. This unit free approach means his method can be applied to data that have undergone preprocessing pipelines."

Reviewer G: "Going forward, I believe Dr. Jiang's skills will be in high demand. His blend of statistical, computational, bioinformatics and genomics expertise will be useful in both collaborative research as well as in the development of methods and software for the rapidly expanding field of data-driven genome science."

Reviewer H: "Dr. Jiang is among the best in his cohort and many of his cohort have been promoted to tenured positions at other leading research universities."

Summary of Recommendation:

Professor Jiang is an excellent teacher and an outstanding researcher, who provides the department with key expertise and leadership in the areas of computational statistics, statistical genomics and bioinformatics. It is with the support of the School of Public Health Executive Committee that I recommend Hui Jiang for promotion to associate professor of biostatistics, with tenure, Department of Biostatistics, School of Public Health.

Cathleen M Connell, Ph.D.
Interim Dean, School of Public Health

May 2018