

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

Xiaoquan W. Wen, associate professor of biostatistics, with tenure, Department of Biostatistics, School of Public Health, is recommended for promotion to professor, with tenure, Department of Biostatistics, School of Public Health.

Academic Degrees:

Ph.D.	2011	University of Chicago, Statistics, Chicago, IL
M.S.	2002	University of Illinois at Chicago, Computer Science, Chicago, IL
M.S.	2000	University of Illinois at Chicago, Mathematics, Chicago, IL
B.S.	1998	Peking University, Chemical Physics, Peking, China

Professional Record:

2017 – Present	Associate Professor, Department of Biostatistics, University of Michigan, Ann Arbor, MI
2011 – 2017	Assistant Professor, Department of Biostatistics, University of Michigan, Ann Arbor, MI
2007 – 2011	Research Assistant, Department of Statistics, University of Chicago, Chicago, IL
2002 – 2007	Research Computer Scientist, University of Chicago, Chicago, IL

Summary of Evaluation:

Teaching: Professor Wen has played an important role in teaching machine learning courses for the new Department of Biostatistics Health Data Science sub-plan. BIOS 626 is a new elective course on machine learning created by Professor Wen in 2017, that supported the launch of this new program in Fall 2019. In addition, Professor Wen has taught BIOS 680, Applications of Stochastic Processes I, a total of three times at his current rank. Overall, his Q1 and Q2 scores have been very good to excellent (Q1: 4.56 – 4.78; Q2: 4.65 – 4.85). Since 2017, Professor Wen has chaired or co-chaired three doctoral student committees, and he has served as a committee member for 10 students, primarily in the Department of Biostatistics, but also in the Department of Computational Medicine and Bioinformatics and the Department of Ecology and Evolutionary Biology at the University of Michigan.

Research: Professor Wen's research program focuses on the development of statistical and computational methods to address emerging scientific problems in genetics, genomics, and other areas. His research innovations span both traditional statistics and statistical genetics and prioritize statistical rigor and reproducibility as well as computational efficiency and scalability. Specifically, Professor Wen has made methodological contributions to integrative analysis of high throughput genetic, genomic, and phenotype data by developing Bayesian methods for colocalization analysis and transcriptome-wide association studies (TWAS). These contributions include methods and software that use probabilistic annotations to study the degree of enrichment of quantitative trait loci (QTLs), such as ENLOC, fastENLOC, DAP-G and BAGSE. He and his collaborator also developed probabilistic transcriptome-wide association studies (PTWAS) to perform TWAS scans and estimate cell type/tissue-specific gene-to-trait effects, as well as PhenomeXcan, that nicely combines colocalization and TWAS methods to improve integrative whole genome analysis. In addition, Professor Wen has played a leading analytic role in the Genotype-Tissue Expression (GTEx)

consortium by developing methods for analysis of genomewide SNPs and expression data and applying these methods to analysis of the GTEx data.

Professor Wen has published a total of 60 papers (12 as first author), 28 at the rank of associate professor. Of the 28 papers published since 2017, he is first or senior author for nine. Professor Wen's work has been published in prestigious scientific journals, such as *Nature*, *Science*, *Cell*, *Nature Methods*, *Nature Genetics*, *Genome Biology*, *American Journal of Human Genetics*, *PLOS Genetics*, and *Nature Communications*, as well as leading statistical journals, such as *Annals of Applied Statistics*, *Biostatistics*, and *Biometrics*. He notably co-authored several high profile GTEx consortium papers, including one GTEx consortium paper in *Science* in 2020. According to Google Scholar, his publications have been cited over 18,000 times. In addition, Professor Wen has developed 14 software tools. Of these, three were developed since 2017 and derive directly from his research program and scientific publications: INTRIGUE (software package for reproducibility assessment in high-throughput experiments), fastENLOC (colocalization analysis of molecular QTLs and SWAS hits), and PTWAS (causal inference of molecular and complex traits). Professor Wen has a well-established record of funding. He is the principal investigator of a prestigious MIRA (R35) award from the National Institute of General Medical Sciences (NIGMS) to study causality, risk prediction, and reproducibility in genomic research. Additionally, he serves as a multiple principal investigator (subcontract primary investigator) for a National Institutes of Health (NIH) R01 grant entitled "Functional genomics of G x E in cardiovascular disease," and he is a co-investigator for three other NIH R01 grants. He also served as a subcontract principal investigator for an R01 while in rank.

Recent and Significant Publications:

- Hukku, A., Pividori, M., Luca, F., Pique-Regi, R., Im, H. K., and Wen, X. (2021). Probabilistic colocalization of genetic variants from complex and molecular traits: promise and limitations. *The American Journal of Human Genetics*, 108(1), 25-35. PMID: 33308443
- Zhao, Y., Sampson, M. G., Wen, X. (2020). Quantify and control reproducibility in high-throughput experiments. *Nature Methods*, 17(12), 1207-1213. PMID: 33046893
- Chen, Y., Quick, C., Yu, K., Barbeira, A., Luca, F., Pique-Regi, R., Im, H.K., and Wen, X. (2020). PTWAS: Investigating tissue-relevant causal molecular mechanisms of complex traits using probabilistic TWAS analysis. *Genome Biology*, 21: 232. PMID: 32912253
- Hukku, A., Quick, C., Luca, F., Pique-Regi, R. and Wen, X. (2020). BAGSE: A Bayesian Hierarchical Model Approach for Gene Set Enrichment Analysis. (original paper). *Bioinformatics*, 36(6): 1689-95.
- Wen, X., Pique-Regi, R., Luca, F. (2017). Integrating Molecular QTL Data into Genome-wide Genetic Association Analysis: Probabilistic Assessment of Enrichment and Colocalization. *PLOS Genetics*, 13(3):e1006646.

Service: Professor Wen's service record at rank includes participation in departmental committees and the summer institute, as well as service and leadership for scientific journals. In the past four years, Professor Wen has served on three departmental committees (Curriculum Committee for three years, Admissions Committee for one year, and Faculty Search Committee for two years) and has served as program faculty for the Big Data Summer Institute at the University of Michigan for three years (2018-2021). He is also review editor for *Frontiers in Genetics* and was a guest editor for *PLOS Genetics* in 2018. Additionally, Professor Wen regularly serves as a reviewer for a number of high impact journals in genetics and statistics.

External Reviewers:

Reviewer A: “Dr. Wen’s publication record is outstanding...What is impressive is that 15 of these publications are since 2020 and it is likely that this tremendous trajectory will only accelerate. What is impressive about Dr. Wen’s publication record is that breadth of his papers. His highlighted publications describing novel statistical methodologies for the analysis of genetic data as well as new directions in reproducibility research...Some of these are published in high impact genetics journals while others are published in statistics journals. He also has several papers on analysis of large genetic datasets as part of consortia. There relatively few researchers with this breadth of work.”

Reviewer B: “Overall, Dr. Wen’s research is of outstanding quality and he has made significant contributions to the field of statistical genetics and genomics. Compared to his peers at similar career stage, Dr. Wen’s research productivity, quality and impact are all highly impressive.”

Reviewer C: “Integrative analysis of genetic, genomic and phenotype data, such as GWAS, gene expressions and complex traits, is of substantial interest in genetic research to understand the molecular mechanism of human diseases and traits. ... These methods provide valuable tools to integrate different types of data to understand molecular mechanisms in genetic associations.”

Reviewer D: “The contributions of Dr. Wen in the development of new methods for genomic data put him in the top tier of statisticians working in this area.”

Reviewer E: “One common thread of Dr. Wen’s work is the formulation of the statistical problem in a Bayesian setting and the consideration and modeling of uncertainty in detecting genetic association signals, causal inference, and enrichment analysis. His work is novel, insightful, and thorough. ... Given his outstanding publications, both in methodology and collaborations, Dr. Wen is clearly among the very best statistical geneticists.”

Summary of Recommendation: Professor Wen’s research centers on developing statistically sound and computationally efficient methods to address emerging scientific problems from genetics, genomics, and other natural sciences. His work is characterized by statistical rigor, computational scalability, creative elegance, and significant impact. He is an excellent teacher, playing an important role in the teaching of machine learning at the school and is an active member of the school, university, and professional communities. It is with the support of the School of Public Health Executive Committee that I recommend Xiaoquan W. Wen for promotion to professor of biostatistics, with tenure, Department of Biostatistics, School of Public Health.



F. DuBois Bowman, Ph.D.
Dean, School of Public Health

May 2022