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

Seunggeun Lee, 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.   2010   University of North Carolina, Chapel Hill (Biostatistics)
B.S.   2005   Seoul National University (Biology & Statistics)

Professional Record:
2013 - present   Assistant Professor, Department of Biostatistics, University of Michigan
2010 - 2013   Research Fellow, Department of Biostatistics, Harvard University

Summary of Evaluation:
Teaching: Professor Lee is a versatile teacher who has taught both core courses in our masters program and specialized courses for our doctoral students. His teaching load has been relatively light as a condition of his NIH K99/R00 award, which covers 75% of his salary but requires that he teach no more than one course per year. Professor Lee has taught BIOSTAT 651 (the second course in our 3-course series on regression models) for three years, with generally great evaluations. He has also taught a special topics course on advanced models for genetic association studies and interaction analyses with excellent scores (Q1=4.38, Q2=4.60). In this course, he introduces students to emerging ideas from his own research and other cutting edge methods. Professor Lee is very active in doctoral student advising, serving as an advisor or co-advisor to seven biostatistics students; this unusual level of engagement for a junior faculty member with doctoral students demonstrates the esteem in which his research is held. He currently chairs four dissertation committees and funds three GSRA positions.

Research: Professor Lee is an outstanding researcher who provides the department with key expertise and leadership in the areas of computational biology and statistical genetics, next generation sequencing and high dimensional data analysis. His work is widely recognized as setting the standard for effective analysis of large DNA variation datasets. Professor Lee broadly works in the quickly developing field of statistics that seeks to develop and apply methods for the analysis of emerging genomic datasets. Within this rich and fertile research area, Professor Lee has focused particularly on the analysis of genetic association studies, especially those studies that seek to analyze rare genetic variants (such as might be discovered through the application of new sequencing technologies) and on the analysis of large datasets, with 10,000s or 100,000s of individuals (as are now available through the application of social media and electronic health record based phenotyping). The analysis of these studies poses unique challenges. For example, when analyzing datasets with 100,000s of individuals many have observed that traditional regression based approaches (such as logistic regression and score tests) have poor statistical properties, particularly when outcomes or predictors are rare. Also challenging, these analyses must account for population structure and relatedness among

samples. The methods developed by Professor Lee tackle these and other challenges in innovative and computationally efficient ways and are now widely used both by other statisticians (as the foundation for new methods) and by geneticists and biologists who are seeking to understand large datasets. These methods help scientists understand the genome, identify disease associated genetic variants and, ultimately, obtain the knowledge that will allow us to precisely understand the biology of human disease and identify new opportunities for treatment and intervention.

Professor Lee has 41 published articles (including 14 as first author). He has provided opportunities for doctoral students to co-author with him. Many of these publications are in top journals (*Nature Genetics, American Journal of Human Genetics, Biometrika, Journal of the American Statistical Association* and *Biostatistics)* and, cumulatively, his work has been cited >3,000 times.

Professor Lee is a sought after collaborator and his research is supported through multiple NIH grant proposals including some as the principal investigator which are focused on his methodological research, and as a collaborator, which are typically focused on the analysis and interpretation of challenging datasets. He is currently the PI on an R01 grant. Professor Lee was also the recipient of a prestigious NIH Pathway to Independence K99/R00 award, which provides support to promising investigators to jump start their careers. He is the first member of the Department of Biostatistics at the University of Michigan to be the recipient of such an award. Professor Lee is or has been a co-investigator on five additional federal grants.

Recent and Significant Publications:
Dey R, Schmidt EM, Abecasis GR, and Lee S. (2017) A fast and accurate algorithm to test for binary phototypes and its application to PheWAS. *American Journal of Human Genetics*, 101(1): 37-49.
Lee S, Sun W, Wright FA, and Zou F. (2017) An improved and explicit surrogate variable analysis procedure by coefficient adjustment. *Biometrika*, 104: 303-316.
Shi J, and Lee S. (2016) A novel random effect model for GWAS meta-analysis and its application to trans-ethnic meta-analysis. *Biometrics*, 72: 945-954.
Lee S, Teslovich T, Boehbke M, and Lin X. (2013) General framework for meta-analysis of rare variants in sequencing association studies. *American Journal of Human Genetics*, 93: 42-53.
Lee S, Emond MJ, Bamshad MJ, Barnes KC, Rieder MJ, Nickerson DA, NHLBI GO Exome Sequencing Project, Christiani DC, Wurfel MM, and Linn X. (2012) Optimal unified approach for rare variant association teting with application to msall sample case-control whole-exome sequencing studies. *American Journal of Human Genetics*, 91: 224-237.

Service: Professor Lee is a regular contributor to department life and committees. He is a thoughtful contributor to faculty meetings and has served as a member of departmental search committees and the admissions committee, which both involve relatively heavy workloads. Professor Lee has also been an important contributor to the profession. He has organized sessions for the Joint Statistical Meetings and the International Chinese Statistical Association. He served as a program committee member for the Eastern North American Region spring

meeting, which is one of the premier annual meetings for biostatisticians. In addition to these roles, he is a regular reviewer for several top biostatistics and genetics journals.

External Reviewers:

Reviewer A: "Frankly and honestly speaking, this is a rare and strong case that an outside reviewer does not need to elaborate much on the candidate's exceptional achievements and bright future…I most enthusiastically support his promotion to a tenured associate professor."

Reviewer B: "I personally find his recent work on fast and accurate score tests for genome wide association of large numbers binary phenotypes (fastSPA) to be particularly exciting."

Reviewer C: "In the field of rare variant analysis, he was the first author of a series of milestone papers that developed the extremely well-received method for rare variant association tests, i.e. SKAT-O which smartly combines the two commonly used yet complementary strategies in a data adaptive fashion."

Reviewer D: "Dr. Lee has published extremely high quality work with important scholarly impact. Dr. Lee is in the very top of his field and has made a large number of important contributions to statistical genetics. His many successes are reflected in his high-profile papers, the number of times his software has been downloaded, and his receipt of a number of grants."

Reviewer E: "Professor Lee's contributions to the area have been of great significance and his methods have far-reaching applications within the field…He is an outstanding statistical geneticist with significant contributions to date, and huge potential for an even bigger transformational role in the field of human genetics going forward."

Reviewer F: "Most of his papers appeared in top statistical and genetic journals…This publication record is truly outstanding. I am not aware of anyone in his peer group who has a stronger publication record."

Summary of Recommendation:

Professor Lee is an outstanding researcher working in a rapidly growing and informative area of statistics that is expected to provide many insights about human biology and other big data problems. It is with the support of the School of Public Health Executive Committee that I recommend Seunggeun Lee 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