Approved by the Regents
May 17, 2018

PROMOTION RECOMMENDATION
THE UNIVERSITY OF MICHIGAN
MEDICAL SCHOOL
DEPARTMENT OF COMPUTATIONAL MEDICINE AND BIOINFORMATICS
DEPARTMENT OF HUMAN GENETICS

Ryan Mills, Ph.D., assistant professor of computational medicine and bioinformatics, Department of Computational Medicine and Bioinformatics, and assistant professor of human genetics, Department of Human Genetics, Medical School, is recommended for promotion to associate professor of computational medicine and bioinformatics, with tenure, Department of Computational Medicine and Bioinformatics, and associate professor of human genetics, without tenure, Department of Human Genetics, Medical School.

Academic Degrees:

Ph.D.	2006	Georgia Institute of Technology
M.S.	2003	Georgia Institute of Technology
A.B.	2000	Wabash College

Professional Record:

2012-present	Assistant Professor of Computational Medicine and Bioinformatics, University of Michigan
2012-present	Assistant Professor of Human Genetics, University of Michigan

Summary of Evaluation:

Teaching: Since 2014, Dr. Mills has been the Course Master for Bioinformatics 527: Introduction to Bioinformatics. He has also been the Course Master for Bioinformatics 606 since 2016. This is a five-day workshop (five hours each day) on the Introduction to Biocomputing that introduces new graduate students to computational methods, tools, techniques, and best practices that foster reproducible research in bioinformatics, genome informatics, and biostatistics. This workshop is given jointly with the Department of Biostatistics in SPH with outstanding evaluations. In addition, he gives lectures in Bioinformatics 525: Foundations in Bioinformatics and Systems Biology; Human Genetics 551: Computational Genomics; Human Genetics 632: Experimental Genetics Systems; and in Human Genetics 803: Advanced Topics in Genetics. Dr. Mills currently mentors three bioinformatics graduate students and one human genetics graduate student; he also has one graduate student co-mentored with Dr. Sally Camper. He has had one graduate student successfully defend her thesis, and this individual is now completing a post-doctoral fellowship at Harvard Medical School. He has also mentored two post-doctoral fellows, one currently, and one who is now doing a second fellowship at the University of Minnesota. Dr. Mills has served on 15 dissertation committees and 19 preliminary examination committees. Dr. Mills received the 2014 Endowment for the Basic Sciences Teaching Award.

Extramurally, Dr. Mills continues to teach in the annual Mathematical and Theoretical Biology Institute (MTBI) at Arizona State University, as a member of the UM Genome Sciences Training Program (GSTP) faculty. This involves multiple lectures over two days, covering mathematical genetics as part of a joint REU undergraduate program with Arizona State University. This workshop is aimed in part at encouraging underrepresented minorities (URMs) to consider graduate level education. In addition, in 2014, Dr. Mills developed an online Coursera course: Introduction to Bioinformatics that consists of three modules (15 minutes each) covering introductory concepts in genomics, genetic variation, and disease genes.

Research: Dr. Mills' primary research thrust is that of sequencing and analyzing genomes to identify the underlying genetic variation between individuals and to explore what role those changes have on human phenotypes. His research laboratory develops and implements methods to precisely identify and resolve diverse types of genomic variation with the goal of integrating this information with other forms of biologically and medically relevant data to improve the overall understanding of human health and disease. He has applied this research in funded work in Schizophrenia (with John Moran) and in Neurological Diseases (with Peter Todd). Dr. Mills currently has 52 total publications across a variety of bioinformatics and genomics related themes, and has three additional senior author papers soon to be submitted. Dr. Mills' research is primarily funded through an R01 awarded by the NIH, for which a competitive renewal application titled "Discovery and Analysis of Structural Variation in Whole Genome Sequences" was recently submitted (July 2017). He also has funding through various collaborative projects including "Schizophrenia Genetics and Brain Somatic Mosaicism," a NIH U01, and "An Integrative Analysis of Structural Variation for the 1000 Genomes Project," also a NIH project through a consortium with the Jackson Laboratory. In addition, he has another NIH R01 pending as a co-PI, entitled "Characterization and Impact of Structural Variation on Gene Regulatory Elements."

Dr. Mills' vision is to build upon the novel methodological foundations his lab has developed and disseminated, and to develop new avenues for analysis that will traverse individual data layers and allow an integrated examination of complex cellular and tissue systems. He believes that the future advancements of knowledge into the complex interplay of cellular systems and disease phenotypes will require such integrative solutions, and will allow for a deeper understanding of their medical implications. He is also continuing his well-respected efforts to improve structural variation detection in whole genome sequence data, using short- and long-read data sources. His efforts in this area should continue to have a major impact on how the genomics field identifies and addresses structural variation, and will likely lead to new insights into their impact on human health and disease. Dr. Mills was an invited speaker at the Wellcome Trust Sanger Institute (2012); and was a speaker and platform moderator for the American Society of Human Genetics Annual Meeting in 2014. He also was an invited speaker in 2013 for the Radiation Effects Research Foundation in Hiroshima, Japan; and in 2016 he gave an invited presentation at the Ewha Woman's University in July of 2016, in Seoul, South Korea. As this record indicates, his work is widely appreciated and respected both nationally and internationally.

Recent and Significant Publications:

Zhao X, Weber AM, Mills RE: A recurrence based approach for validating structural variation using long-read sequencing technology. *Gigascience* 6:1-9, 2017.

Zhao X, Emery SB, Myers B, Kidd JM, Mills RE: Resolving complex structural genomic rearrangements using a randomized approach. *Genome Biology* 17:126, 2016.

Chun SY, Rodriguez CM, Todd PK, Mills RE: SPECtre: a spectral coherence--based classifier of actively translated transcripts from ribosome profiling sequence data. *BMC Bioinformatics* 17:482, 2016.

Sudmant PH, Rausch T, Gardner EJ, Handsaker RE, Abyzov A, Huddleston J, Zhang Y, Ye K, Jun G, Hsi-Yang Fritz M, Konkel MK, Malhotra A, Stutz AM, Shi X, Paolo Casale F, Chen J, Hormozdiari F, Dayama G, Chen K, Malig M, Chaisson MJ, Walter K, Meiers S, Kashin S, Garrison E, Auton A, Lam HY, Jasmine Mu X, Alkan C, Antaki D, Bae T, Cerveira E, Chines P, Chong Z, Clarke L, Dal E, Ding L, Emery S, Fan X, Gujral M, Kahveci F, Kidd JM, Kong Y, Lameijer EW, McCarthy S, Flicek P, Gibbs RA, Marth G, Mason CE, Menelaou A, Muzny DM, Nelson BJ, Noor A, Parrish NF, Pendleton M, Quitadamo A, Raeder B, Schadt EE, Romanovitch M, Schlattl A, Sebra R, Shabalin AA, Untergasser A, Walker JA, Wang M, Yu F, Zhang C, Zhang J, Zheng-Bradley X, Zhou W, Zichner T, Sebat J, Batzer MA, McCarroll SA, Genomes Project C, Mills RE[#], Gerstein MB[#], Bashir A[#], Stegle O[#], Devine SE[#], Lee C[#], Eichler EE[#], Korbel JO[#]: An integrated map of structural variation in 2,504 human genomes. *Nature* 526:75-81, 2015. ([#]co-senior authors)

Dayama G, Emery SB, Kidd JM, Mills RE.: The genomic landscape of polymorphic human nuclear mitochondrial insertions. *Nucleic Acids Research* 42:12640-12649, 2014.

Service: Dr. Mills has a good record of regional and national service engagement. He is on the program committee for the 2017 Great Lakes Bioinformatics Conference, a conference associated with the International Society for Computational Biology (ISCB), in which he been a member of the since 2011. Dr. Mills is also a member of the American Society of Human Genetics (ASHG), most recently serving as an abstract reviewer for the 2016 ASHG Meeting. Dr. Mills has served an ad hoc member of the 2016 NIH GCAT and MIRA Study Sections. He has also served on as an ad hoc member of several NIH and NIH/NHGRI Study Sections. Dr. Mills serves on the editorial boards of *Scientific Reports* and *PeerJ.* He also serves as an ad hoc journal reviewer for the *American Journal of Human Genetics*, *BMC Bioinformatics*, *Bioinformatics*, *Genome Biology*, *Genome Research*, *Nature Genetics*, *Nature Communications*, *Nature Protocols*, *Human Genetics*, and *PLoS Computational Biology and Methods*.

Locally, Dr. Mills is a member of the Bioinformatics Ph.D. and Master's Program Admission Committees, and was a co-chair of the DCM&B Seminar Series Committee from 2014-16; in addition, he has served as the committee chair of DCM&B's Website Committee for the past two years. Dr. Mills is a member of the new EBS Basic Science Faculty Research IT Committee and will serve as a faculty advisor to the Bioinformatics Core Biomedical Research Core Facilities in Medical School Administration in the upcoming year.

External Reviewers:

Reviewer A: "As a faculty member, Dr. Mills has also contributed as a middle author to the most recent 1000 Genomes structural variant catalog (Nature, 2015). This has provided the most

extensive catalog of structural genetic variants now existing, and it is widely used. The associated catalog of mobile element insertions made by the 1000 Genomes collaborative, which Dr[.] Mills has also contributed to, is absolutely a *tour-de-force*—the most encompassing, high-quality collection existing today."

Reviewer B: "Dr. Mills has gotten some outstanding publications out of his collaborative interactions, including Genome Research, Science, Nature, and Genome Biology, among others. However, Dr. Mills has also made an impact beyond those collaborations with his own methodology development."

Reviewer C: "Dr. Mills is making important contributions to our understanding of genetic polymorphisms. Of particular note is the work he has done to uncover and understand structural variations in the human genome, and their relation to human disease....Dr. Mills is clearly emerging as a leader in the large arena of disease related genetic polymorphism."

Reviewer D: "Dr. Mills entertains very high standing in the academic community. That high standing and his productivity is attested to by his excellent funding record....This impressive range of activities demonstrates his versatility and his likely ongoing contributions both the basic science and to clinically relevant research."

Reviewer E: "Dr. Mills has generated a body of work that is of outstanding quality with a highly significant impact on the field of human genetics and genomics....Dr. Mills' involvement in the 1000 Genomes Project's Structural Variation Analysis Group, has led to some of his best papers and contributions to the entire research community."

Summary of Recommendation:

Dr. Mills has gained an impressive national and international reputation for his work in developing methodology for genomic and bioinformatics analysis. His publication and sponsored research records are exemplary. In addition, Dr. Mills has been a dedicated teacher and mentor. I am pleased to recommend Ryan Mills, Ph.D. for promotion to associate professor of computational medicine and bioinformatics, with tenure, Department of Computational Medicine and Bioinformatics, and associate professor of human genetics, without tenure, Department of Human Genetics, Medical School.

Marschall S. Runge

Marschall S. Runge, M.D., Ph.D.
Executive Vice President for Medical Affairs
Dean, Medical School

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