OMB No. 0925-0001 and 0925-0002 (Rev. 09/17 Approved Through 03/31/2020)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.  
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: FREDERICK JOSEPH BOEHM, III

eRA COMMONS USER NAME (credential, e.g., agency login): fjboehm

POSITION TITLE: Postdoctoral associate

EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

| INSTITUTION AND LOCATION | DEGREE  (if applicable) | Start Date  MM/YYYY | Completion Date  MM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- | --- |
| University of Wisconsin-Madison, Madison, Wisconsin, USA | B.S. | 09/1996 | 05/2001 | Chemistry, mathematics, biochemistry |
| University of Wisconsin-Madison, Madison, Wisconsin, USA | M.S. | 01/2003 | 08/2007 | Population health sciences |
| University of Wisconsin-Madison, Madison, Wisconsin, USA | M.D. | 08/2003 | 08/2007 | Medicine |
| University of Wisconsin-Madison, Madison, Wisconsin, USA | Ph.D. | 09/2011 | 05/2019 | Statistics |
| University of Massachusetts Medical School, Worcester, Massachusetts, USA |  | 09/2019 |  | Statistical genetics |

**A. Personal Statement**

**I will use this fellowship training to develop Bayesian statistical methods to advance complex trait genetics. Specifically, I will implement a Bayesian hierarchical model for inferring allelic series at QTL. I will then apply this approach to traits in Diversity Outbred and Collaborative Cross mice. I first infer the allelic series at a QTL in Diversity Outbred mice. Then, because Diversity Outbred and Collaborative Cross mice share the same founders, I use the inferred allelic series to reduce the number of parameters fitted in the QTL scan in Collaborative Cross mice. This provides more statistical power to detect QTL with the specified allelic series.**

**My previous research in developing frequentist (not Bayesian) statistical methods for complex trait genetics resulted in multiple published journal articles reporting new methods, applications, and software. I now use the proposed fellowship training to elaborate my statistical methods skills set with research in a Bayesian framework. I anticipate leveraging both Bayesian and frequentist methods in subsequent methods development research.**

**B. Positions and Honors**

***Honors***

**Best poster award, International Mammalian Genome Society, 2018**

**Travel scholarship, International Mammalian Genome Society, 2018**

**Research ethics fellowship, University of Wisconsin-Madison, 2013**

**New arts venture challenge award, University of Wisconsin-Madison, 2013**

**Medical student research training fellowship, Howard Hughes Medical Institute, 2006**

**Family medicine research stipend, University of Wisconsin-Madison, 2004**

**Shapiro research award, University of Wisconsin-Madison, 2004**

**University Bookstore award for outstanding thesis, University of Wisconsin-Madison, 2001**

**Meyerhoff excellence award, University of Wisconsin-Madison, 2001**

**Graduate research fellowship, National Science Foundation, 2001**

**Panek memorial research scholarship, University of Wisconsin-Madison, 2000**

**Hilldale research fellowship, University of Wisconsin-Madison, 1999**

**Wisconsin Idea fellowship, University of Wisconsin-Madison, 1999**

**Chemistry research scholarship, University of Wisconsin-Madison, 1998**

**Wisconsin academic excellence scholarship, 1996**

***Positions***

**Senior fellow, University of Washington, Department of Biostatistics, November 2007 to September 2009**

**Assistant researcher, University of Wisconsin-Madison, Value-added Research Center, January 2011 to August 2011**

**Postdoctoral fellow, University of Wisconsin-Madison, Molecular and environmental toxicology center, February 2012 to January 2014**

**C. Contributions to Science**

***1. Developing multivariate QTL mapping methods for systems genetics studies***

***2. D****iverse applications of text analysis methods*****

*****3. Creating and implementing a quality control pipeline for genome-wide association studies*****

*****4. Epidemiological studies of HIV and other STDs in resource-poor settings*****

*****5. Chemical tools to explore immune cell recognition*****

**D. Additional Information: Research Support and/or Scholastic Performance**

| YEAR | COURSE TITLE | GRADE |
| --- | --- | --- |
|  | | |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |