NATIONAL LIBRARY OF MEDICINE, NIH
BOARD OF SCIENTIFIC COUNSELORS
MEETING MINUTES
April 7, 2022

The Board of Scientific Counselors of the National Library of Medicine (NLM) convened by webcast on April 7, 2022, between 11:00 a.m. and 4:30 p.m. The meeting was open for viewing via NIH VideoCast.

BSC Members Participating
Peter Tarczy-Hornoch, MD, University of Washington *(BSC Chair)*
Graciela Gonzalez Hernandez, PhD, University of Pennsylvania
Hyun Min Kang, PhD, University of Michigan
Kateryna Makova, PhD, Pennsylvania State University
Lucila Ohno-Machado, MD, PhD, University of California San Diego
Ming Jack Po, MD, PhD, Google Health
Donna Slonim, PhD, Tufts University
Pamela Soltis, PhD, University of Florida
Jessica Tenenbaum, PhD, Duke University
Valerie Florance, PhD, NLM *(Executive Secretary)*

BSC Ad Hoc Member
Bonnie Berger, PhD, Massachusetts Institute of Technology

NIH Staff Presenting
Patricia Flatley Brennan, RN, PhD, NLM
Valerie Florance, PhD, NLM

NLM Tenure-Track Investigators Receiving Review
Xiaofang Jiang, PhD, NCBI, NLM
Lauren Porter, PhD, NCBI, NLM

1. Welcome and logistics – Peter Tarczy-Hornoch

Dr. Tarczy-Hornoch welcomed participants to the meeting and outlined the schedule for the day.

2. Remarks from NLM Director – Patricia Flatley Brennan

Dr. Brennan thanked the BSC members for their service to NLM. She highlighted recent NLM activities, including:

- Plans for staff to return to the workplace and anticipated flexibilities
- Progress on NLM's Strategic Plan
- Development of video vignettes of NLM researchers
- Submission to NIH of NLM's Racial and Ethnic Equity Plan (REEP) and empanelment of an NLM Inclusiveness, Diversity, Equity and Accessibility (IDEA) Council
- Progress on the renovation of NLM's building
- Search for a new NLM Scientific Director

Dr. Brennan also updated the BSC on NIH's Policy for Data Management and Sharing, which goes into effect in January 2023, as well as on NLM's budget. She noted NLM's intent to provide additional investigator tracks and to modernize its computer infrastructure.

3. Remarks from NLM Acting Scientific Director – Valerie Florance

Dr. Florance summarized the findings of a report to the NIH Equity Committee (NEC), which reviews diversity, inclusion, and equity metrics for each Intramural Research Program (IRP) at NIH. She presented tables on the gender and race/ethnicity of NLM investigators and scientists, noting that the lack of gender parity and the minimal number of underrepresented minorities indicates NLM has "work to do in order to get to the place where we want to be." Dr. Florance added that one recommendation she made to the NEC was for increased visibility on the NIH IRP website of clinical informatics and biomedical data science to help with recruitment.

Dr. Florance also described NLM's Diversity in Data Science and Informatics (DDSI) Research program, which provides interns with a mentored research project, cohort activities (e.g., a codeathon and a journal club), mentorship and role model activities (e.g., a career panel with NLM alumni working in bioinformatics and computer science), and workshops hosted by the NIH Office of Intramural Training. The summer program has matched five DDSI interns to investigators in NLM's IRP. The next cycle of applications will be in November 2022 for 2023 internships.

Dr. Florance also described plans for the 9th floor of building 38A, which will be home to the Scientific Director of NLM's IRP, the IRP Training Coordinator, and offices and cubicles for a mix of IRP staff from the Computational Biology Branch and the Computational Health Research Branch.

In the Q&A session following Dr. Florance's presentation a BSC member asked whether there were plans to increase the visibility of the DDSI intern program beyond HBCUs since many institutions might have candidates. Dr. Florance responded that NLM started with a very targeted focus, but that going forward the program will be broader in scope.

4. Presentation and Review of Xiaofang Jiang, Tenure-Track Investigator

Dr. Jiang noted that her group's focus has been on using comparative genomics to predict microbial function, but that with the emergence of the COVID-19 pandemic, they shifted approximately 35% of their efforts to COVID-19-related research.
Dr. Jiang focused her presentation on three of her group's research projects:

- Functional annotation of health-relevant features of the microbiome,
- Adaptation of bacteria taxa to the vertebrate gastrointestinal tract, and
- Wastewater-based epidemiology on SARS-CoV-2

She also briefly described her group's plans for future research, which, in the area of health-relevant features of the microbiome, include improving the functional annotation framework (GutFunFind) and incorporating additional functional models. The group plans to establish collaborations with wet-lab scientists to study bilirubin reductase, which could lead to ideas for new preventative treatments for jaundice. Lastly, she described planned work exploring the application of de Bruijn graphs in microbiome research.

Following Dr. Jiang's presentation there was a Q&A session, after which the BSC went into closed session with her.

5. Presentation and Review of Lauren Porter, Tenure-Track Investigator

Dr. Porter described her group's research into protein fold switching, which she described as a rearrangement or remodeling of secondary and tertiary structure that leads to changes in function or regulation. She noted various human diseases to which fold switching is relevant, including cancer, tuberculosis, Alzheimer's, and gastroenteritis.

The lab's research has three major aims: to develop computational approaches to predict fold-switching proteins from their amino acid sequences, to validate their predictions experimentally, and to experimentally characterize fold-switching mechanisms.

Dr. Porter explained that while AlphaFold2 can predict protein structure from sequences, it does not do well in predicting the structures of fold-switching proteins, and thus an alternative method was needed. Her lab approached the problem with the hypothesis that because fold-switching proteins are changing their secondary structures, they are likely to have secondary structure propensities for both folds, not just one. She described how her group tested this hypothesis on the NusG protein family.

Dr. Porter noted that future research directions fall in two areas – observational and mechanistic. She briefly outlined six future projects, the first three of which are observational, while the latter three are mechanistic:

- In-depth prediction assessment through high-throughput protein purification and circular dichroism analysis
- Predict not only whether a protein switches folds but also which folds it assumes

- Phylogenetic analysis of fold switching in the NusG protein family
- Identify local interactions that foster RfaH fold switching
- Determine mutational pathways that convert singe-fold NusGs to fold switchers
- Measure the folding free energies of both RfaH C-terminal domain (CTD) conformations and the CTD:N-terminal domain interface

Following Dr. Porter's presentation there was a Q&A session, after which the BSC went into closed session with her.

6. Poster Session with Trainees (Closed Session)

7. Report to NLM Acting Scientific Director and DDIR Designee (Closed Session)

8. Adjournment

Peter Tarczy-Hornoch Digitally signed by Peter Tarczy-Hornoch Date: 2022.06.09 10:19:24 -07'00'

Dr. Tarczy-Hornoch, Chair (Date)
Board of Scientific Counselors

Valerie Florance -S Digitally signed by Valerie Florance -S Date: 2022.06.10 08:31:37 -04'00'

Dr. Valerie Florance (Date)
Acting Scientific Director, NLM