NIH Establishes Early Version of Personalized Medicine Platform

Stephen Barlas

Congress has been pumping money into the precision-medicine initiative at the National Institutes of Health (NIH). The first, early results of that spending were announced on May 7, when the All of Us research project went live with three types of aggregate health data on 142,000 individuals. It was the first wave of what is expected to amount to, or hoped to amount to, one million participants. All of Us grew out of the 21st Century Cures Act and is a favored target for federal funding. President Trump has proposed a 12% cut in NIH funding for fiscal 2020 (starting on October 1, 2019), which Congress is likely to reverse, as it has done in the last few years when similar cuts were asked for by the White House. However, the President’s 2020 budget does contain $313 million for All of Us.

The program was kicked off one year ago in seven cities around the country, with a particular emphasis on convincing members of underrepresented and minority communities to come forward with their health data. The idea is eventually to be able to check genomic data against environmental experience with a view to finding clues on the origin of various health conditions, so as to better target prevention and treatment measures. So far, more than 206,000 people have begun the enrollment process, and more than 142,000 have completed all the steps in the protocol. Most participants (> 75%) are from communities that have been underrepresented in biomedical research. “Those people are often left behind,” said Francis Collins, Director of NIH. “We’re hoping to chip away at vexing health disparities.”

A number of universities around the country have received grants to pay for participant enlistment efforts, including the University of Alabama at Birmingham (UAB).

Bruce Korf, MD, Chief Genomics Officer, UAB Medicine, says, “The All of Us research program is creating an unprecedented rich set of medical and biological data on one million participants who reflect the diversity of the United States. It will provide the foundation for the broad application of precision medicine for years to come, including the development of approaches to predict individuals at risk of disease and more precise and effective treatments.”

The NIH program is headed by Eric Dishman, former vice president of the Health and Life Sciences Group at Intel Corporation, where he was responsible for driving global strategy, research and development, product and platform development, and policy initiatives for health and life science solutions. Dishman—and Collins, among others—spoke at the one-year anniversary conference held at NIH on May 6. He explained that All of Us works with a consortium of 2,000 organizations and people from local communities to convince individuals to provide three types of data: electronic health records, responses to survey questions, and physical measurements. The data are available on the All of Us website (https://databrowser.researchallofus.org/), where one can view, for example, the top 10 health conditions and then drill down in each category to get breakdowns, such as the age of those people affected and other measures.

Dishman was honest in his appraisal of the initial product. “Our tools are pretty crude,” he said. “Over time, the viewer experience will get better.” He noted that the early data can’t be sorted by ethnicity or race, which would seem like a pretty important goal considering that the project’s overarching objective is mining health statistics from the African American and Hispanic populations.

Gary Gibbons, MD, Director of the Heart, Lung and Blood Institute at NIH, posited the potential by explaining that further study of genomic variations among African Americans could help explain the root causes of sickle cell disease. He noted that individuals’ African roots may have caused variations in their hemoglobin genes via interaction with malaria vectors, and ultimately resulted in the sickle cell trait. An individual could have one genetic copy of that trait, or two, and that difference would have health implications. On one hand, the variations could have been protective, against malaria. On the other hand, that same sickle cell trait may predispose African Americans to chronic kidney disease, for which they are at higher risk.

Beyond sickle cell disease, Gibbons noted that genomic/environmental interaction could identify people who are at increased risk for heart disease, hypertension, coronary disease, and asthma. “We’re working toward a day when we can predict that you’ll have atrial fibrillation, which today may only become manifest when you come to an emergency room feeling dizzy and short of breath with a rapid heartbeat. But if we already know from your polygenic risk score that you are [susceptible to] atrial fibrillation, you may be wearing a watch that detects your heart rhythm, allowing us to detect the arrhythmia and provide an electric jolt to short-circuit it.”

Much of the promise of the All of Us initiative appears to rest on genomic exploration, and there are no genomic data available at present. Collins said that the data would be included in 2020 and that the program has a “bold timetable” for enrolling the 800,000 individuals who would complete the cohort of one million.

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