**Capitol Hill Science Advocacy Visit Application**

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**Research Project and Presentation Summary**

Medicine and genetic research are far from being one-size-fits-all. This is particularly true when building genetic reference panels, which are crucial for interpreting data from genetic studies accurately. The existing reference panels, such as those from the Thousand Genome Project, offer robust data for European populations but fall short for admixed populations like Latinx, and are significantly underrepresented for South Asian and East Asian groups. To address this gap, I am leading a collaboration with researchers from UC San Diego and UC San Francisco to create the most comprehensive reference panel to date. Utilizing sequencing data from the NHLBI Trans-Omics for Precision Medicine (TopMed) program, this new panel compiles over 1.02 billion genetic variants—approximately ten times more than the Thousand Genome Project—and includes data from over 50,000 participants representing a rich tapestry of ancestries. This is about fifty times the participant diversity of the previous project. Our TopMed Reference Panel (TRP) not only boasts a higher count of genetic variants but also features a richer collection of rare variants thanks to advanced sequencing technologies. This enhancement is critical for investigating Mendelian diseases, which are influenced by rare genetic variations. Early tests and benchmarks of the TRP have shown its ability to fine-tune the mapping of genome-wide association study summaries with unprecedented resolution, revealing more significant genetic loci linked to various diseases and phenotypic traits. This is especially vital for populations that have historically been underrepresented in medical research. I am thrilled and honored to present this pioneering work at Capitol Hill through a detailed poster that 1) briefly describes the methods and making of the TRP, 2) visualizes the breakdown of the TRP in terms of participant ancestry and genetic diversity, comparing TRP to previously established reference panels, and 3) illustrates the new reference panel's broad applications, demonstrating the transformative power of bioinformatics and genetics in advancing precision medicine.

**Why Policy and Why this Visit**

My passion for policy and policymaking began in high school during my involvement in the Model United Nations, where I was captivated by the detailed process of crafting policy and the complex interactions among stakeholders. This interest deepened recently through a science-policy course at UCSF, which exposed me to the various dimensions of policymaking. As a bioinformatician in training, I recognize that our field is fundamentally grounded in data, which in turn is heavily influenced by policy. Effective policies can facilitate the establishment of extensive biobanks or increase access to de-identified electronic health records, significantly advancing research. Conversely, gaps in these policies can allow for the unethical use of private data by genetic testing companies. Understanding that both genetics and bioinformatics are deeply intertwined with policy, due to their reliance on data, I am eager to learn not only how to navigate these fields scientifically but also how to influence them through thoughtful policymaking. Participating in a Capitol Hill science advocacy visit would provide an invaluable opportunity to learn directly from leading scientists and policymakers. This experience would equip me to contribute effectively to policy changes that support scientific advancement and ethical standards in bioinformatics and genetics.