- The FASEB Journal 36(S1)
- DOI: 10.1096/fasebj.2022.36.S1.R4308
- Conference: Experimental Biology

Building a Distributed Research Network for Undergraduate Opportunities in Molecular Biochemistry

Jeremy W. Prokop, Adam Underwood, William Faber, Amy Wilstermann, Audrey Shor, Cynthia Stenger, Sara Cline, Michele Morris

First published: 13 May 2022

https://doi.org/10.1096/fasebj.2022.36.S1.R4308

The COVID-19 pandemic brought to light the continued issues in access to research opportunities. Many of our undergraduate students at research-intensive institutes lost their ability to go into labs to gain experience. However, students at most smaller colleges and universities faced these challenges to bring research opportunities to students long before the pandemic. Thus, our lower-cost community colleges and higher education institutes with diverse students lack equity when it comes to research investments. This highlights the need for bringing research into diverse institutes using novel approaches. Over the past ten years, our team has built a strategy for integrating genomic and molecular bioinformatics tools into undergraduate opportunities. Developing bioinformatics training material, professor training opportunities, summer research opportunities, and organized large scale research projects, our team has developed a distributed research network. Our goal is to bring genomic and bioinformatic literacy to early undergraduate training to increase STEM retention while improving research equity issues. Having students work on characterizing challenging clinical variants, known as Variants of Uncertain Significance (VUS), brings novel research projects to students while filling the growing needs of clinical variant characterizations. At the core training, we focus on bringing tools to professors and instructors, lowering the initiation efforts to performing bioinformatics research. These include the optimization of protein homology modeling, molecular dynamic simulations through analysis with a few mouse clicks (or two lines of code for Linux users), 3D protein printing, deep evolutionary profiling with hundreds of species using user-friendly tools, assessing expression from the NCBI SRA, and integrating genomic databases (GTEx, Human Protein Atlas, Geno2MP, gnomAD, Comparative Toxicogenomics Database, PharmGKB, Open Targets Genetics). Once in the hands of professors, they have implemented these tools into independent research projects for their students, coursework design such as bioinformatics classes, and research clubs. Over the past ten years, we have thus impacted hundreds of students with these tools. This can best be highlighted by the student's successes integrating the tools into publications on the NMDA receptors (PMID:34726335), CFTR database for cystic fibrosis (PMID: 32734384), NAA10 variant analysis (PMID: 33335012), multiple sclerosis genetics (PMID: 31482761), COVID-19 immune response (PMID:34335605), the SARS-CoV-2 evolution/structural dynamicome (PMID: 32587094), CCR5 role in diverse phenotypes and

bioethics (accepted), and SOX gene developmental biology (in review). Thus, the development of tools and strategies and the distribution of research projects can reach students and faculty at any institute, bringing equitable research opportunities to those who traditionally do not have many opportunities.