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AB - We are seeking to incorporate authentic inquiry into an undergraduate biochemistry lab course. Students on six campuses are combining computational (?in silico?) and wet lab (?in vitro?) techniques as they characterize proteins whose three dimensional structures are known but to which functions have not been previously ascribed. The in silico modules include protein visualization with PyMOL, structural alignment using Dali and ProMOL, sequence exploration with BLAST and Pfam, and ligand docking with PyRX and Autodock Vina. The goal is to predict the function of the protein and to identify the most promising substrates for the active sites. In the wet lab, students express and purify their target proteins, then conduct enzyme kinetics with substrates selected from their docking studies. Their learning as students and their growth as scientists is being assessed in terms of research methods, visualization, biological context, and mechanism of protein function. The lab course is an extension of successful undergraduate research efforts at RIT and Dowling College. The modules that are developed will be disseminated to the scientific community via a web site (promol.org), including both protocols and captioned video instruction in the techniques involved. Over the course of the project, we will also be following changes in faculty and teaching assistant competence in two areas: effective teaching with structural biology tools and the development of skills in the area of measuring learning gains by students. As we conduct the lab on these different campuses, we will also focus on advantages of our approach and barriers to implementation that exist on each campus, from the level of student acceptance and faculty training, to resources that are needed to changes in the culture at the departmental and institutional levels. As we analyze the feasibility of this approach on other campuses, we will seek input from other potential adopters about their level of interest and the barriers that they anticipate on their campuses. Support or Funding Information This project is supported in part by NSF IUSE 1503811.
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