

Student Feedback on Implementing a Molecular Visualization Tool in General Biochemistry in Class and Online

MIT is positioned for widespread adoption of hybrid education due to the growing momentum of blended learning approaches in higher education, popularity of MITx courses on edX, and its technologically-oriented academic culture. However, like many higher education institutions, there is inertia in traditional instruction. For example, introductory biology courses can consist of a couple hundred students lectured by a research professor in a large auditorium. This teacher-centered style can result in fewer high grades and reduced interest in biology compared to student-centered active learning formats (Burrowes 2003). One way to create a student-centered classroom is to use authentic learning practices, in which students are active participants in their discipline (Lombardi 2007). Since we know active learning is more effective than passive formats (Freeman et al. 2014), how can we combine authentic learning strategies and hybrid techniques in a large enrollment lecture course to increase student understanding? We hypothesized using a widely-used molecular visualization software would enhance student understanding of the biochemical structure of nucleic acids and proteins.

We instituted a promising practice in a General Biochemistry course by integrating the use of a molecular visualization software (PyMOL) both in the classroom and through online assignments. PyMOL is a powerful open-source molecular visualization software that allows users to manipulate and investigate crystallographic structures of proteins and nucleic acids archived in the Protein Data Bank. This tool is widely used by researchers, and thus could promote an authentic learning environment. Using molecular visualization tools has potential for increasing active learning if integrated into classroom activities (Canning & Cox 2001) and may hone skills using and interpreting biochemical representations (Wilder & Brinkerhoff 2007). We created and piloted a single PyMOL assignment in collaboration with the professor in 2016, and due to positive student responses, expanded PyMOL assignments into seven weekly problem sets in 2017. These assignments administered through the learning management site (Open edX) instructed students to use local instances of PyMOL software to explore DNA and protein features and answer computer-gradable questions. In 2018, as an additional course strategy to involve PyMOL, the professor provided students with 3D glasses during lecture and demonstrated PyMOL sessions in stereo view using seven different protein structures throughout the course. In this way, the teaching staff reinforced PyMOL exposure weekly in 2018, students watched demonstrations in class, and then completed graded assessments online using the tool.

To gauge the impact of introducing molecular visualization into the course, we collected surveys from students about their experiences using PyMOL, and compiled the average scores of these assignments. 72 out of 170 enrolled students in 2017 responded, and currently 48 out of 160 in 2018 responded to the active survey. 82% of responding students in 2017 thought that PyMOL assignments helped them visualize and understand the structure of nucleic acids and proteins. Whereas in 2018, 72% of responding students did. In regards to demonstrations in class, 85% of students enjoyed using the 3D glasses, and 91% thought that the professor should continue demonstrating PyMOL in class. Performance on the PyMOL assignments across these two years were comparable, enrolled students that attempted at least three PyMOL assignments scored an average of 83% and 82%, in 2017 and 2018, respectively.

Do students better understand the structures of nucleic acids and proteins after using PyMOL? The majority of students in both years believe the exercises help their understanding of structural biochemistry. Furthermore, the use of PyMOL in class and online fosters an authentic learning environment where students learn from an expert modelling an activity that

demonstrates how structural biochemistry is applied by scientists in research contexts, and subsequently engage with this activity through online assignments (Herrington and Kervin 2007). Support that we exposed students to an authentic learning experience is reflected by the fact that well over 80% of responding students had never used PyMOL before General Biochemistry. Students also seem to enjoy the PyMOL demonstrations in class, but it seems unlikely they are deriving much benefit from solely watching the professor use the tool if there is not corresponding discussion of the demonstration, as has been shown in an introductory physics class (Crouch et al. 2004). Furthermore, the in-class demonstrations do not seem to be affecting student performance on related online assignments. In fact, student perception of the usefulness of these assignments has decreased with additional exposure to the tool in class. However, caution should be taken in the interpretation of student perceptions. Students had more polarized responses to a biology course when comparing a hybrid class structure to lectures without online components (Riffel & Sibley 2005).

General Biochemistry is in the process of integrating hybrid elements to encourage authentic student understanding of structural biochemistry. Using visualization tools has the promise of promoting student understanding, but more research is needed to assess its implementation in an interactive blended learning environment. Evaluating the impact of design elements on student understanding of visualizations and comparing pre- and post-tests of PyMOL learning objectives in future iterations of the course will provide valuable insight.

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