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Leveraging Bioinformatics to Enhance Remote Learning During COVID-19

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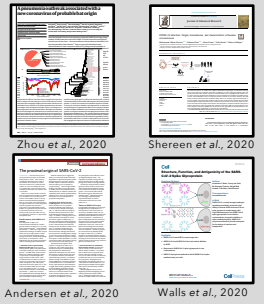
Introduction

In March 2020, the COVID-19 pandemic triggered an unprecedented and rapid transition to remote teaching and learning at all U.S. colleges and universities. Instructors were challenged to flip undergraduate lecture and lab courses online at mid-semester and strategically adapt summer courses. This radical pedagogical shift presented an opportunity to engage students in the science of COVID-19 by leveraging online bioinformatics platforms. We rapidly developed and implemented two inquiry-based bioinformatics modules in undergraduate molecular biology courses at Loyola University New Orleans and the University of Montana. During synchronous class meetings, students explored coronavirus genome sequences using NCBI Virus and framed research questions about the origins of SARS-CoV-2. Evaluation of mutation fitness and virus phylogeny was demonstrated with the T-BioInfo Platform. In addition, the viral spike glycoprotein was investigated as a critical target for neutralizing antibodies and vaccine development. Completion of these modules resulted in gains in perceived learning about the novel coronavirus and an increased understanding of sequencing data. We recommend incorporation of similar modules into undergraduate courses to enhance remote learning and increase opportunities for research training during and beyond the pandemic.

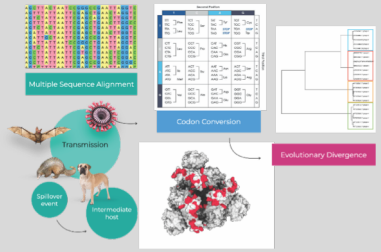
Methods

Molecular Genetics (BiolA326 / 327): This undergraduate course was taught as a traditional lecture and parallel laboratory section in Spring 2020 at Loyola University New Orleans. The course focused on the Central Dogma of molecular biology, analysis of primary scientific literature, and laboratory research techniques. A foundational study on SARS-CoV-2 emergence was discussed in class on March 3 (Zhou., 2020). Local outbreak in New Orleans forced an immediate shift to remote learning on March 16 and this course rapidly adapted to increase focus on the molecular biology of SARS-CoV-2. Two bioinformatics modules incorporating recent pandemic literature were introduced to the laboratory section of the course. PineBiotech led a virtual hands-on investigation of full-length coronavirus genome and spike glycoprotein sequences using NCBI Virus. The T-BioInfo Platform was used to demonstrate methods to analyze mutation fitness, virus phylogeny, and mechanisms of spike glycoprotein evasion from host immune. Post-course assessment was conducted with a customized SALG (student assessment of learning gains) online survey. Results from the lecture alone group (n=8) were compared to the lecture plus lab group (n=13) by t-test. This study was exempt from IRB review, however informed consent was obtained from students completing the survey.

Students analyzed SARS-CoV-2 literature during face-to-face and virtual sessions.



Students tested hypotheses about the origins of SARS-CoV-2 and explored the structure and function of the spike glycoprotein through virtual hands-on bioinformatics modules.



Cellular and Molecular Biology (BIOB260): This undergraduate course was taught fully online in Summer 2020 at the University of Montana. The course focused on cellular and subcellular biology, including the Central Dogma, signal transduction, and regulation of the cell cycle. This course consisted of weekly synchronous lectures, discussions, and asynchronous activities to support learning. A foundational study on SARS-CoV-2 emergence was discussed in the third week of class (Zhou., 2020). A bioinformatics module focused on the origins of the novel coronavirus was incorporated into the fifth week of the course. A similar virtual hands-on investigation of coronavirus genome sequences using NCBI Virus and the T-BioInfo Platform was delivered by PineBiotech. Students explored the structure and function of genes in SARS-CoV-2 in a follow-up group activity. Online presentations focused on host-virus interactions relevant for vaccine and therapy development. Pre and post-course assessments were conducted with customized SALG (student assessment of learning gains) online surveys. Results from the pre-course assessment (n=27) were compared to the post-course assessment (n=23) by t-test. This study was exempt from IRB review, however informed consent was obtained from students completing the survey.

Results

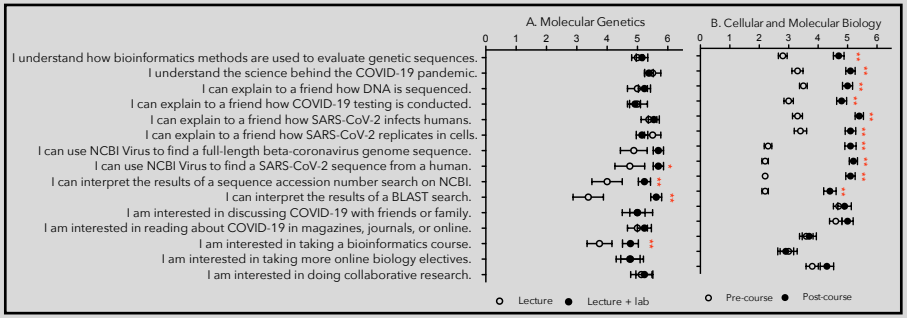


Figure 1. Student Assessment of Learning Gains. Online SALG surveys were administered to students enrolled in both courses in this study. A) Molecular Genetics post-course results were compared between lecture alone (n=8) and lecture + lab (n=13). B) Cellular and Molecular Biology pre- and post-course results were compared (n=27 & 23). T-tests were used to determine statistical significance between groups. *p<0.05. **p<0.005

Students proposed relevant high-level research questions about SARS-CoV-2 that could be addressed using bioinformatics approaches from these modules.

Are there significant differences between SARS-CoV-2 sequences isolated from patients in Italy and the rest of the world?

Is it possible for SARS-CoV-2 to be spread via fecal-oral transmission, in addition to the already know respiratory droplet transmission?

How do SARS-CoV-2 sequences isolated from patients in Louisiana compare to sequences isolated from early patients in Washington?

Students were enthusiastic to be learning about SARS-CoV-2 during the pandemic.

"We were able to study the structure of the virus and evaluate how it is different from other coronaviruses. Study of the virus fit perfectly into our class."

"I took a lot from observing the multiple sequence alignments and how much information that can tell about a specific set of sequences. "

"My understanding of COVID-19 has allowed me to stay up to date about the latest information about the virus including its genetic makeup. "

Conclusions

- High-impact bioinformatics modules were developed for undergraduate molecular biology courses and implemented online during the COVID-19 pandemic.
- These modules provide a framework to investigate SARS-CoV–2 transmission and origin hypotheses with NCBI Virus, BLAST, and the T-BioInfo Platform.
- Students demonstrated significant gains in their perceived understanding of SARS-CoV-2 pathogenesis and sequence analysis methods.

This study was presented at the ISMB Education COSI on July 13-14, 2020. Further details of the study and teaching materials will be made available to collaborators upon request.

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