

Making Change Sustainable: Network for Integrating Bioinformatics into Life Sciences Education (NIBLSE) Meeting Review

Inimary Toby¹, Jason Williams², Guoqing Lu³, Chao Cai⁴, Keith A. Crandall⁵, Elizabeth A. Dinsdale⁶, Jennifer Drew⁷, Nicholas P. Edgington⁸, Carlos C. Goller⁹, Neal F. Grandgenett¹⁰, Barry J. Grant¹¹, Charles Hauser¹², Keith A. Johnson¹³, Christopher J. Jones¹⁴, Nathaniel K. Jue¹⁵, John R. Jungck¹⁶, Jacob Kerby¹⁷, Adam J. Kleinschmit¹⁸, Kathryn G. Miller¹⁹, William R. Morgan²⁰, Barbara Murdoch²¹, George Noutsios²², Janelle Nunez-Castilla²³, Mark Pauley²⁴, William R. Pearson²⁵, Sabrina D. Robertson²⁶, Srebrenka Robic²⁷, Anne Rosenwald²⁸, Yee Mey Seah²⁹, Marcia Shofner³⁰, Michael Sierk³¹, Jessica Siltberg-Liberles³², Todd Smith³³, Naomi A. Stover¹³, William Tappich³, Eric W. Triplett³⁴, Elizabeth F. Ryder^{35*}

¹Department of Biology, University of Dallas; ²DNA Learning Center, Cold Spring Harbor Laboratory; ³Department of Biology, University of Nebraska at Omaha; ⁴Libraries and School of Information Studies, Purdue University; ⁵Computational Biology Institute, George Washington University; ⁶College of Science and Engineering, Flinders University; ⁷Microbiology and Cell Science, University of Florida; ⁸Biology Department, Southern Connecticut State University; ⁹Department of Biological Sciences, North Carolina State University; ¹⁰Department of Teacher Education, University of Nebraska at Omaha; ¹¹Division of Biological Sciences, University of California San Diego; ¹²Department of Biological Sciences, St. Edward's University; ¹³Department of Biology, Bradley University; ¹⁴Department of Biological Sciences, Moravian University; ¹⁵Biology and Chemistry, California State University, Monterey Bay; ¹⁶Delaware Biotechnology Institute, University of Delaware; ¹⁷Department of Biology, University of South Dakota; ¹⁸Department of Natural and Applied Sciences, University of Dubuque; ¹⁹Department of Biology, Washington University, St Louis; ²⁰Department of Biology, College of Wooster; ²¹Biology Department, Eastern Connecticut State University; ²²Mathematical and Natural Sciences, Arizona State University; ²³Department of Biological Sciences, Florida International University; ²⁴Division of Undergraduate Education, National Science Foundation; ²⁵Biochemistry and Molecular Genetics, University of Virginia; ²⁶Psychology and Neuroscience, University of North Carolina; ²⁷Department of Biology, Agnes Scott College; ²⁸Department of Biology, Georgetown University; ²⁹Department of Laboratory Medicine and Pathology, University of Washington Medical Center; ³⁰Department of Entomology, University of Maryland, College Park; ³¹Interdisciplinary Sciences Department, Saint Vincent College; ³²Department of Biological Sciences, Biomolecular Sciences Institute, Florida International University; ³³Digital World Biology; ³⁴Microbiology and Cell Science, University of Florida; ³⁵Department of Biology and Biotechnology, Worcester Polytechnic Institute

Abstract

The purpose of the meeting described in this review was to decide how best to ensure the sustainability of the [Network for Integrating Bioinformatics into Life Science Education](#) (NIBLSE; pronounced “nibbles”). Biology research today generates large and complex datasets, and the analysis of these datasets is becoming increasingly critical to progress in the field. The long-term goal of NIBLSE is to address this need and achieve the full integration of bioinformatics into undergraduate life sciences education. Meeting participants supported several next steps for NIBLSE, including further development and dissemination of bioinformatics learning resources through our novel incubators and Faculty Mentoring Networks, vigorously pursuing assessment strategies for our learning resources, connecting learning resources with open educational resource (OER) textbooks, learning more about barriers to bioinformatics implementation for underrepresented groups, and developing future workshops and meetings. About half the participants at the meeting were newcomers to NIBLSE, a positive sign for the future. NIBLSE has many exciting opportunities available, and we welcome life science educators with any level of bioinformatics expertise as new members.

Citation: Toby I, Williams J, Lu G, Cai C, Crandall KA, Dinsdale EA, Drew J, Edgington NP, Goller CC, Grandgenett NF, Grant BJ, Hauser C, Johnson KA, Jones CJ, Jue NK, Jungck FR, Kerby J, Kleinschmit AJ, Miller KG, Morgan WR, Murdoch B, Noutsios G, Nunez-Castilla J, Pauley M, Pearson WR, Robertson SD, Robic S, Rosenwald A, Seah YM, Shofner M, Sierk M, Siltberg-Liberles J, Smith T, Stover NA, Tappich W, Triplett EW, Ryder EF. 2022. Making change sustainable: Network for Integrating Bioinformatics into Life Sciences Education (NIBLSE) meeting review. CourseSource. <https://doi.org/10.24918/cs.2022.10>

Editor: Carrie Diaz Eaton, Bates College

Received: 4/9/2021; **Accepted:** 2/1/2022; **Published:** 7/17/2022

Copyright: © 2022 Toby, Williams, Lu, Cai, Crandall, Dinsdale, Drew, Edgington, Goller, Grandgenett, Grant, Hauser, Johnson, Jones, Jue, Jungck, Kerby, Kleinschmit, Miller, Morgan, Murdoch, Noutsios, Nunez-Castilla, Pauley, Pearson, Robertson, Robic, Rosenwald, Seah, Shofner, Sierk, Siltberg-Liberles, Smith, Stover, Tappich, Triplett, and Ryder. This is an open-access article distributed under the terms of the Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International License, which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original author and source are credited.

Conflict of Interest and Funding Statement: None of the authors has a financial, personal, or professional conflict of interest related to this work.

***Correspondence to:** Elizabeth F. Ryder 100 Institute Rd., Worcester, MA 01609. Email: ryder@wpi.edu.

PURPOSE AND GOALS OF THE NIBLSE MEETING

The Network for Integrating Bioinformatics into Life Science Education (NIBLSE) is a community of educators whose goal is to promote the integration of essential bioinformatics skills into undergraduate life sciences education. The main purpose of the NIBLSE meeting, held in October 2019, was to determine how best to sustain the Network; our goal was to identify the next steps for the future. Since many meeting attendees were new to NIBLSE, meeting presentations first reviewed the network's major accomplishments to provide a context to discuss which components of NIBLSE work are critical to its sustainability. Presentations included our work to create and implement bioinformatics core competencies for life science majors, our findings on barriers to implementation of bioinformatics in life sciences classrooms, and our novel approaches to create, curate, and assess bioinformatics learning resources through new collaborative mechanisms called incubators and Faculty Mentoring Networks (FMNs). In addition, outside speakers from two organizations representing models for possible future structures for NIBLSE spoke about their history and goals: the [Partnership for Undergraduate Life Sciences Education](#) (PULSE), and the [Society for the Advancement of Biology Education Research](#) (SABER). These sessions were followed by small group work to generate and discuss ideas for sustainability, suggest next steps, and facilitate further planning by the leadership team. We conclude this meeting review with a call for new members and a summary of the directions NIBLSE will be pursuing as a result of the meeting.

CORE COMPETENCIES

To facilitate bioinformatics integration into life science curricula, NIBLSE previously published a set of nine bioinformatics core competencies for undergraduate life science students (1), summarized in Table 1. These competencies are intended to address the needs of life science students, rather than bioinformatics specialists. They were developed through a process involving a nationwide survey of life sciences faculty, followed by further refinement from faculty representing diverse undergraduate institutions. To informally assess the implementation of the NIBLSE core competencies in the biology courses of educators predisposed to bioinformatics integration, we asked meeting participants to report which NIBLSE core competencies they use in their teaching. The most common core competency taught was C4) use of bioinformatics tools to solve biological problems (Figure 1). Also implemented frequently were competencies C5) approaches to retrieve biological data; C1) role of computation and data mining in addressing hypothesis-driven and hypothesis-generating questions; and C7) use of command line tools in bioinformatics. We were impressed that all of the competencies proposed by NIBLSE were being taught in multiple courses across the country, attesting to their usefulness and demonstrating the feasibility of bioinformatics integration into undergraduate life science curricula. The observation that some competencies were implemented to a lesser extent may suggest a need for more learning resources in these areas.=

BARRIERS TO BIOINFORMATICS INTEGRATION

As we reported previously (2), our national survey of biology faculty identified several major barriers facing biology faculty in

integrating bioinformatics into their curriculum, including the need for adaptable learning resources and faculty professional development (discussed later in this review). Unfortunately, with fewer than 7% of survey respondents from racial/ethnic minority groups (e.g., Hispanic, Black, and Native American), we were unable to reach strong conclusions regarding particular barriers members of these groups may face. To better promote equity and access in bioinformatics education, meeting participants concluded that NIBLSE should delve more deeply into the needs of underrepresented minority faculty and faculty at minority serving institutions (MSIs). After the meeting, we worked with faculty members from these groups to develop a new inclusive survey that proactively targeted experiences and viewpoints we may not have captured sufficiently in our initial survey. The survey was deployed in December 2021, closed in March 2022, and results are currently being analyzed.

Table 1. NIBLSE Core Competencies

(adapted from Sayres et al., 2018)

Core Competencies
C1-Explain the role of computation and data mining in addressing hypothesis-driven and hypothesis-generating questions within the life sciences.
C2-Summarize key computational concepts, such as algorithms and relational databases, and their applications in the life sciences.
C3-Apply statistical concepts used in bioinformatics.
C4-Use bioinformatics tools to examine complex biological problems in evolution, information flow, and other important areas of biology.
C5-Find, retrieve, and organize various types of biological data.
C6-Explore and/or model biological interactions, networks, and data integration using bioinformatics.
C7-Use command-line bioinformatics tools and write simple computer scripts.
C8-Describe and manage biological data types, structure, and reproducibility.
C9-Interpret the ethical, legal, medical, and social implications of biological data.

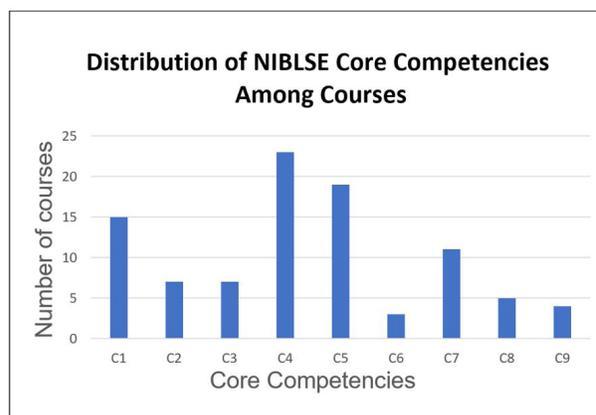


Figure 1. Distribution of NIBLSE core competencies covered by those courses taught by the attendees of the NIBLSE meeting in October 2019.

INCUBATORS

One important finding of the 2016 survey was that many life sciences faculty members lack the time and training necessary to implement bioinformatics in their courses (2). As the NIBLSE Resource Review Committee (RRC) began to assemble a set of existing online [bioinformatics learning resources](#) mapped to the [core competencies](#), we discovered another problem: we found very few available learning resources that were accurate, engaging, current, and accessible to non-expert faculty. Working with the [Quantitative Undergraduate Biology Education and Synthesis](#) (QUBES) network, we have begun to address both these problems through a new mechanism called “incubators.” The goal of these small online faculty groups is to develop new bioinformatics curricular modules and also nurture a growing network of faculty implementing bioinformatics modules in their courses (3).

An incubator is a short (6–10 week), focused, online community that refines an existing module submitted by its author into a more polished and widely usable learning resource (3). Incubator participants are chosen to include both experts and novices on the resource topic in order to ensure both accuracy and accessibility of the finished product. In addition, NIBLSE members are actively sought out to participate in an incubator. The incubators themselves can provide useful support networks; faculty who participate in the incubator are also likely to implement the resource in their classrooms. Each completed incubator module is assigned a DOI, allowing incubator participants to publish their work, and the QUBES infrastructure also allows publication of adaptations of the original module.

At the meeting, NIBLSE members described the incubator process, using the incubation of a DNA barcoding module as an example. In this exercise, students are introduced to DNA barcoding, which is the identification of species using a short nucleotide sequence from a standard genetic region, such as ribosomal RNA or cytochrome C oxidase. Students use the software platform [DNA Subway](#) to “clean” the provided sequence data, identify the species using BLAST, build a multiple sequence alignment, create a phylogenetic tree, and interpret its meaning.

Participating in an incubator requires active engagement. The goals of the incubator are decided jointly by the group, and individuals contribute different components to the resource, discuss and edit each other’s contributions, and discuss ideas for classroom implementation. Over the course of the DNA barcoding incubator, for example, the authors added a new dataset on mosquitos to engage student interest, and they incorporated better explanations of phylogenetic tree-building and more structured questions to guide students through the exercise. In addition, instructor resources were prepared, including an analysis of the dataset and answers to associated questions. The learning resource was published on the QUBES site (4). Several incubator participants subsequently implemented the module in their courses.

The example above illustrates the multiple benefits of incubators. Incubators serve to create engaging community-validated bioinformatics learning resources that are mapped to core competencies and can be implemented by non-

bioinformatics specialists. They also create small networks of faculty who help each other implement the modules. Importantly, authors receive recognition and publication of their educational scholarship. Incubated modules are also ideal resources for the longer-lived and more structured Faculty Mentoring Networks (FMNs), described below. The NIBLSE RRC is eager to recruit more lessons for incubation as well as more incubator participants from the bioinformatics community.

FACULTY MENTORING NETWORKS (FMNS)

Faculty Mentoring Networks, sponsored and facilitated through QUBES, bring together faculty to develop, implement, and refine teaching materials in quantitative biology. FMNs typically last 3–4 months, a timeframe that allows ongoing support as faculty implement new teaching materials in their courses. FMNs capitalize on the experience of mentors who lead network activities and peers with a shared educational goal, and these networks provide a bridge between pedagogical theory and actionable classroom practice. By providing knowledge and support to faculty with little training in bioinformatics, FMNs address a major barrier to implementing bioinformatics in life science courses (2).

NIBLSE partnered with QUBES and initiated the development of the FMN titled *Bring Bioinformatics to Your Biology Classroom*, with the common goal of using bioinformatics strategies to address biological concepts and competencies in introductory life science courses. The NIBLSE FMN brought together a group of faculty representing a diverse range of sub-disciplines to implement and adapt the NIBLSE learning resource titled *Sequence Similarity: An inquiry based and “under the hood” approach for incorporating molecular sequence alignment in introductory classrooms* (5). This resource had been previously incubated at NIBLSE prior to publication in *CourseSource*. The resource introduces students not only to the use of important bioinformatics software such as BLAST and multiple sequence alignment, but involves students in exercises that result in an understanding of the algorithms underlying these tools. The module also includes a choice of several short projects in which students use the tools they have just learned to analyze real data.

For all QUBES FMNs, participating faculty are required to adapt the common learning resource to fit the learning environment and learning objectives of their specific course. These adaptations are linked to the original learning resource to establish a suite of related modules that faculty can review and adopt according to their specific needs and goals. All adaptations are supported by teaching notes and documents that guide implementation. The adaptations also provide a summary of differences that distinguish the new resource from the original, including adaptation-specific learning objectives. In the NIBLSE FMN, adaptations were published for several biology courses, including *Developmental Biology* (6), *Plant Biology* (7), and *Virology* (8).

The NIBLSE Conference FMN panel and faculty participants shared their experiences with the development, adaptation, and dissemination of learning resources using the FMN model. Within the confines of the FMN, participants and mentors discussed their successes and challenges in implementing the module(s) in their classrooms and traded ideas related to their course-specific module adaptations. The many benefits

provided by FMNs include professional development support from peers, the availability of experienced mentors, the efficiency of development and implementation happening in parallel, regular discussion of implementation successes and challenges in real time, and adaptations occurring along the way. Faculty participants in the FMN were teaching in different contexts and on different timelines, and thus learned from each other's varied experiences. The publication of adaptations on QUBES provided some faculty with products useful for professional advancement. Support from the QUBES FMN facilitators was outstanding, with regular communication and problem-solving throughout the semester.

Given the success of the initial NIBLSE FMN, conference participants organized two additional FMNs subsequent to the meeting. One FMN repeated the use of the Sequence Similarity resource, resulting in additional adaptations (9-13). An FMN using the learning resource "RNA-seq data analysis using Galaxy" (14, 15) was recently completed. Plans to organize future FMNs are described in "Next Steps" below.

DISSEMINATION, ASSESSMENT, AND VALIDATION OF LEARNING RESOURCES

Thus far, eight NIBLSE incubators and the FMNs described above have been completed; resulting learning resources, including a number of adaptations, are published on the [NIBLSE Learning Resource Collection](#) site within QUBES. There is a need to improve dissemination and tracking of the learning resources. Currently, we only know the number of times resources have been viewed and downloaded; information is needed on how often they have been implemented in courses.

In addition, an important step to ensure the adoption of learning resource modules is assessment of their effects on student learning and retention. The NIBLSE Assessment and Validation Committee (AVC) presentation to participants stressed the difficulty in finding generalizable assessment instruments for learning resources teaching bioinformatics competencies, as might be expected for a newly emerging field. In response, the AVC has generated a 'Tip Sheet' on assessment that is a high-level review of methods of constructing assessment instruments (16).

In cooperation with the AVC, groups of NIBLSE members designed an assessment instrument associated with the Sequence Similarity learning resource. The assessment instrument was created during the initial Sequence Similarity incubator and was then refined during the subsequent FMN. The Sequence Similarity resource was implemented and assessed by NIBLSE members at seven institutions across the US, in educational settings ranging from large universities to small liberal arts colleges, and in courses from introductory biology to advanced specialty life science classes. Subsequent to the meeting, this work culminated in a publication that showed significant learning gains at all institutions (17), including several where the instructor considered themselves a "novice" bioinformatics instructor and had not previously implemented bioinformatics in the classroom. Given the success of this effort, the NIBLSE community plans to pursue this strategy for future learning resources.

STRUCTURES FOR SUSTAINABILITY

Two models for sustainability were discussed at the meeting: 1) attending pre-existing society meetings to offer workshops or perhaps a half- or full-day associated NIBLSE meeting or 2) organizing annual meetings by creating a framework for starting a formal society of our own. Two invited speakers shared their insights on these models. Dr. Kathryn Miller represented the Partnership for Undergraduate Life Sciences Education (PULSE), which uses a workshop model, while Dr. Mary Pat Wenderoth represented the Society for the Advancement of Biology Education Research (SABER), which established its own society. Key points made by both speakers are summarized below.

Dr. Miller described the primary goal for PULSE, which is to help life sciences departments at all institutions of higher education align with national education reform initiatives arising from the *Vision and Change* report (18). Their goal is to develop inclusive, student-centered, evidence-based teaching and learning in order to cultivate the development of scientists who reflect the diversity of American society (19). An important initiative developed by the PULSE network is the Ambassadors Program. This program facilitates discussions in biology and life science departments to aid them in implementing transformative resources. During workshops, PULSE ambassadors work with faculty members and department leadership to create a shared vision for the future and provide them with the skills to work with one another using dynamic governance.

Dr. Wenderoth shared a detailed background about the inception of SABER. The primary reason for SABER's formation was the need for a society focused on education research, and in particular, on evidence-based teaching and learning (20). Dr. Wenderoth's suggestions for education models that could be leveraged by NIBLSE included the HHMI Summer Institute and the [National Center for Case Study Teaching in Science](#). To promote its activities and vitality, SABER utilizes social media for advertising and generating awareness for the organization. Members of the organization also publish their work in educational research journals.

After much discussion of the merits of these two approaches, the consensus of the group was that NIBLSE would be best served by the flexibility of integrating workshops into existing meetings rather than expending time and energy on forming our own society and meeting structure at the present time.

NEXT STEPS

Several goals for NIBLSE future work emerged from the meeting. We need to make our learning resources as easy as possible for educators to adopt. In addition, we plan to expand our incubator, FMN, and assessment efforts. Finally, we need to better publicize and disseminate our work.

As a result of suggestions from the meeting, we are currently mapping curricula to the [OpenStax](#) introductory biology textbook *Biology 2e*. We are also creating online documents that highlight resources appropriate to particular kinds of classes (e.g., sophomore-level genetics) as well as with associated Vision and Change concepts.

To facilitate the vertical integration of bioinformatics into the life science curriculum, we are identifying [NIBLSE learning resources](#) appropriate for different levels in the curriculum and sponsoring FMNs for these resources. Dissemination will be enhanced by scaffolding FMNs; faculty who participate in an FMN are encouraged to be mentors in a subsequent FMN. These activities will help to mitigate lack of expertise or training, the most common barrier faculty face for bioinformatics integration (2).

Assessment of modules will be an important step toward convincing faculty that modules are worthy of adoption in their courses. FMNs provide excellent venues for development of assessment tools hand-in-hand with the implementation of modules in courses (15). NIBLSE members who led the recent FMN on RNA-seq Analysis followed this model by discussing assessment strategies as the FMN proceeded.

We discussed strategies to improve communication and dissemination of the work NIBLSE is doing and to increase the size of the network. NIBLSE is planning on launching a new communications and social media initiative to broaden participation and increase awareness of our work. In addition, we plan to identify institutions that have faculty willing to integrate NIBLSE resources into their curricula. The NIBLSE AVC will measure the success of the resulting integration efforts, which will be publicized through conference presentations and publications.

The general consensus from the meeting was that (1) NIBLSE is making progress towards its goals of creating, disseminating, assessing, and integrating bioinformatics learning resources as well as supporting faculty development; (2) life science curricula are challenging to change overnight; (3) NIBLSE will achieve more by integrating our work into that of other societies rather than forming our own society. Several strategies were discussed to increase the resources available for NIBLSE to continue to grow and especially to incorporate the “next generation” of graduate students, post-docs, and early-career faculty. We anticipate bringing the NIBLSE community together annually at large conferences such as the annual SABER meeting. We plan to offer workshops at such conferences that would serve as training experiences for instructors on the processes of embedding bioinformatics materials into courses. Long term, these workshops would be supported by implementation of small annual membership dues (and possibly workshop registration fees). In addition, NIBLSE leadership will investigate possible new sponsors.

SUMMARY AND CALL FOR PARTICIPATION

NIBLSE seeks to expand our membership and to increase the involvement of existing members. There are many opportunities for involvement by members, for example:

- Participating in Incubators and FMNs to develop, assess, and disseminate new learning resources
- Connecting learning resources to OER textbook publishers
- Conducting focus groups to further explain findings from our new barriers survey
- Working to broaden participation in NIBLSE
- Developing the format and content of future meetings and workshops

- Volunteering their department to serve as a model for bioinformatics integration

Please join [NIBLSE](#) online and contact Inimary Toby, NIBLSE Membership Director, itoby@udallas.edu, to let her know of your specific interests.

SCIENTIFIC TEACHING THEMES

All learning resources that NIBLSE adds to the Learning Resource Collection and uses as the basis for Faculty Mentoring Networks must pass a review that ensures they adhere to the standards of Scientific Teaching. Learning Resources must be aligned with at least one of the NIBLSE Bioinformatics Core Competencies.

Active Learning

This meeting report describes two NIBLSE resources in some detail to illustrate the active nature of learning resources developed by NIBLSE incubators and FMNs. In addition, incubators and FMNs are themselves examples of active learning processes for the participants, as they collaborate to create and implement new learning resources.

Assessment

We describe the assessment of one resource that has been implemented at multiple institutions; we plan similar future joint assessments. The NIBLSE Assessment and Validation Committee is developing further strategies for learning resource assessment.

Inclusive Teaching

Resources recommended by NIBLSE include instructor resources to engage students from varied backgrounds. Our goal with introductory resources in particular is to assist instructors with little or no bioinformatics expertise with integration of bioinformatics into biology courses for students with varied backgrounds. We make an effort to include instructors with little or no bioinformatics experience in incubators and FMNs.

ACKNOWLEDGMENTS

Support for this work was provided by a grant from the National Science Foundation (DBI 1539900). Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the National Science Foundation.

REFERENCES

1. Wilson Sayres MA, Hauser C, Sierk M, Robic S, Rosenwald AG, Smith TM, Triplett EW, Williams JJ, Dinsdale E, Morgan WR, Burnette JM, Donovan SS, Drew JC, Elgin SCR, Fowlks ER, Galindo-Gonzalez S, Goodman AL, Grandgenett NF, Goller CC, Jungck JR, Newman JD, Pearson W, Ryder EF, Tosado-Acevedo R, Tappich W, Tobin TC, Toro-Martínez A, Welch LR, Wright R, Barone L, Ebenbach D, McWilliams M, Olney KC, Pauley MA. 2018. Bioinformatics core competencies for undergraduate life sciences education. PLOS ONE 13:e0196878. doi:10.1371/journal.pone.0196878
2. Williams JJ, Drew JC, Galindo-Gonzalez S, Robic S, Dinsdale E, Morgan WR, Triplett EW, Burnette III JM, Donovan SS, Fowlks ER, Goodman AL, Grandgenett NF, Goller CC, Hauser C, Jungck JR, Newman JD, Pearson WR, Ryder EF, Sierk M, Smith TM, Tosado-Acevedov R, Tappich W, Tobin TC, Toro-Martinez A, Welch LR, Wilson MA, Ebenbach D, McWilliams M, Rosenwald AG, Pauley MA. 2019. Barriers to integration of bioinformatics into undergraduate life sciences education: A national study of US life sciences faculty uncover significant barriers to integrating bioinformatics

- into undergraduate instruction. *PLOS ONE* 14:e0224288. doi:10.1371/journal.pone.0224288
3. Ryder EF, Morgan WR, Sierk M, Donovan SS, Robertson SD, Orndorf HC, Rosenwald AG, Triplett EW, Dinsdale E, Pauley MA, Tapprich WE. 2020. Incubators: Building community networks and developing open educational resources to integrate bioinformatics into life science education. *Biochemistry and Molecular Biology Education* 48:381-390. doi:10.1002/bmb.21387
 4. Williams J, Enke RA, Hyman O, Lescak E, Donovan SS, Tapprich W, Ryder EF. 2018. Using DNA Subway to analyze sequence relationships (Version 2.0), QUBES Educational Resources. doi:10.25334/Q4J111.
 5. Kleinschmit A., Brink B., Roof S, Goller C, Robertson SD. 2019. Sequence Similarity: An inquiry based and “under the hood” approach for incorporating molecular sequence alignment in introductory undergraduate Biology courses. CourseSource. <https://doi.org/10.24918/cs.2019.5>
 6. Murdoch, B. 2019. Sequence Similarity in developmental biology -- A bioinformatics exercise using myostatin. Bring Bioinformatics to Your Biology Classroom, QUBES Educational Resources. doi:10.25334/Q45F3H
 7. Erickson A. 2019. Bioinformatics: Investigating Sequence Similarity - A plant biology approach. Bring Bioinformatics to Your Biology Classroom, QUBES Educational Resources. doi:10.25334/Q4H458
 8. Tapprich W. 2019. Sequence Similarity resource adaptation: Exploring Ebola virus. Bring Bioinformatics to Your Biology Classroom, QUBES Educational Resources. doi:10.25334/Q47X63
 9. Sollberger DE. 2021. Sequence Similarity: A quick introduction to Bioconductor. QUBES Educational Resources. doi:10.25334/Q45F3H
 10. Katcher J. 2021. Sequence Similarity: Introducing biological databases to community college biology students. QUBES Educational Resources. doi:10.25334/1EAH-3E24
 11. Lenahan M, Cinquemani S. 2021. Developing a phylogram from computational resources. QUBES Educational Resources. doi:10.25334/DP07-5Q37
 12. Tarun A. 2021. Introductory video and worksheets on Module 1 and 2 on “Sequence Similarity: An inquiry based and under the hood...” QUBES Educational Resources. doi:10.25334/RSKV-D240
 13. Hultgren K. 2021. Inquiry-based hypothesis testing using phylogenetic trees in MEGA. QUBES Educational Resources. doi:10.25334/FYP1-0G44
 14. Escobar M, Donovan SS, Makarevitch I, Morgan B, Robertson S. 2021. RNAseq data analysis using Galaxy. NIBLSE Incubator: RNAseq data analysis using Galaxy, (Version 4.0). QUBES Educational Resources. doi:10.25334/XHW8-7189
 15. Escobar MA, Morgan W, Makarevitch I, Robertson SD. 2019. Tackling “big data” with biology undergrads: A simple RNA-seq data analysis tutorial using Galaxy. CourseSource. <https://doi.org/10.24918/cs.2019.13>
 16. Drew JC, Grandgenett N, Dinsdale EA, Vázquez Quiñones LE, Galindo S, Morgan WR, Pauley M, Rosenwald A, Triplett EW, Tapprich W, Kleinschmit AJ. 2021. There is more than multiple choice: Crowd-sourced assessment tips for online, hybrid, and face-to-face environments. *J Microbiol Biol Educ* 22:e00205-21. <https://doi.org/10.1128/jmbe.00205-21>
 17. Kleinschmit AJ, Ryder EF, Kerby JL, Murdoch B, Donovan S, Grandgenett NF, Cook RE, Siriwardana C, Mogan W, Pauley M, Rosenwald A, Triplett E, Tapprich W. 2021. Community development, implementation, and assessment of a NIBLSE bioinformatics sequence similarity learning resource. *PLOS ONE* 16(9): e0257404. <https://doi.org/10.1371/journal.pone.0257404>
 18. American Association for the Advancement of Science (AAAS). 2011. Vision and change in undergraduate biology education: A call to action. Retrieved from <http://visionandchange.org/files/2011/03/Revised-Vision-and-Change-Final-Report.pdf>
 19. Peteroy-Kelly M, Brancaccio-Taras L, Awong-Taylor J, Balsler T, Jack T, Lindsay S, Marley K, Romano S, Uzman JA, Pape-Lindstrom P. 2019. A qualitative analysis to identify the elements that support department level change in the life sciences: The PULSE Vision & Change Recognition Program. *PLOS ONE*, 14(5), e0217088. doi:10.1371/journal.pone.0217088
 20. Offerdahl EG, Balsler T, Dirks C, Miller K, Momsen JL, Montplaisir L, Osgood M, Sirum K, Wenderoth MP, White B, Wood WB, Withers M, Wright R. 2011. Society for the Advancement of Biology Education Research (SABER). *CBE Life Sci Educ*, 10(1), 11-13. doi:10.1187/cbe.10-11-0135