

# Integration of Bioinformatics into Life Science Curricula: Community Development, Dissemination, and Assessment of a NIBLSE Learning Resource

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## Introduction and Context

*The Network for Integrating Bioinformatics into Life Science Education (NIBLSE)*

- Big data and computational tools have transformed the way we address biological questions. To prepare undergraduates for tomorrow's challenges in the biological sciences, life science curricula should integrate the understanding and use of these tools at all levels. NIBLSE has developed a framework to facilitate achieving this goal (Dinsdale et al., 2015).

See our accompanying poster (460A): "The Network for Integrating bioinformatics into Life Sciences Education (NIBLSE): Barriers to Integration" Rosenwald et al.

*Limitations of Traditional Pedagogical Bioinformatics Exercises Introducing Sequence Similarity*

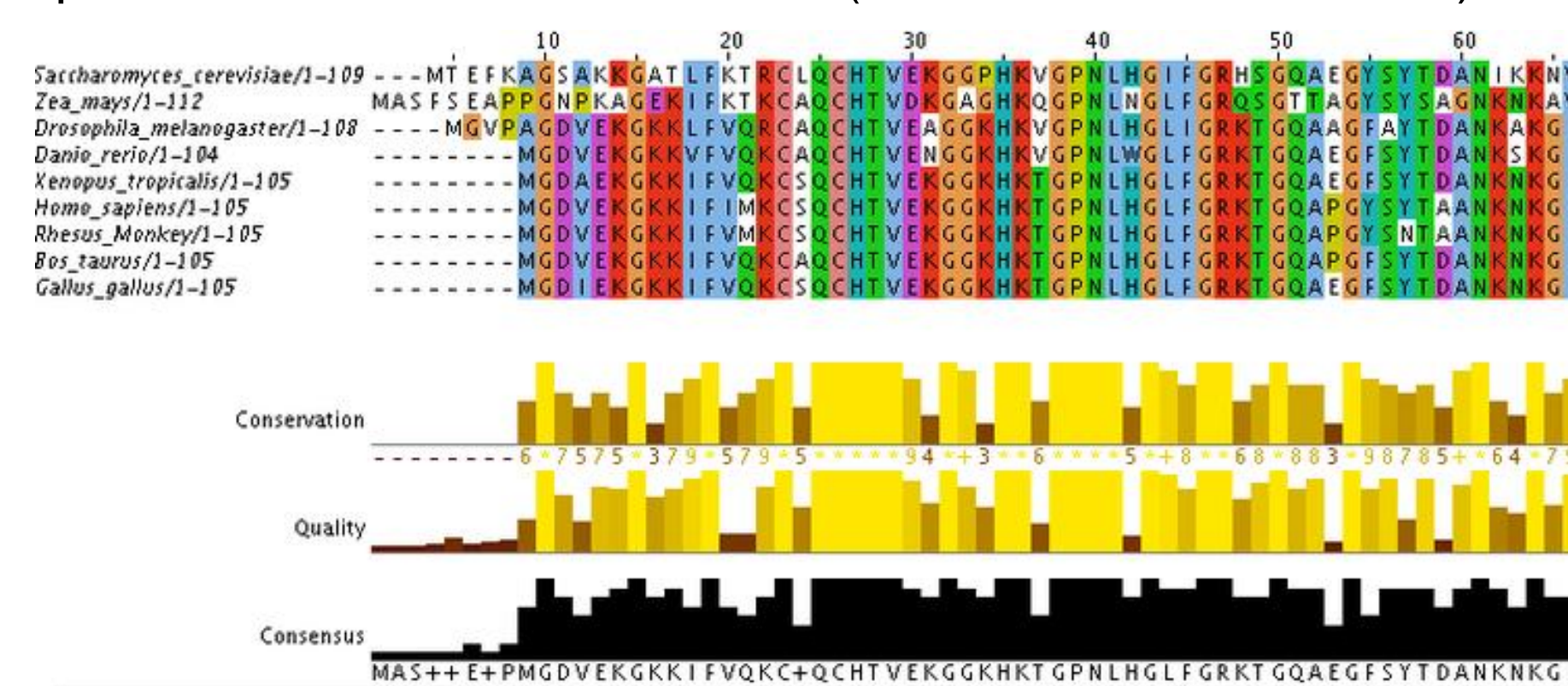
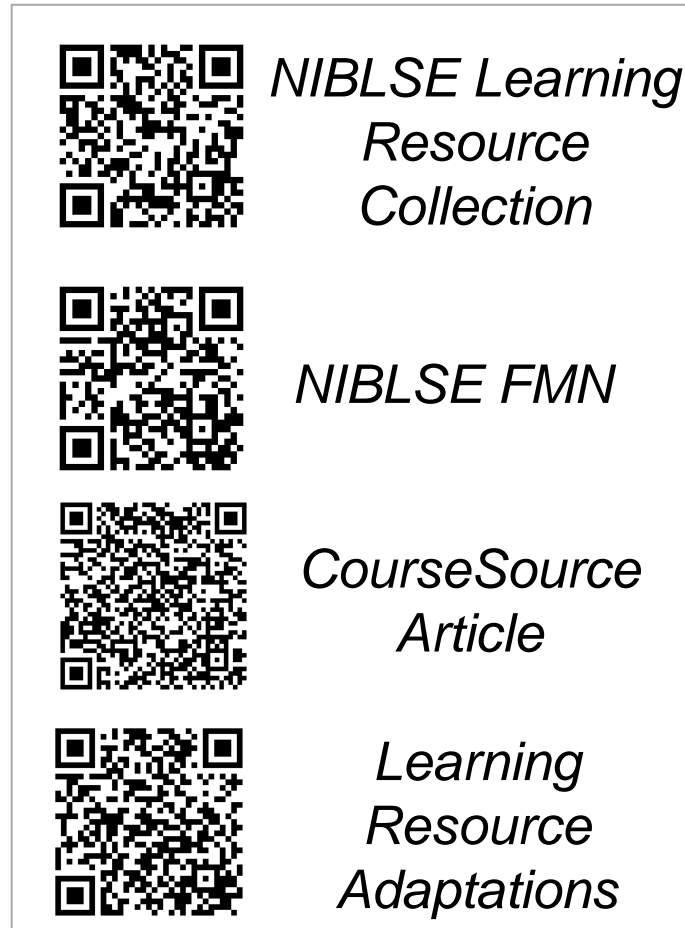
- Introductory bioinformatics exercises typically walk students through the use of computational tools, but often provide little understanding of what a tool does "under the hood." A solid understanding of how computational algorithms function, including their limitations, is essential for interpreting the output in a biologically relevant context. Here we describe the development, assessment, and dissemination of an introductory learning resource that focuses on the core concept of sequence similarity and its biological applications, using the NIBLSE framework.

*Development and Dissemination of a NIBLSE Learning Resource*

- The resource which focuses on the core concept of sequence similarity and its biological applications was built upon the bioinformatics core competencies developed by NIBLSE and established in August of 2016 (Sayres et al., 2018).
- An initial version of the resource was converted into modular format and expanded for a wider audience by a community of faculty operating within the collaborative NIBLSE Incubator model and made publicly available on via the NIBLSE Learning Resource Collection in June of 2017 (see associated QR code).
- After multiple pilot rounds of classroom implementation and refinement, a polished version of the resource was formally published in the journal CourseSource in April of 2019 (see associated QR code).
- The resource was further disseminated using the QUBES Faculty Mentoring Network (FMN) model in the Spring of 2019 (see associated QR code).
- In addition to implementing the resource into classrooms across the nation, a subset of FMN participants produced course and learning goal specific adaptations (i.e., virology, developmental biology, botany) of the original resource that are linked as part of the collection on QUBES (see associated QR code).

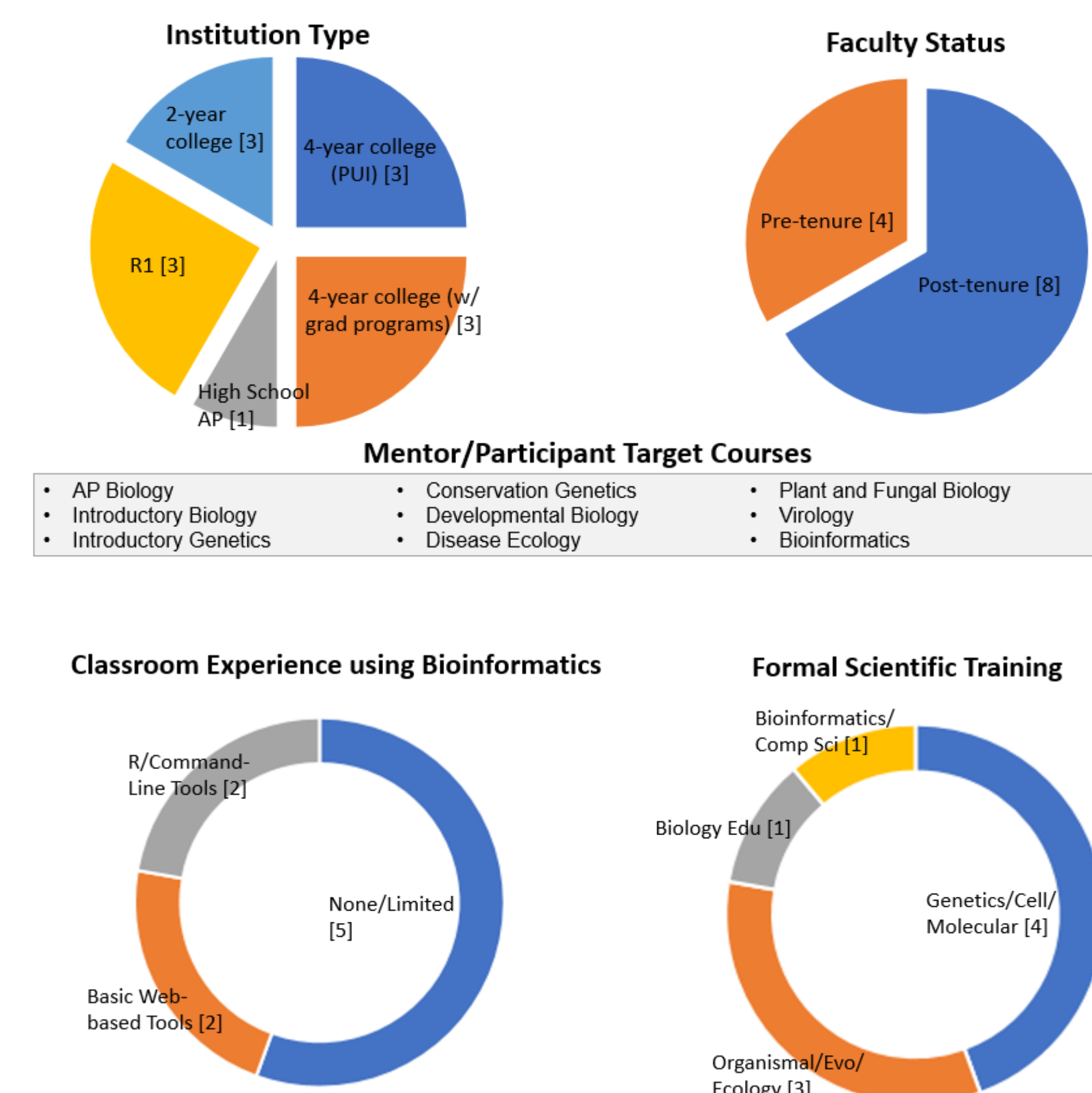
See our accompanying poster (464B): "Incubators: Building community networks and developing open educational resources to integrate bioinformatics into life science education" Morgan et al.

### QR Codes



**Figure 1. Multiple sequence alignment output of homologous cytochrome C protein sequences using Jalview viewer (above).** This visual is produced by students during a learning module to visualize conserved domains within cytochrome C, while the nearest-neighbor distance matrix values are used to generate a phylogram.

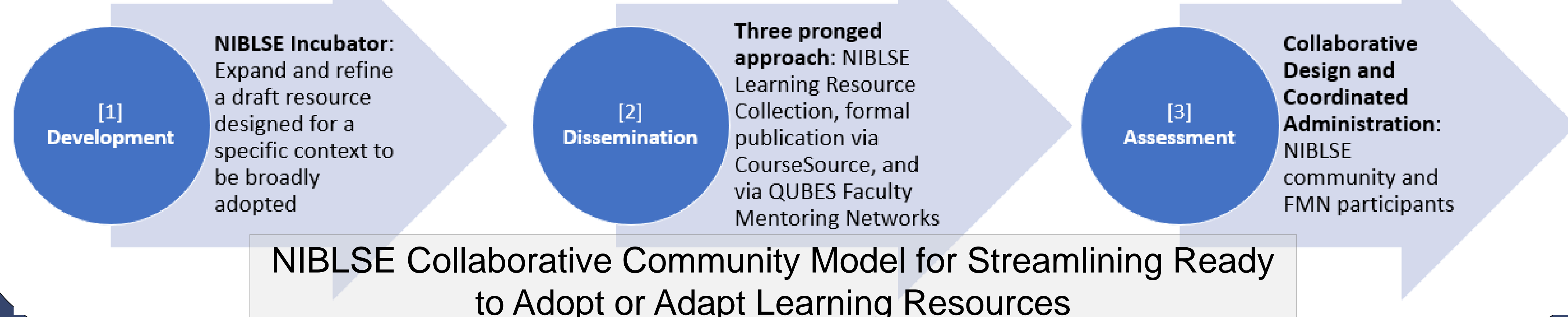
**Figure 2. NIBLSE FMN participant composition descriptive metrics (right).** The FMN was run during the spring 2019 semester with 12 faculty members in the learning community (9 mentees and 3 mentors). The professional development opportunity targeted recruitment of faculty from a variety of biological professional society listservs and encouraged instructors that were interested in integrating bioinformatics principles into their classroom for the first time to apply. The group of faculty was diverse on many fronts (e.g., institution type, tenure status, targeted course, previous experience using bioinformatics, biological training emphasis).



## Research Goal

- To assess if modules from a NIBLSE Incubator learning resource implemented across diverse classrooms types and institution classifications can yield measurable learning gains and changes in student perception of learning.

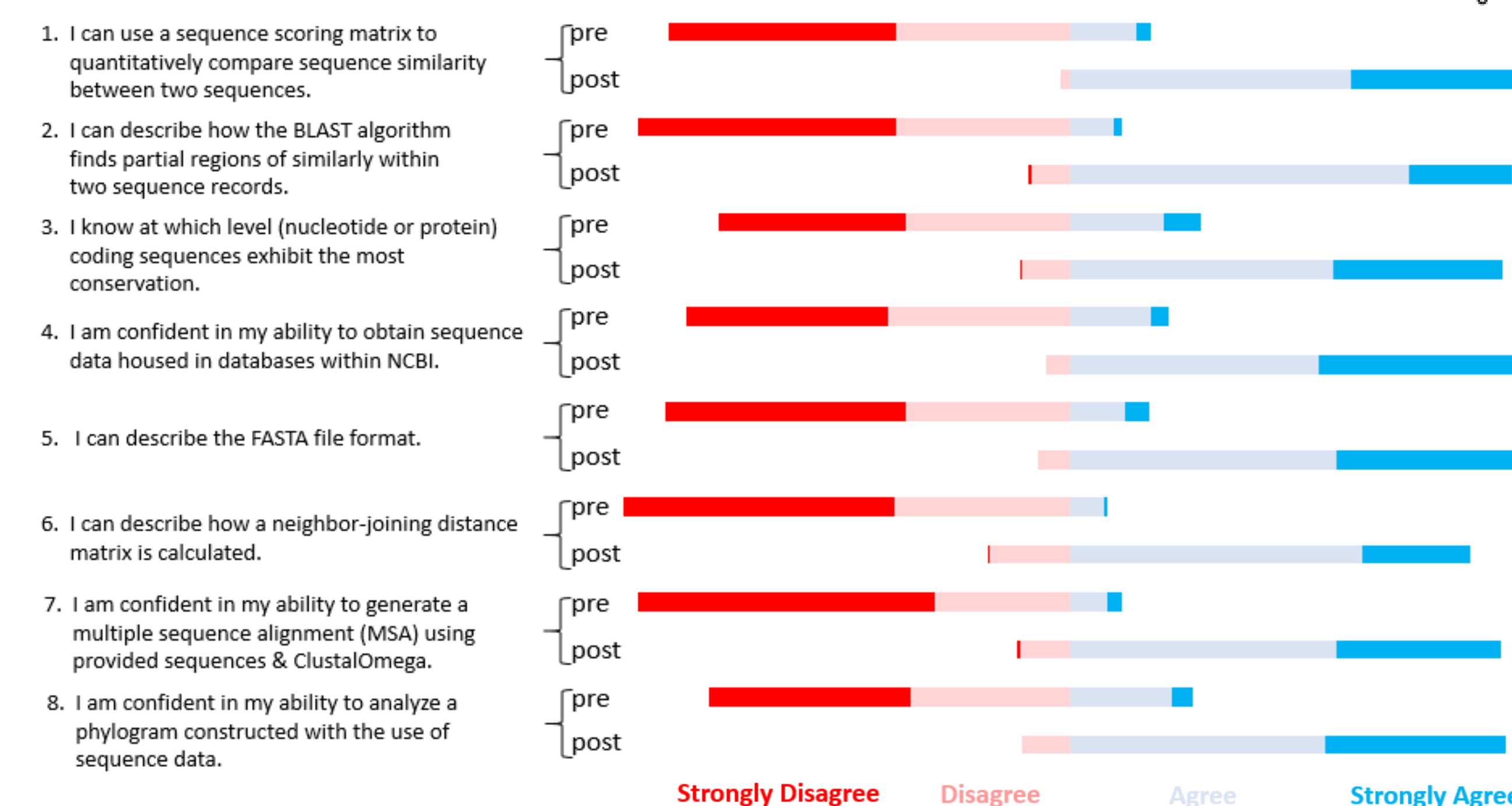
## Methods



## Results

Course Content Focus	Undergraduate Course Level	Institution Classification
Bioinformatics and Computational Biology	100	Research Intensive
General Biology	200	Liberal Arts College
Developmental Biology	300	Liberal Arts College
Molecular Biotechnology	300	Liberal Arts College
Molecular Biology of the Cell	300	Research Intensive
Virology	300	Research Intensive

**Figure 3. Matched pre-/post-assessment quiz scores indicate significant participant learning gains.** A fifteen-item assessment consisting of a combination of multiple choice and multiple selection questions was administered pre- and post-completion of the interactive learning modules. Six cohorts of student participants (n=175) at independent institutions completed the assessment instrument with a range of 7-28 days between pre- and post-assessment. A two-tailed paired t-test indicated significant difference ( $p < 0.00001$ ) between pre- (4.95) and post-quiz (7.38) means. + = mean; box notches =  $\pm 1.58 \cdot \text{IQR} / \sqrt{n}$  and represent the 95% confidence interval for each median. Non-overlapping notches give roughly 95% confidence that two medians differ.



## Conclusion

- Matched pre-/post-quiz scores (n=175) showed an improvement of 40% ( $p < 0.00001$ ), indicative of objective learning gains in both understanding and utilizing computational tools.
- A retrospective attitudinal survey indicated that students self-reported perception of competence in performing learning outcomes was also significantly higher ( $p < 0.0001$ ), with medians on all questions shifting from negative to positive responses after module completion.
- This resource and its developmental process serves as an exemplar for the ability of the NIBLSE collaborative model to address barriers for the integration of bioinformatics into undergraduate curricula and to harness community intellectual capital.

## References

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- Kleinschmit, A., Brink, B., Roof, S., Goller, C., & Robertson, S. D. (2019). Sequence Similarity: An inquiry based and "under the hood" approach for incorporating molecular sequence alignment in introductory undergraduate biology courses. *CourseSource*.
- Sayres, M. A. W., Hauser, C., Sierk, M., Robic, S., Rosenwald, A. G., Smith, T. M., Triplett, E.W., Williams, J.J., Dinsdale, E., Morgan, W.R. & Burnette III, J. M. (2018). Bioinformatics core competencies for undergraduate life sciences education. *PloS one*, 13(6).

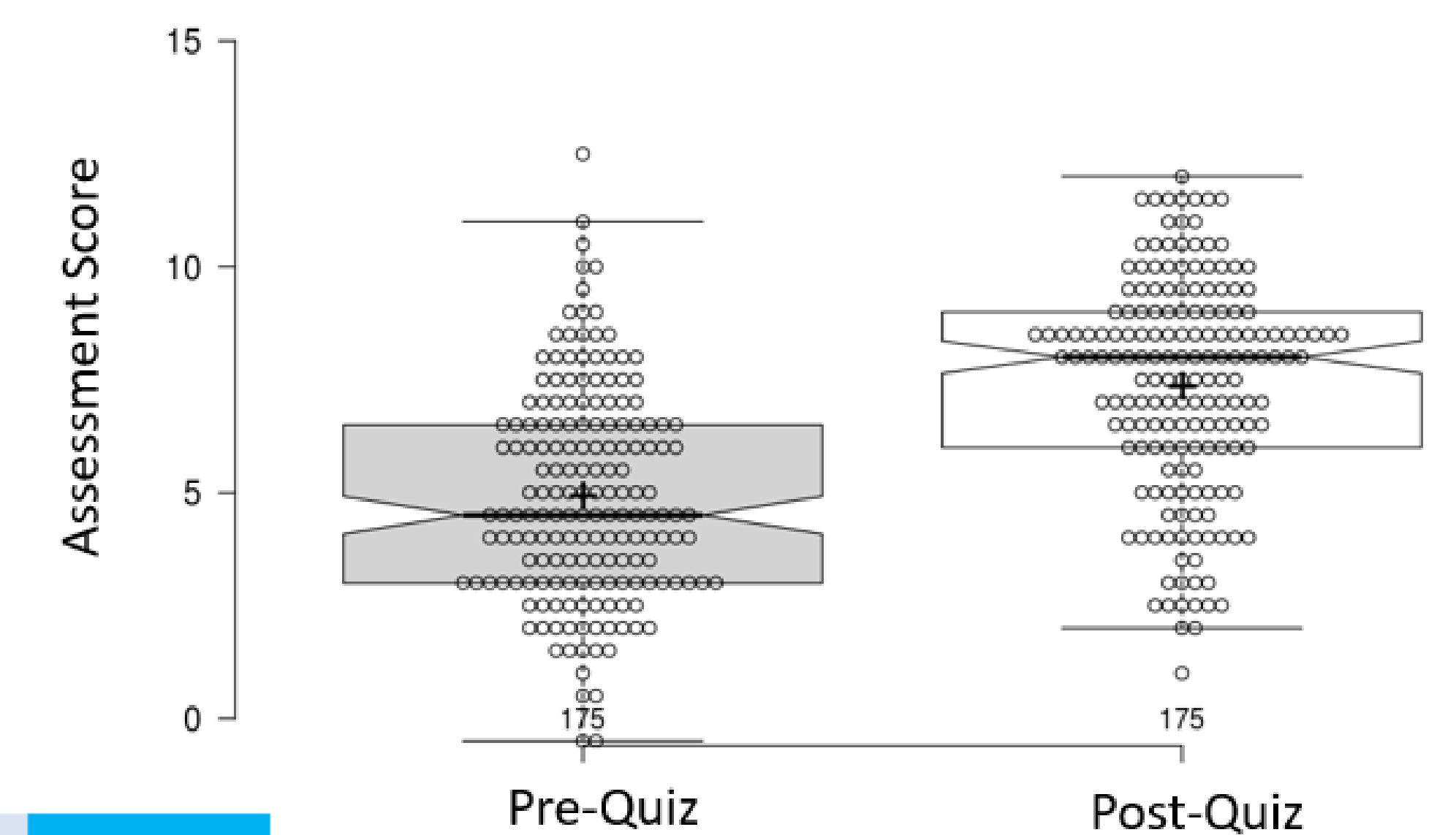
## Acknowledgements

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- Sam Donovan (University of Pittsburgh), Hayley Orndorf (University of Pittsburgh), and Deb Rook (QUBES) were instrumental in coordinating the logistics and streamlining the QUBES FMN. Sam Donovan also served as a lead mentor of the NIBLSE FMN.
- The NIBLSE leadership team: Mark Pauley, Anne Rosenwald, Elizabeth Dinsdale, William Morgan, Eric Triplett, and William Tapprich.

## NIBLSE Contact Information

- Webpage: <https://qubeshub.org/community/groups/niblse>
- Join the NIBLSE Group: <https://qubeshub.org/community/groups/niblse/getinvolved>

**Table 1. The bioinformatics learning resource was implemented and assessed in a diversity of courses across program-level and institution classification.** The versatility of the learning resource and the ability of bioinformatics to be integrated across the curriculum for biology majors is highlighted by the variety course content types in addition to the diversity of programmatic course level codes. Disaggregated pre-/post-assessment data and retrospective post survey results exhibited significant learning gains and changes in participant perceptions independent of institution classification, programmatic level of a course, and the focus of course-content.



**Figure 4. Student participants self-reported perceived learning gains.** Retrospective pre- and post-survey aggregate data utilizing a four-point Likert-type scale is depicted as a divergent stacked bar graph. Six cohorts of student participants (n=165) at independent institutions completed the survey instrument. All questions were statistically significant ( $p < 0.0001$ ) when comparing median Likert-type scale response between retrospective pre- and post-ratings using the Wilcoxon signed-rank test.



NIBLSE  
Webpage  
QR Code

