## Letter to the Editor

# The *CourseSource* Bioinformatics Learning Framework

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To The Editor:

According to the *Oxford English Dictionary* (OED), bioinformatics is defined as "the branch of science concerned with information and information flow in biological systems, esp. the use of computational methods in genetics and genomics" (OED, 2015). Because the use of bioinformatics tools and approaches is becoming increasingly important for life scientists of all disciplines at all levels, it would be particularly advantageous for life sciences undergraduates to have some training in this field.

As of yet, there is little agreement on a set of bioinformatics learning goals appropriate for undergraduate biology students. In an effort to move toward consensus in this area, we have developed a learning framework for a bioinformatics course that is part of the *CourseSource* initiative (Supplemental Material Table 1). *CourseSource* builds on the goals of *Vision and Change in Undergraduate Education: A Call to Action* (American Association for the Advancement of Science, 2011) by serving as a repository for tested teaching resources in a variety of different biological disciplines (Wright *et al.*, 2013). *CourseSource* organizes teaching materials into courses that are part of the standard biology curriculum (http://coursesource.org). Each course is informed by a framework that has been vetted by an appropriate disciplinary society (e.g., the *CourseSource* framework for a genetics course was developed by representatives from the Education Committee of the Genetics Society of America).

Core competencies for bioinformatics have been defined by the Curriculum Task Force of the Education Committee of the International Society for Computational Biology (Welch *et al.*, 2014). The task force related the competencies to three different types of individuals requiring bioinformatics training: 1) bioinformatics engineers, who create novel computational methods needed by bioinformatics users and scientists; 2) bioinformatics scientists, who employ computational methods to advance the scientific understanding of living systems; and 3) bioinformatics users, who access data resources and bioinformatics tools to perform duties in specific application domains (e.g., medicine, law, agriculture, food science, education, etc.). As the starting place for the framework we used the bioinformatics user and bioinformatics scientist personas in particular (see table 2 in Welch *et al.*, 2014) as well as our collective experience of integrating bioinformatics into our teaching.

Three of us (M.A.P., A.G.R., and L.W.) worked collaboratively on the framework over several months, with input from S.C.R.E. and R.W. We then asked for feedback on the framework from groups with an interest in bioinformatics education, including members of the Genomics Education Partnership (http://gep.wustl.edu), the Network for Integrating Bioinformatics into Life Science Education (NIBLSE; http://niblse.unomaha.edu), and the Genome Consortium for Active Teaching NextGen Sequencing (http://lycofs01.lycoming.edu/~gcat-seek), and participants in the Howard Hughes Medical Institute–sponsored Bioinformatics Workshop for Student/Scientist Partnerships that took place in June 2012 (http://gep.wustl.edu/hhmi_bioinformatics_workshop/index.html). The feedback we received was used to revise the framework. We are currently working with the International Society for Computational Biology to vet the framework. In addition, we expect that NIBLSE will also play a role in its ongoing development.

As with most of the frameworks for other courses, the bioinformatics framework is organized around major topics with associated learning goals (framed as questions). A set of sample learning objectives, not meant to be exhaustive, is associated with each learning goal. In devising the framework (Supplemental Material Table 1), we organized the information around biological topics and computational

ideas needed to address them. The first topic involves the role of computation in the life sciences. Subsequent topics involve concepts associated with the central dogma, beginning with DNA as the repository of genetic information, then considering RNA and proteins as means to express the genetic information. We next considered metabolomics and systems biology, exploring cellular homeostasis, and then examined topics in ecology and evolution, including metagenomics, thus moving from the level of individual cells to environmental samples. The final topic describes computational skills.

*CourseSource* learning frameworks, including this one for bioinformatics, are not meant to be proscriptive. That is, there is no implication that a course should necessarily contain all of the elements in the associated framework. Instead, a course based on the learning framework will make use of an agreed-upon set of learning goals, and can take advantage of the associated expertise and materials posted in that particular field on *CourseSource*. For example, several of us teach bioinformatics courses that do not include substantial time spent on computer science skills, yet adhere to the overall learning goals and learning objectives within the framework. Overall, we feel that the existing framework will be generally applicable and useful to those attempting to launch a bioinformatics course at their institution for the first time. We therefore encourage all faculty members who are currently teaching bioinformatics to help populate the *CourseSource* bioinformatics framework with useful teaching materials to maximize utility of the site.

Bioinformatics is an excellent way to introduce students to authentic research and is thus an effective means to achieve the goals of *Vision and Change*. We envision that the bioinformatics learning framework will continue to evolve as the field of bioinformatics grows. We welcome feedback from the life sciences community and encourage members to consider submitting their lessons, whether in bioinformatics or in other disciplines, to *CourseSource*.

## REFERENCES

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