Editorial: International, interdisciplinary, multi-level bioinformatics training and education

Bioinformatics is central to biology in the 21st century. The generation of terabytes to petabytes of data per day has increased the complexity and challenges of contemporary biological research. The use of computer-based analytical tools on electronically stored and distributed data is fundamentally changing not only core life science research but also its application to problems in medicine, agriculture, conservation and forensics. In light of this ‘information revolution’, school, college and university curricula as well as various forms of postgraduate training and informal education must be redesigned to prepare the next generation of life scientists. In this special issue of Briefings in Bioinformatics, we continue to report on various initiatives in bioinformatics education and training begun in a previous special issue published here in 2010 [11 (6)].

To address the needs of diverse learners and citizenries from multiple cultures, there is a tremendous need for heterogeneous approaches. The articles included herein are drawn from (i) multiple countries: Australia, Costa Rica, Israel, the Netherlands, New Zealand, UK, United States; (ii) multiple curricular levels: public citizenry, secondary level, college and university level, graduate students, postgraduate level (PhD and postdoctoral fellows), faculty development, scientific research community; (iii) multiple pedagogies that range from informal education to training and transmission to engagement in open-ended, collaborative and problem-based learning environments; and (iv) software use that range from Wikis and spreadsheets to high-end research suites. All authors desire to enhance, expand and empower an international community of bioinformatics educators, trainers and researchers. Most operate in the copyleft paradigm of sharing software, databases and analytical tools in an open access environment. The authors report that the current revolution in biological research is a wonderful opportunity to reform the way we teach life sciences. Three factors in particular make this a unique time to explore new ways to enhance learning:

- The research data and analytical tools are now easily accessible in the public domain;
- Faculty recognize that they need to seek professional development to stay abreast of the changes in biological knowledge and techniques; and
- Students are aware of the changes in biology and related disciplines, understand that solving biological problems is relevant to their lives and realize that bioinformatics skills hold possibilities for future employment.

Taken together, the convergence of these factors affords us the opportunity to move curriculum reform beyond the relatively small group of ‘early adopters’ to engage the much larger ‘early majority’ of biology faculty.

Bioinformatics is a subject in transition subject to being defined differently by life scientists, computer scientists, engineers, experimentalists, mathematicians and so forth. However, despite these differences, when it comes to education and training, there is widespread agreement that to use the databases, software, primary literature, theoretical lenses and applications, users need to develop more quantitative reasoning skills to conceptually understand the bioinformatics challenges faced today. Techniques may change such as recently occurred in the shift away from microarrays to analyze gene expression to RNA-seq analyses of transcriptomes or from a reliance on strictly bifurcating phylogenetic trees based on sequences to network models based on complete genomes that accommodate horizontal gene transfer and endosymbiosis. So the challenge is how do we educate for such a rapidly changing, ill-formed discipline? The authors inside describe exciting possibilities that are adoptable, adaptable and implementable in a wide variety of contexts.

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