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Essay

A Survey of Scholarly Literature Describing the Field of Bioinformatics Education and Bioinformatics Educational Research

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Bioinformatics education can be broadly defined as the teaching and learning of the use of computer and information technology, along with mathematical and statistical analysis for gathering, storing, analyzing, interpreting, and integrating data to solve biological problems. The recent surge of genomics, proteomics, and structural biology in the potential advancement of research and development in complex biomedical systems has created a need for an educated workforce in bioinformatics. However, effectively integrating bioinformatics education through formal and informal educational settings has been a challenge due in part to its cross-disciplinary nature. In this article, we seek to provide an overview of the state of bioinformatics education. This article identifies: 1) current approaches of bioinformatics education at the undergraduate and graduate levels; 2) the most common concepts and skills being taught in bioinformatics education; 3) pedagogical approaches and methods of delivery for conveying bioinformatics concepts and skills; and 4) assessment results on the impact of these programs, approaches, and methods in students' attitudes or learning. Based on these findings, it is our goal to describe the landscape of scholarly work in this area and, as a result, identify opportunities and challenges in bioinformatics education.

MOTIVATION FOR THE STUDY

Many complex problems in biomedical systems and public health research and development require cross-disciplinary approaches to integrate diverse perspectives into a collective whole (Adams *et al*., 2010). Cross-disciplinary approaches encompass "a set of practices associated with thinking and working across perspectives such as multidisciplinary, interdisciplinary, and transdisciplinary" (Adams *et al*., 2010, p. 1158). Bioinformatics is a cross-disciplinary field that resulted from the advancement of biological sciences due to the integration and application of information technology and computational science to solve biological problems in emerging fields such as genomics and systems biology. This advancement has resulted in a massive amount of biological data that has impacted the manner in which research and education has and will continue to be conducted in our pursuit of improved human health and prolongation of human life (Yang *et al*., 2008). Hence, it is vital to leverage education and training to fulfill the ongoing need for competent scientists and technicians in bioinformatics (Hersh, 2008; Ranganathan, 2005). Moreover, to ensure the efficacy of the education and training, we must have a better understanding of effective educational approaches and strategies for improving student learning in this field.

Bioinformatics education can be broadly defined as the teaching and learning of the use of computer and information technology to gather, store, analyze, interpret, and integrate data to solve biological problems (Counsell, 2003; Koch and Fuellen, 2008). This means that training and education in bioinformatics should encompass knowledge and skills

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from biology, mathematics, statistics, physics, chemistry, medicine, pharmacology, computer science, and information technology (Ranganathan, 2005). However, effectively integrating bioinformatics education into formal and informal educational settings has been a challenge due to: 1) its cross-disciplinary nature; 2) the disparate methods, outlooks, and cultures of its related disciplines (Zauhar, 2001); 3) the lack of an integrated training support structure (e.g., United Kingdom; Brass, 2000); and 4) the lack of collaboration between funding agencies (Brass, 2000). In this article, we seek to provide an overview of the state of research in bioinformatics education and bioinformatics educational research as described in the published literature. Our goal is to 1) help inform current education and training in the field, 2) motivate educators to share the effectiveness or challenges of their efforts through scholarly articles with the broader community, and 3) invite educational researchers to collaborate with educators in helping to shape and evaluate the effectiveness of specific implementation efforts.

Like many other fields, bioinformatics has emerged due to the development of new computing tools and environments that allow researchers to more easily share data. While traditional bioinformatics has been used to perform genome and proteome analysis, this field is growing or morphing rapidly to now encompass simulation-based approaches give rise to computational biology (Kitano, 2002). We argue that, as the technical advances in this area progress, we also need to simultaneously concentrate on how these advances can be effectively integrated into educational settings and on sharing the approaches with the broader community. Coupling advances in technical research and identifying how these advances can be transformed into specific training and educational experiences will allow the development of a future workforce that will be ready to take jobs and conduct research in these emerging fields.

To make steps toward this end, we aim in this survey study to identify: current approaches for integrating bioinformatics at the undergraduate and graduate levels; the most common concepts and skills being taught in bioinformatics education; pedagogical approaches and methods of delivery for conveying bioinformatics concepts and skills; and evaluation or assessment results (when available) on the impact of these programs, approaches, and methods in students' learning. Specific research questions for this survey study were:

How does published literature describe curricular efforts aimed at integrating bioinformatics education?

How does published literature describe specific bioinformatics education content, delivery methods, and assessment?

Our findings identify both the opportunities and challenges that exist in bioinformatics education and reveal a need for further educational assessments in this emerging area.

METHODS

Owing to the recent emergence and continuously evolving nature of the field of bioinformatics, we chose to narrow our searches to key phrases such as "bioinformatics education," "biomedical informatics," or "bioinformatics" in some educational context. We limited our searches to these three key phrases to keep the focus on the field of bioinformatics and to limit the scope of the paper. We expected that, by using this approach, we would identify articles from better established efforts that at the same time could have had an impact in educational programs or classroom implementations. Therefore, findings from this study are limited to those articles with any of those phrases in at least the title, abstract, and keywords and with a publication date of 2013 or earlier.

The research team followed a systematic procedure of searching, categorizing, and analyzing the papers presented in this review. The interdisciplinary research team consisted of four faculty members and two students from backgrounds in educational research (A.M.), biology (M.K.), biotechnology (K.C.), computer science (J.S.), computer and information technology (D.R.), and engineering (M.T.). To account for reliability, A.M., D.R., and M.T. performed all the searches and the initial categorization of the papers. They also took the first step at constructing the tables. Then, the tables, the columns, and the categorization of the articles were reviewed by the rest of the team members to account for validity, with each team member focusing on his or her own discipline. Finally, A.M. and the lead team member from each discipline conducted discussions associated with each of the tables. At times, the discussion was performed by three team members (i.e., mathematics, statistics). Details of the specific procedures are detailed in the following paragraphs.

The publications selected for this analysis were identified by conducting searches in Google Scholar, Web of Science, ACM Digital Library, ERIC, and PubMed. When the searches were conducted, we used the default settings of those databases: searching on multiple fields and matching at least title, abstract, and indexing subject headings/descriptors. In Web of Science, the default "topic" search parameters include title, abstract, and descriptor fields. Default settings of PubMed include all fields, but PubMed also tries mapping the search terms to phrases in the MeSH (medical subject headings), journal, and author databases. For ACM Digital Library, the default search is "any field." In Google Scholar, the default search setting is "anywhere in the article." ERIC default parameters include searches in title, author, source, abstract, and descriptor. Therefore, we can argue that the searches conducted were in at least the title of the document, the abstract, and the keywords. Additionally, we performed a search on the National Science Foundation database to identify awards on the same topic. Using the key term "bioinformatics education," we identified 25 awards. Each award was reviewed individually to identify related lists of publications.

This search returned 113 (out of a total of 140) documents ranging in their publication year from 1998 to 2013 and returned primarily three types of scholarly publications: journal papers, conference proceedings, and magazine articles. The 113 identified papers were analyzed as individual units (as opposed to groups of papers published by the same research groups), potentially resulting in overlapping themes. Multiple levels of analyses were conducted on the 113 documents identified. To provide an overview of our sample, we first started by identifying frequencies of types of articles found as well as the year in which those were published. Then, because the major goals of this study were to identify how literature describes bioinformatics education, we decided to use a qualitative approach that consisted of analyzing the content of the abstracts in each of the categories to identify the themes; the details of this process follow.

In the first level of analysis, we aimed to identify a general perspective on the kinds and number of publications related to bioinformatics education, including the number of papers published per year, the types of publications (i.e., journal or magazine articles or conference papers), and the journals or conferences wherein bioinformatics education is disseminating and finding a community. In the second level of analysis, we categorized the papers based on their primary theme. Four primary themes were identified: 1) description, 2) position, 3) pedagogy, and 4) educational research or evaluation. In the description category, we included papers that described some sort of program, degree, course, or series of courses. In the position category, we considered all papers that described opinions about the need for bioinformatics education, opportunities and challenges of bioinformatics education, and issues related to the interdisciplinary nature of bioinformatics education. In the pedagogy category, we included papers that described a teaching method, multimedia technology, or method for the delivery of bioinformatics education. In the educational research or evaluation category, we considered all of the papers that included some sort of evaluation of programs, materials, knowledge, skills, or attitudes in general. Some papers were assigned to two or more of these categories. Papers describing programs at the K–12 level were omitted.

In the third level of analysis, we qualitatively examined the abstracts of the 113 papers, using categorical analysis to identify themes. Categorical analysis refers to a systematic approach of data analysis in which findings are inductively derived from the data (Strauss and Corbin, 1990). The process of inductive analysis identifies similarities and differences within the data, resulting in a set of interrelated themes (Glaser and Strauss, 1967). Through this analysis, we manually identified common themes among the abstracts, clustered these themes together into similar topics, and used the most descriptive wording or phrase for the topics. Finally, all papers from the same topic were further reviewed to provide a more detailed and in-depth description of each of the newly identified topics. All papers presented in the tables in the *Results* section are ordered alphabetically based on the first author's last name followed by year of publication.

RESULTS

In this section, we present the results of the three levels of analysis conducted on the articles identified using the search parameters and methodology described earlier. As shown in Figure 1, the publication year for the 113 identified articles ranged from 1998 to 2013.

Results in Figure 1 illustrate that, so far, the maximum number of articles appeared in 2007. Of the three types of publications, journal articles were the majority (81%), with conference papers (16%) and magazine articles (3%) forming much smaller contributions. On the other hand, Figure 2 shows that the published papers classified by discipline or field of study fell into four main categories. The biology education category (Figure 2, Biology Ed.) included 37 papers (34%) in education journals or conference proceedings focusing on microbiology, biology, pharmaceutical, biochemistry, or life sciences. The bioinformatics category included 38 papers (35%) discussing topics about bioinformatics, medical informatics, biomedical informatics, or computational biology. Computer or technology education (Figure 2, Computer Ed.) contained 14 papers (13%) published in journals or as conference papers related to technology education or computer science education. The biology and biotechnology category (Figure 2, Bio. and Biotech.) included 12 papers (11%) related to medical and biological engineering, biotechnology, science, and systems biology. The remaining seven papers (6%) were categorized as published in journals and as conference papers related to engineering education, education or science education, and information science or information science technology (Figure 2, Eng. Ed. & Inf. Science).

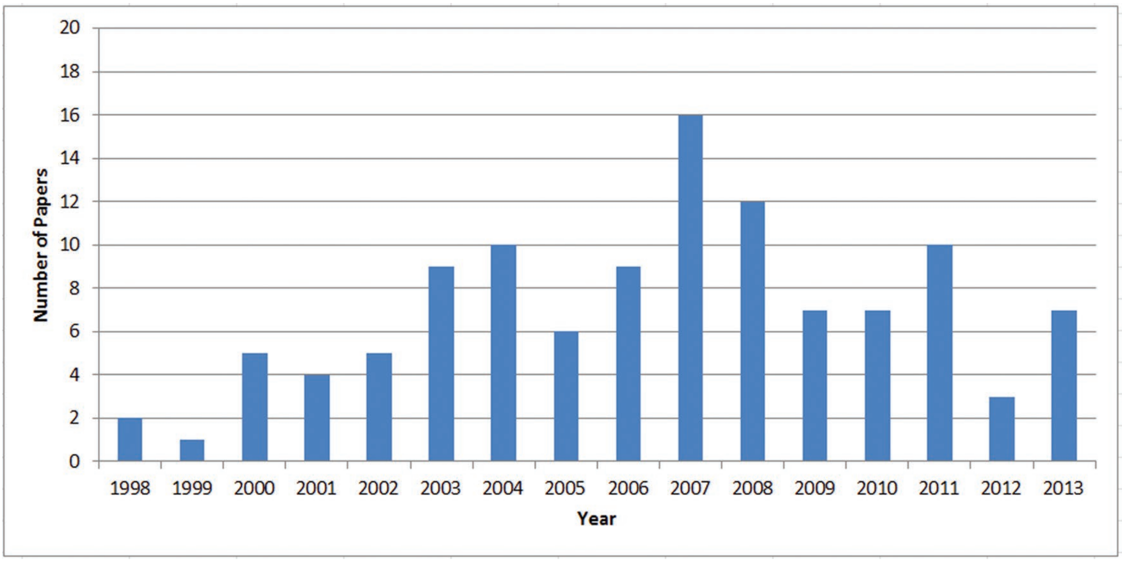

Figure 1. Distribution of articles published in the years 1998 through 2013.

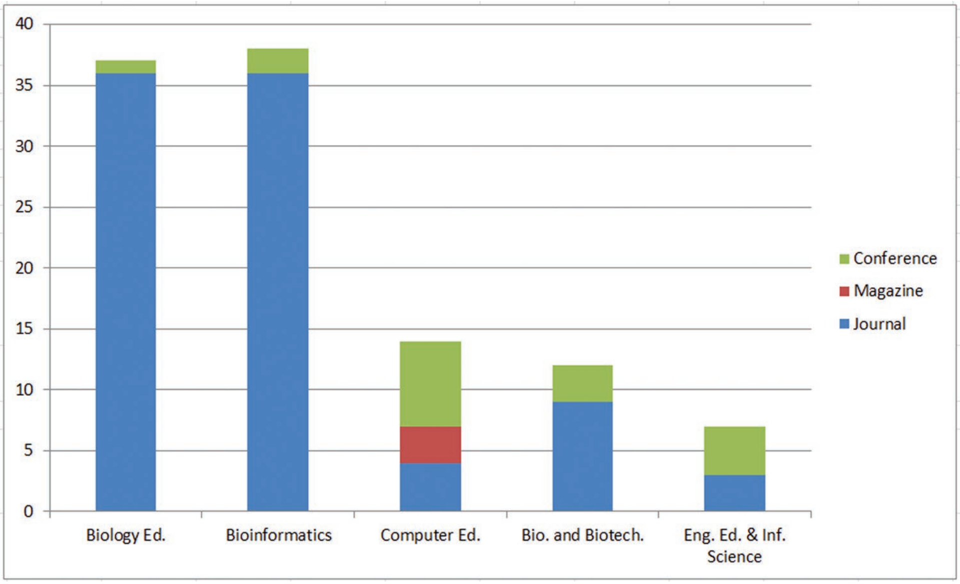

Figure 2. Distribution of manuscripts by type of publication and category.

The next step in the analysis consisted of a qualitative analysis of the abstracts to identify themes. Four preliminary themes emerged from the data and evolved into the following topics: 1) current curricular approaches for integrating bioinformatics at the undergraduate and graduate levels; 2) the most common concepts, skills, tools, and resources being taught and used in bioinformatics education; 3) pedagogical approaches and methods of delivery for conveying bioinformatics concepts and skills; and 4) evaluation results on the impact of these programs, approaches, and methods on students' attitudes or learning. We describe in the following sections each of the four identified topics by means of the content in each of the corresponding articles. A fifth theme also emerged that could be described as position papers. Papers found as part of this fifth theme discussed the need for bioinformatics education and a trained workforce within the discipline. However, because the content of these articles focused primarily on policy, and not content or pedagogy, they were omitted from the final analysis.

How Does the Published Literature Describe Curricular Efforts Aimed at Integrating Bioinformatics Education?

This section describes our findings in terms of individual courses, programs, degrees, and outreach efforts. In these papers, bioinformatics has been described as being incorporated into undergraduate or graduate curricula through either a course or a series of courses or as a university degree or program. Table 1 lists the articles that fell into these categories and describes how bioinformatics has been integrated.

Table 1 also shows that bioinformatics content is most commonly presented through a course or a series of courses. The target audience for these courses ranges from students in interdisciplinary courses to students in courses designed specifically for biology, biotechnology, life sciences, or pharmacy majors or for computer science and information technology majors at both the undergraduate and graduate levels. This distribution supports the notion of bioinformatics as interdisciplinary.

When bioinformatics is integrated as a university degree or program, the course of study is mainly focused on degrees for graduate students or geared toward a combination of undergraduate and graduate students. A less common focus is in the area of degrees for undergraduate students only. This may exemplify a trend observed in other new fields that emerge and are taught first at a graduate level and then, as the discipline evolves and becomes more clearly defined, at the undergraduate level.

How Does the Published Bibliography Describe Specific Bioinformatics Education Content, Delivery Methods, and Assessment?

This discussion starts by describing the content related to bioinformatics education in terms of subject matter expertise; specific concepts, methods, and tools; and services. This section also describes specific pedagogical methods described in the literature and delivery methods such as online learning. Finally, the analysis concentrates on literature that describes evaluation and assessment components.

Concepts, Methods, Tools, and Services in Bioinformatics Education

We divide this section into four parts: concepts, methods, tools, and services. The term "concept" refers to the notion of a subject or topic that any student must know and understand in the area of study in order to solve certain problems. These topics include computer science, biology/genetics, and mathematics/statistics. As for "tools," this refers to all the pre-existing instruments and applications available for students to use in order to facilitate the analysis and solution of a certain problem. Additionally, "methods" refers to the experimental, statistical, and computational processes. Finally, "services" refers to all the resources available for

Table 1. Summary of articles in category "course, series of courses or university degree or program"

Reference	Area	Format	Level	Discipline
Brame *et al*., 2008	Bioinformatics, molecular biology, and genetic approaches and research	Course	Undergraduate	Genetics
Brazeau and Brazeau, 2006	Human genetics and genomics in drug therapy, optimization, and patient care and counseling	Course	Undergraduate	Pharmacy students
Campbell, 2003	Genomics, proteomics, and bioinformatics	Course	Undergraduate	Biology
Cattley, 2004	Bioinformatics	University degree or program	Undergraduate	Science
Craddock *et al*., 2007	Pathosystems biology	Course	Undergraduate	Interdisciplinary
Feig and Jabri, 2002	Data mining	Integrated collection of exercises	Undergraduate	Biochemistry
Fetrow and John, 2006	Bioinformatics	Course	Graduate and undergraduate	Interdisciplinary
Floraino, 2008	Bioinformatics	Course	Upper undergraduate	Biological sciences, chemistry, and computer science
Furge *et al*., 2009	Bioinformatics	Modules	Undergraduate	Interdisciplinary
Goode and Trajkovski, 2007	Molecular biology, biochemistry, and bioinformatics	University degree or program	Undergraduate	Interdisciplinary
Hack and Kendall, 2005	Bioinformatics	University degree or program	Graduate	Life sciences
Haux, 2004	Health, medical, and biomedical informatics	University degree or program	Graduate and undergraduate	Biomedicine and health sciences
Hersh, 2007	Biomedical informatics	University degree or program	Graduate	Health science
Honts, 2003	Genomics and structural biology, cell biology, bioinformatics	Three courses	Undergraduate	Biology
Hughey and Karplus, 2003	Bioinformatics	University degree or program	Graduate and undergraduate	Engineering
Kane and Brewer, 2007	Biomedical informatics	Three courses	Undergraduate	Information technology
Kane *et al*., 2006	Biomedical informatics	Courses	Undergraduate	Information technology
Khuri, 2008	Computer science	Track collection of courses	Undergraduate	Health, medical, and life sciences
Koch and Fuellen, 2008	Bioinformatics	Courses	Graduate and undergraduate	Interdisciplinary
Krilowicz *et al*., 2007	Bioinformatics	Summer program	Graduate and undergraduate	Interdisciplinary
Kulkarni-Kale *et al*., 2010	Information technology and biotechnology	Course	Graduate	Biotechnology
Lim *et al*., 2003	Bioinformatics	Online course	Graduate and undergraduate	Interdisciplinary
Luo, 2013	Online bioinformatics resources	One semester course	Graduate	Biology
Rainey *et al*., 2007	Bioinformatics	Two course	Undergraduate and workforce	Interdisciplinary
Ranganathan, 2005	Bioinformatics	University degree or program	Graduate	Interdisciplinary
Reisdorph *et al*., 2013	Genomics, proteomics, and bioinformatics	Hands-on workshops	Graduate	Biology
Sahinidis *et al*., 2005	Bioinformatics	University degree or program	Graduate	Interdisciplinary
Sczyrba *et al*., 2008	Sequence analysis and programming in bioinformatics	Two courses	Undergraduate and graduate	Bioinformatics
Smith and Emmeluth, 2002	Bioinformatics	Learning modules	Undergraduate	Biology
Tolvanen and Vihinen, 2004	Bioinformatics	Two courses	Graduate	Interdisciplinary
Toth and Connelly, 2006	Sequence analysis	Course	Upper undergraduate	Biology and computer science
Yang and Zhang, 2008	Bioinformatics	Conferences, workshops, and tutorials	General	Interdisciplinary
Zatz, 2002	Bioinformatics	University degree or program	Graduate	Medical
Zauhar, 2001	Bioinformatics	University degree or program	Graduate and undergraduate	Interdisciplinary
Zhang, 2011	Bioinformatics and cystic fibrosis	Lab exercises	Undergraduate	Biology
Zhang *et al*., 2007	Bioinformatics	Track collection of courses	Graduate and undergraduate	Computer science
Zhong *et al*., 2003	Bioinformatics	Courses and programs	Graduate and undergraduate	Bioinformatics

users to access information, including reference and literary databases such as GenBank and PubMed. We recognize that the "database" term is burdened with multiple meanings, including a simple container for data (such as a file or even a written record), a means to manage data (i.e., a database management system), and even a Web-based interface providing access to an underlying database. For our purposes, we place "database" in the services category due to databases' need for a retrieval mechanism to provide their fullest value; consider that, if one did not have the need to eventually retrieve the data, then the need to store it is highly dubious. These services can be paired with several tools to organize and analyze data.

These categories are not mutually exclusive, in that items may appear in two or more of the categories based on context and audience. For instance, the term "BLAST" subsumes concepts such as DNA sequencing and pattern-matching; methods involving algorithms, statistics, and experimental processes/workflows; tools implementing the BLAST algorithms, such as the software supplied by the National Center for Biotechnology Information (NCBI); and services such as the BLAST search capabilities provided by the NCBI on its website (http://blast.ncbi.nlm.nih.gov/Blast.cgi). Given the richness of the field, some overloading of terms is natural, and when such cases occur in our analysis, we attempted to include such items in the most applicable category while recognizing others with different perspectives may place them elsewhere.

The most basic computer science concepts introduced within bioinformatics-related courses are databases, algorithms, and the Perl programming language, along with proper uses of the BLAST, Clustal, and FASTA tools and the NCBI, GenBank, PubMed, and MEDLINE services (see Table 2). Effective use of these tools requires data-mining skills and object-oriented programming skills. Additional skills are systems analysis and design, database design, software engineering, and human–computer interaction (HCI).

Table 3 shows that the application of bioinformatics methods to biological problems is the most common method for integrating bioinformatics and biology. Other less common applications relate to demonstration of evolution-related concepts and uses of information technology, such as conducting searches and mining data. The most frequent biological concepts include genomics, proteomics, and DNA sequence concepts, as well as biochemistry and molecular biology. Methods commonly taught include sequence analysis and alignment, DNA microarray data analysis, and the use of protein structure prediction and classification tools.

From results depicted in Table 4, we can identify probability and statistics as main concepts highlighted by different authors. No specific tools or statistical analysis or methods in this area were identified in any of the reviewed papers.

Pedagogical Approaches and Methods for the Delivery of Bioinformatics Education

During the content analysis, we attempted to identify the most common pedagogical methods used to convey bioinformatics-related concepts and procedures (see Table 5). In the process, we also determined that bioinformatics education has been delivered through both traditional face-to-face classroom formats and online distance-learning experiences, as described in Table 6.

Results from Table 5 indicate that bioinformatics has been introduced primarily through problem-to-be-solved methods (i.e., challenge-based learning) including student-centered approaches such as inquiry learning and collaborative learning. This also supports the trend discussed earlier, that within an educational context, bioinformatics is introduced as a tool to solve biological problems.

Diverse multimedia and delivery methods have been used in bioinformatics education. Primarily, we can identify the use and development of Web-based applications and learning environments to support inquiry learning and also the use of distance learning as a means of delivering content.

Impact of Programs, Approaches, and Methods on Students' Attitudes or Learning

During the analysis stage we attempted to identify whether some educational research or program evaluations have been conducted in the area of bioinformatics education and the kinds of constructs that have been measured. In Table 7, we present the summary of articles that fall within this category.

We note that that most of these articles are focused on evaluation of learning materials in the form of final course grades and student self-assessments, perceptions of the materials, confidence in attaining specific learning outcomes, and attitudes toward the learning experience. When assessment of learning was provided, results reported positive outcomes on student learning and perceptions in most cases. In cases in which learning data were reported, gains were related to working knowledge of bioinformatics concepts and methods.

DISCUSSION

This analysis provides a broad perspective of the state of scholarly work in bioinformatics education on the following dimensions: 1) a spectrum of the literature related to bioinformatics education; 2) ways of integrating bioinformatics into educational settings; 3) concepts, methods, computational tools, and services used in bioinformatics education; 4) pedagogical approaches for integrating bioinformatics education; and 5) evidence of the effectiveness of bioinformatics education.

Looking at trends of research in bioinformatics education, we can identify interesting patterns. The data reveal that publishing on bioinformatics education has been increasing since 1998. After 2007, a relatively constant rate of fewer than 12 papers a year is observed. It is possible that this decline can be attributed to the bioinformatics education community using additional terms (i.e., such as terms described in U.S. Department of Energy, 2010) to describe fields that are using some of the tools and curricula developed by the bioinformatics field and that are now applying them to new emerging areas of need. Additional terms may include "genomics," "proteomics," "quantitative biology," "systems biology," "computational biology," "biological systems," and "computing for biological systems," among others.

The most common method found for integrating bioinformatics into the undergraduate curriculum is either through a series of stand-alone courses or through learning modules integrated into existing courses. In contrast, university degrees

Table 2. Summary of computer science concepts, tools, and services

Reference	Concepts	Tools and services
Bagga, 2012	Data mining and programming	Perl
Beck *et al.*, 2007	Data mining	BLAST, GenBank, NSF, MAGI, and Inter-ProScan
Bednarski *et al.*, 2005	Data mining	BLAST, ClustalW, LocusLink, PSIPRED, DeepView, NCBI, OMIM, ExPASy's, KEGG, and Swiss-Prot
Boyle, 2004	Data mining	BLAST, Biology Workbench of San Diego Super-computer Center, NCBI, OMIM, PubMed, and Google
Burhans and Skuse, 2004	Object-oriented programming, information management, data mining, and HCI	Perl, algorithms and complexity, and human–computer interaction
Campbell, 2003	Data mining and object-oriented programming	PubMed, PubCrawler, Perl, Perl programming
Cattley and Arthur, 2007	Data mining and object-oriented programming	BLAST, Clustal, BioManager, Phylip, Course DNA, GenBank, MEDLINE, Sydney Bioinformatics, AGIC, AGNIS, UniProt, Swiss-Prot, Uniform Resource Locator URL, and UNIX
Cooper, 2001	Data mining	BLAST, Biology Workbench of San Diego Super-computer Center, Protein Explorer, Chime, and RasMol
Craddock *et al.*, 2007	Data mining	NCBI, GenBank, PATRIC, PathInfo, and MINet
Doom *et al.*, 2003	Data mining, database design, object-oriented programming, and HCI	Introductory programming, entity-relationship models, Perl, artificial intelligence algorithms, formal and comparative languages, pattern recognition, human–computer interaction, and evolutionary computation
Feig and Jabri, 2002	Data mining	Chime plug-in module
Fetrow and John, 2006	Data mining, systems analysis and design, and software engineering	Software engineering protocol, waterfall model, dynamic programming algorithms, clustering methods, and artificial neural networks
Furge *et al.*, 2009	Data mining, data structures, and machine learning	BLAST, BLASTp, FASTA, ClustalW, ClustalX, CBS, Trident, GlobPlot, VAST, FoldIndex, Swiss Deep View, ConSurf, MSA, Protein Explorer, MAFFT, MapViewer, dbSNP, tBLASTx, ENTREZ, CDD-CDART, CN3D, NetPhos 2.0, Phi-Blast, UniGene, BioQUEST, GARLI, GCG, LAMARC, MrBayes, PAML, PAUP*, PHYLIP, NetPhos, SignalP, Spartan, FirstGlance, NCBI, OMIM, PubMed, KEGG, ExPASy, PDB, BRENDA, data structures, machine learning, Perl, GUI programs, and query
Gelbart and Yarden, 2006	Data mining	BLAST
Gollery, 2006	Data mining and object-oriented programming	BLAST, PFAM, Linux, and Perl
Goode and Trajkovski, 2007	Data mining and object-oriented programming	Perl and database management
Haux, 2004	Data mining, object-oriented programming, data structures, and software engineering	Algorithms, data structures, software engineering, programming, and information systems
Honts, 2003	Data mining	BLAST, FASTA, VAST, ClustalW, GrailEXP, RasMol, OpenRasMol, Chime, CN3D, Deep View, SwissPDBViewer, TreeView, BCM Search Launcher, COILS Server, NCBI, OMIM, GenBank, PubMed, CDART, PDB, Human Genome Project, UCSC, RCSB, and Perl
Howard *et al.*, 2007	Data mining	BLAST, RPSBLAST, ClustalW, and PROSEARCH
Hughey and Karplus, 2003	Object-oriented programming	Perl
Kane and Brewer, 2007	Data mining, systems analysis and design, database design, and HCI	BLAST, FASTA, Clustal, managing databases, information systems, information management, evolving systems modeling, microarray, development languages, client–server architectures, algorithms, queries, data structures, human–computer interaction, data modeling, data organization architecture, system architecture, and system integration
Kane *et al.*, 2006	Data mining	BLAST and Clustal
Kane and Springer, 2007	Data mining and object-oriented programming	mpiBLAST, FASTA, NCBI, GenBank, Visual Basic .NET, SDK, and hands-on training in blade server architecture
Khuri, 2008	Data mining and object-oriented programming	BLAST, FASTA, ClustalW, GenBank, Swiss-Prot, PDB, C, Perl, UNIX, algorithms, and assembly packages
Koch and Fuellen, 2008	Data mining, object-oriented programming, and database design	Database design, algorithm design, pattern matching, programming paradigms, Perl, Phyton, C, C++, and Java
Krilowicz *et al.*, 2007	Data mining, object-oriented programming, systems analysis and design, and software engineering	C++, Phyton, Perl, and basic programming methods including but not limited to: data representations, data processing, file input/output, user interfaces, software engineering, algorithms, documentation, testing, debugging, and data structures
LeBlanc and Dyer, 2004	Data mining and object-oriented programming	Algorithms, and complexity programming fundamentals
Luo, 2013	Data mining	Dot plots

(*Continued*)

Table 2. Continued

Reference	Concepts	Tools and services
Marceglia *et al*., 2007	Data mining, object-oriented programming, and database design	Database management systems, relational database theory, relational models, entity-relationship diagrams, database design, and SQL
Moll *et al*., 2006	Data mining and object-oriented programming	BALLView and Python
Nehm and Budd, 2006	Data mining	GenBank, NMITA, and analyzing the Human Genome Project
Nichols *et al*., 2003	Data mining	Navigation through DNA data banks, NCBI, Sequence Manipulation Suite, Nucleotide Frequency Program, DHPLC Melt Program, Biology Workbench, Cold Spring Harbor Sequence Server, Codon Usage Database, T-COFFEE Sequence Alignment
Obom and Cummings, 2009	Data mining, object-oriented programming, and software engineering	Perl, microarrays, algorithms, and software engineering
Perez-Iratxeta *et al*., 2007	Data mining	MEDLINE
Pevzner and Shamir, 2009	Data mining	BLAST and principal component analysis
Rainey *et al*., 2007	Data mining	Course management system, CART, and BSC
Rao *et al*., 2008	Data mining and object-oriented programming	FASTA, EMBOSS, PHYLIP, GCG Wisconsin, ArrayQuest, NCBI, GenBank, SRS, PubMed, UniProt, PDB, KEGG, MUSC, GEO, Human Genome Project, EMBL, database, SOAP, algorithm, Web services, Web server, BioPerl, C++, microarray, and information systems
Sahinidis *et al*., 2005	Data mining and object-oriented programming	Databases, algorithms, microarrays, integer programming, and computational complexity
Sansom and Smith, 2000	Data mining	BLAST, FASTA, Prints, ProDom, TREMBL, Kabat ENZYME, PSI-Blast server, HGMP-RC Dali, Pfam, PROSITE, Jpred, NCBI, OMIM, EMBL, GenBank, DDBJ, Human Genome Mapping Project Resource Centre, PBD, and Swiss-Prot
Sczyrba *et al*., 2008	Data mining	BLAST, FASTA, GenBank, PubMed, EMBL, DDBJ, InterPro, PDB, UniProt, FlyBase, Wormbase, NCBI, and NEWT
Smith and Emmeluth, 2002	Data mining	NCBI, PubMed, MEDLINE, NLM, Human Genome Project
Toth and Connelly, 2006	Data mining and object-oriented programming	BLAST, Folding@Home, Clustal, Perl, regular expressions, dynamic programming, call stack, call tree, and memoization
Umarji *et al*., 2009	Data mining and object-oriented programming	Extreme programming and requirements engineering and documentation
Yang and Zhang, 2008	Data mining	BLAST, Genome Browser, Ensembl, UCLC, NCBI, and PDB
Zauhar, 2001	Data mining and object-oriented programming	Databases, algorithms, C, C++, Java, and Perl
Zhang *et al*., 2007	Data mining	BLAST, FASTA, OMIM, GenBank, and GEO

or programs are mostly oriented toward graduate degrees. A more recent trend seems to be the integration of bioinformatics education via online educational resources and programs. Kampov-Polevoi and Hemminger (2011) conducted a systematic comparison of curricula among bioinformatics programs. They developed a categorization scheme that is grounded in the analysis of the content of existing academic programs. Categories of their proposed scheme align with our categorization of bioinformatics domains such as informatics and computer science, statistics and research methods, domain-specific information systems (e.g., tools and services), and domain-specific knowledge (e.g., biology). In addition, they identified management- and business-related concepts, ethical and societal issues, and communication skills.

As we observed earlier, we may demarcate bioinformatics education into four main areas: concepts, methods, computational tools, and services. The conceptual basis for bioinformatics is found in topical areas such as genomics and proteomics; as for analysis tools, these include approaches such as data mining and object-oriented programming. In addition to concepts and analysis tools, we naturally see the wide deployment of computational tools and methods such as BLAST and databases such as GenBank. We also note services as playing a significant role in bioinformatics research and, hence, in education; in fact, we may characterize BLAST as provided by the NCBI as a service. Moreover, the capacity to search databases such as GenBank—again provided by the NCBI—as a service available to researchers and students alike. Underlying all four of these areas are threads that suggest a more conceptual basis for considering and incorporating computational elements as warranted. For example, moving beyond the specifics of BLAST into reflections on and investigations of string pattern matching and, even more broadly, pattern recognition will enable students to move beyond the current state of the art computationally and into a future of computing that will complement and enhance the next generation of biotechnologies. It is also interesting to point out that, from patterns found in Tables 2–4, little emphasis has been placed on mathematical and statistical concepts and procedures. Computational thinking—including a stronger focus on mathematics and statistics curriculum—serves to provide the ties that bind the aforementioned threads into a stronger weave surrounding bioinformatics education. Two additional topics that were found in more recent literature

Table 3. Summary of biology and genetics concepts and methods

Reference	Concepts	Method
Beck *et al*., 2007	Global gene expression and shoot apical meristem	
Butler *et al*., 2008	Microscopy	
Cattley and Arthur, 2007	Multiple sequence alignment, PCR primer design, restriction mapping, evolution, phylogeny, gene detection, microarray analysis, protein structure and function prediction, proteomics, protein identification and characterization, motif searching, and sequence assembly	
Craddock *et al*., 2007		Obtain pathogen information from Patho-Systems Resource Integration Center and Center for Pathogen Information
Doom *et al*., 2003	Chemistry, biochemistry, molecular biology, genetics, DNA sequencing, gene expression, X-ray crystallography, protein structure and function, gene structure and density, introns and exons, transposition and repetitive elements, introduction to gene microarrays, and proteomics	Comparative model of protein structure, DNA isolation, gel electrophoresis, molecular visualization, structural modeling, ligand screening, inhibition, and drug design
Feig and Jabri, 2002	Exploring concepts of information content of different biopolymers, the relationship between primary sequence and tertiary structure, and how sequence conservation can be used to find an enzyme active site	
Fetrow and John, 2006		Pairwise sequence alignment, protein secondary structure prediction, gene expression, gene prediction, and gene sequencing
Fuselier *et al*., 2011	Sequencing and PCR	NCBI and BLASTN
Goode and Trajkovski, 2007	Organic chemistry	
Harmon *et al*., 2002	Genomics and proteomics	DNA research and sequencing
Honts, 2003	Phylogenetic trees, molecular biology, cellular biology, DNA sequence, protein structure and function, gene structure and expression, and genome	
Howard *et al*., 2007	Biochemistry, genetics, cell biology, molecular biology, bacterial diversity, microbial genetics, microbiology, genes, protein sequence, protein structure, nucleotide sequence, amino acid sequence, DNA sequence, genetic mutation, and proteomics	
Hughey and Karplus, 2003	Molecular biology, chemistry, biochemistry, organic chemistry, cell biology, basics of DNA, RNA, protein sequence and structure, enzymes, regulation, metabolism, amino acids, genomics, phylogeny, and proteomics	Biochemistry laboratory, protein structure prediction, mRNA expression analysis, gene finding, RNA prediction and alignment, X-ray crystallography, and NMR spectroscopy
Kane and Brewer, 2007	Amino acids, nucleotides, genes, proteins, and single-nucleotide polymorphisms	Pairwise sequence alignments, multiple sequence alignments, and DNA microarray
Kane *et al*., 2006	Single nucleotide polymorphisms, protein sequence and function, genomics, DNA microarrays, proteomics, and atomic force	Mass spectrometry and cellular imaging
Kerfeld and Scott, 2011	Evolution and biological principles	BLAST
Khuri, 2008	Genetics, molecular biology, biochemistry, genomics, and proteomics	Macromolecular structures and machines and DNA microarray technology
Koch and Fuellen, 2008		Sequence/structure analysis, microarray data, and phylogenetic tree inference
Krilowicz *et al*., 2007	Molecular biology, biochemistry, genetics, microarrays, molecular life science, and bioethics	
Luo, 2013	Data mining, DNA and protein sequence analysis, motif identification, gene structure prediction, tree construction, and protein structure visualization and analysis	PubMed searches, UniProt database queries, sequence alignments, dot plots, BLAST, WebLab, Jemboss, MEGA, and SPDBV
Medin and Nolin, 2011	Primers and data mining	Blast, GenBank, Protein Data Bank, Science Direct, PubMed
Miskowski *et al*., 2007	Biology, transcription, translation, mutations, microbiology, genetics, evolutionary conservation, biochemistry, protein structure and function, enzyme kinetics, cell biology, phylogeny, protein sequence alignments, conserved protein domains, molecular biology, genomics, developmental biology, model organisms/comparative genomics, bacterial diversity, diversity of morphologies, physiologies and ecological niches throughout the microbial phylogenetic tree, DNA replication, structural RNA, and proteomics	Gene expression
MacMullen and Denn, 2005	Microarray gene expression, gene function, and molecular biology	

(*Continued*)

Table 3. Continued

Reference	Concepts	Method
Nehm and Budd, 2006	Evolution, geochemistry, molecular biology, paleobiology, and genetics	
Nichols *et al.*, 2003	Illustrate the different percentage of guanine-cytosine content present in the same gene across various organisms; variations in codon usage for each amino acid among organisms; relationships between nucleotide frequency, codon usage, and melting temperatures; and building phylogenetic trees based on a single gene from different organisms	
Obom and Cummings, 2009	Molecular biology, cell biology, human genetics, immunology, stem cell biology, proteomics, microbial genomics, molecular structure, and systems biology	Gene organization and expression, genome analysis, microarrays and analysis, and simulation of biological complex systems
Perez-Iratxeta *et al.*, 2007	Genomics and protein sequences	DNA microarray data
Rao *et al.*, 2008	Genomics	DNA microarray technology and gene-specific measurements and detections
Robertson and Phillips, 2008	PCR	
Sahinidis *et al.*, 2005	Proteomics, metabolic networks, biochemistry, molecular biology, cell biology, organic chemistry, and genomics	DNA microarray data, complex feedback and control mechanisms
Saier, 2003	Bioinformatic and biosystematic approaches to address fundamental questions about transmembrane transport systems and to develop probable answers based on systematic phylogenetic analyses	Bioinformatic tools applied to macromolecular evolution
Tolvanen and Vihinen, 2004	Biochemistry, molecular biology, proteins, and DNA	
Toth and Connelly, 2006	Molecular biology	
Wefer and Sheppard, 2008	Evolution, nucleotide sequences, amino acid sequences, DNA sequences, and mutations and variations	Evolutionary models
Wightman and Hark, 2012	Data mining and sequences	PubMed, NCBI, OMIM, and Blast
Yang *et al.*, 2008	Transmembrane proteins, amino acid, amino acid pair composition, RNA, and RNase digestion	Microarray data analysis, Bayesian biclustering model, Gibbs sampling procedure, protein structure prediction and classification, and protein disorder predictor
Yang and Zhang, 2008	Protein structure and function and genomes	Sequence analysis, pairwise sequence alignment, multiple sequence alignment, protein structure comparison and classification, protein structure prediction, and gene expression
Zhang *et al.*, 2007	PCR, DNA, theory of molecular evolution, comparative genomics, phylogenetic trees, sequence alignment, biochemistry, and biology	Isolation of cell DNA and preparation of PCRs

also emphasized the importance of providing bioinformatics students with core skills in scientific communication (e.g., Willighagen, 2010) and knowledge about ethics in the field (Taneri, 2011).

Pedagogical approaches identified to convey bioinformatics-related concepts and procedures include diverse forms of challenge-based learning. Specifically, inquiry-based learning approaches such as problem-based learning and research-based projects are the most common pedagogical methods coupled with the use of learning management systems that provide learners with an entry point where all tools and materials can be organized cohesively. It was also identified that, because of the nature of bioinformatics tools and resources, distance learning another viable approach for delivery of bioinformatics education.

Considering the results on the evaluation and educational research in bioinformatics education, we identified that assessment of educational materials (and not learning in particular) has been the common thread across most of the articles found in this category. The most common assessment mechanisms include pretest and posttest assessments, laboratory reports with their corresponding rubrics, and course examinations. This finding is consistent with the idea that the educational community is at an early stage of the instructional design process, focusing strongly on deciding the content and "what to teach" and the effectiveness of such content. But less progress has been made in identifying most effective ways of how to teach bioinformatics, including a focus on how students learn bioinformatics. This observation can be derived from the descriptions in Table 7, wherein most of the findings relate to student perceptions of learning materials or student self-assessments. These more experimental designs, as well as the introduction of qualitative research methods to identify how learning happens, are needed. Usability studies would also be useful in identifying how the technology supports or limits learning. This finding can also resonate with the circumstance that most of the authors outlined in this research come from disciplines in biology, computer science, and the like, where disciplines such as the social sciences, specifically science

Table 4. Summary of math and statistics concepts

Reference	Concepts
Andersson *et al*., 2001	Mathematics: factorial calculations
Burhans and Skuse, 2004	Mathematics: discrete mathematics
Doom *et al*., 2003	Mathematics: calculus and discrete mathematics Statistics: "statistics and probability," specific concepts not specified
Fetrow and John, 2006	Mathematics: abstract modeling and logical and quantitative problem solving Statistics: specific concepts not specified
Furge *et al*., 2009	Mathematics: calculus, differential methods, and numerical methods
Goode and Trajkovski, 2007	Mathematics: discrete mathematics and calculus Statistics: specific concepts not specified
Hack and Kendall, 2005	Mathematics: mathematical modeling methods, specific concepts not specified Statistics: statistical software tools and methods, specific concepts not specified
Haux, 2004	Mathematics: specific concepts not specified Statistics: biostatistics
Kane and Brewer, 2007	Mathematics: calculus Statistics: "probability and statistics," specific concepts not specified
Koch and Fuellen, 2008	Mathematics: combinatorics, graph theory, and linear algebra/numerics Statistics: structure analysis
Khuri, 2008	Mathematics: specific concepts not specified Statistics: hidden Markov models
Krilowicz *et al*., 2007	Mathematics: college-level mathematics skills, specific concepts not specified Statistics: "statistics and probability," specific concepts not specified
Sahinidis *et al*., 2005	Mathematics: specific concepts not specified Statistics: specific concepts not specified
Wightman and Hark, 2012	Statistics: ratios, probabilities, logarithms

Table 5. Summary of articles in category "pedagogical methods"

Reference	Pedagogical method
Andersson *et al*., 2001	Theory-anchored evaluation research approach and reciprocal evaluation-based collaborative teaching and learning, and design of online learning materials' virtual teacher
Beck *et al*., 2007	Collaborative research project
Bednarski *et al*., 2005	Inquiry-based labs
Boyle, 2004	Problem-based learning
Burhans *et al*., 2004	Laboratory practices
Burhans and Skuse, 2004	Laboratory practices
Butler *et al*., 2008	Close-ended research experience integrating student-centered research projects
Cooper, 2001	Inquiry-based exercises
Craddock *et al*., 2007	Hands-on skills, project-based learning
Fetrow and John, 2006	In-class exercises and a research-based course project
Floraino, 2008	Hands-on experience
Furge *et al*., 2009	Active learning
Hershberger, 1999	Interactive website for student research
Honts, 2003	Computer laboratory problems and group research projects
Jungck and Donovan, 2000	Use of the theme of "evolution" to convey bioinformatics
Jungck *et al*., 2010	Phylogenetic thinking and problem solving
Kane and Springer, 2007	Training modules and applied scientific computing
Lim *et al*., 2009	Problem-based learning
Ranganathan, 2009	Tutorials and symposia
Robertson and Phillips, 2008	Interactive Primer Design Exercise using the principles of scientific teaching
Shapiro *et al*., 2013	Problem-based learning (PBL), process-oriented, guided inquiry learning, and peer-led team learning
Toth and Connelly, 2006	Research project
Williams *et al*., 2010	Informal resources in bioinformatics education
Yang *et al*., 2008	Application-oriented approaches and student-centered instructional strategies

education, engineering education, and computing education, can play a larger role in contributing with pedagogical methods, instructional design theories, and assessment mechanisms.

Finally, through this analysis we also found that little research has focused on 1) how faculty members conceive bioinformatics and education in bioinformatics, 2) the identification of an integrated curriculum describing the required content and skills in bioinformatics education at different levels (K–12, undergraduate and graduate), and 3) how students learn bioinformatics.

The limitations of the study relate to the searching methodology and the categorization of the articles found. Specifically, we only considered articles that resulted from searches conducted in the above-mentioned databases and the use of very specific terminology. Also, the categorization was done manually, and although the categorizations were performed at least two times, there is still a possibility that some papers should have been categorized in additional themes. Also, the main source of the categorizations were title, abstract, and keywords, and while most of the papers were reviewed to identify specific details to include on the tables, a thorough analysis was not performed on the bodies of the documents.

Another limitation is the scope of the level of description for each of the resources. For instance, we do not have a way to identify that all courses reported in Table 1 had the same workload, credits, or content, nor do we have specific details as to format, such as whether a course included a lab, recitation, or just a lecture. This lack of an empirical unit makes it difficult to standardize and compare the actual workload across papers. Similarly, this survey is not reporting specific

Table 6. Summary of articles in category "delivery method"

Reference	Delivery method
Brazas and Ouellette, 2013	Online videos, discussion forums
Butler *et al*., 2008	Active learning and enhanced student–faculty interaction
Buttigieg, 2010	Multimedia presentation and visual communication
Campbell, 2003	Student-based discoveries
Cattley, 2004	Web-based bioinformatics application integrating a variety of common bioinformatics tools for teaching BioManager
Cooper, 2001	Open-ended, inquiry-based exercises
Craddock *et al*., 2007	Problem-based approach, course management service
Crawford, 2007	Inquiry-based strategies
Floraino, 2008	Lecture and computer practice topics, free for academic use, with software and Web links required for the laboratory exercises
Gelbart and Yarden, 2006	Web-based learning environment and inquiry-based processes
Hersh, 2007	Distance-learning program
Jungck *et al*., 2010	Academic community of BioQUEST Curriculum Consortium
Lim *et al*., 2003	Online course distance education
Lim *et al*., 2009	Learning Activity Management System e-learning tool
Machluf and Yarden, 2013	Learning environment
Moll *et al*., 2006	Molecular viewer and modeling tool BALLView.
Obom and Cummings, 2009	Online master of science in bioinformatics program
Perry *et al*., 2013	Games
Ranganathan, 2009	e-Learning tools
Searls, 2012	Online videos virtual course catalogue
Shapiro *et al*., 2013	Hybrid delivery including peer-assisted learning approaches incorporated into a bioinformatics tutorial for a genome annotation research project
Tolvanen and Vihinen, 2004	Distance-learning program
Williams *et al*., 2010	Informal sources of bioinformatics education

major skills needed to use bioinformatics tools other than identifying data-mining skills and object-oriented programming skills (see Table 2). For instance, specific definitions and examples of how those skills must be developed to become a skilled bioinformatics student are missing. These descriptions were not included mainly because they were outside the scope of the study, but also because not enough details were provided in the original sources. We welcome educators to help the broader community to define these skills and report specific examples of how those can be integrated into working classrooms. This limitation extends to the case of the evaluation data reported in Table 7. Specifically, we do not report specific or quantitative measures of learning (e.g., means, SDs, p values or effect sizes), making the evaluation of the effectiveness of the educational initiatives difficult to compare. Finally, for the case of Table 4, several papers identified a need for mathematics and statistics content knowledge, yet authors listed only broad terms such as "college-level statistics," and no specific topics or skills were able to be identified for these fields.

IMPLICATIONS FOR BIOINFORMATICS EDUCATION

The results of this study have implications for both the teaching and learning of bioinformatics at the undergraduate and graduate levels and the development of a more scholarly based body of knowledge in bioinformatics educational research.

The implications of this study, as related to teaching and learning bioinformatics, focus on the design, validation, and implementation of curricular materials and learning resources. The first step toward this goal is to appropriately orchestrate bioinformatics-related learning outcomes, including concepts, skills, and procedures; to identify the evidence of the learning; and to use appropriate pedagogical approaches (Wiggins and McTighe, 1997). The process for coordinating these three main steps toward the design of instructional curriculum has been denominated "understanding by design" (Wiggins and McTighe, 1997). This framework is a simple but complete model, accessible to all audiences. This model has also been suggested to be particularly effective for the design of outcome-based curricula (Streveler *et al*., 2012) and for the practice of scientific teaching (Handelsman *et al*., 2004). Its core consists of a set of tools composed of three main steps: 1) identifying the desired learning outcomes, 2) determining the acceptable evidence of learning, and 3) planning the experiences and instructional approach. Understanding by design is then an educational tool that focuses on the processes essential to the act of teaching and learning and is centered on the design of curriculum and learning experiences to accomplish specified purposes (Wiggins and McTighe, 1997). According to Wiggins and McTighe (1997), effective curricular designs can be accomplished by starting with the desired results, then deriving the curriculum from the evidence of learning and subsequently focusing on the educational methods that will move the students to the desired performance. Through this review of the literature, we have identified a need to clearly define the curriculum and the content that should be taught together with appropriate pedagogical approaches (i.e., inquiry-based learning) and evaluation and assessment mechanisms that go beyond perceptions and motivational aspects and move toward assessing learning outcomes and rigorous research in bioinformatics education.

Along the same lines, educators should also be aware that, as important as the identification of concepts, skills and procedures (i.e., the learning outcomes), is the assessment of the attainment of learning outcomes. Wiggins and McTighe (1997), called for us "to operationalize our goals or standards in terms of assessment evidence as we begin to plan a unit or course" (p. 8). In this work, we have identified that little has been reported in this area. However, a good example is provided by Robertson and Phillips (2008), who utilized this framework to design and implement an active learning activity aimed at designing DNA parameters for PCR. In their implementation, they carefully aligned learning objectives with assessment and activities. They also developed a rubric delineating different levels of performance.

Table 7. Summary of articles in category "educational research or evaluation"

Reference	Focus of evaluation	Learning assessment	Result
Bednarski *et al*., 2005	Student learning and attitudes	Group quiz and a pretest and posttest assessment	Students gained understanding of the Web-based databases and tools and enjoyed of the investigatory nature of the lab
Brame *et al*., 2008	Student knowledge and skills and interest in research	Pretest and posttest assessments and student laboratory reports scored with a rubric	Student response to the project was positive, both in terms of knowledge and skills increases and interest in research
Brazeau and Brazeau, 2006	Student perceptions		Significant improvement on student course ratings on the pedagogical format of the course and the relevance of course material to professional practice
Campbell, 2003	Student academic achievement and perceptions	Course examinations	Students gained the ability to utilize online information to achieve the educational goals of the course and perceived this as a positive experience with respect to how they might contribute to biology
Furge *et al*., 2009	Student learning strategies and learning	Student laboratory reports, solutions to problem sets, and in-class presentations	Largely promotion of active learning in the classrooms and enhanced student understanding of course materials
Honts, 2003	Student learning	A take-home final examination	Students developed working knowledge of bioinformatics concepts and methods
Howard *et al*., 2007	Student confidence and performance		Students gained confidence in solving and ability to solve bioinformatics-related problems. Increased student performance on bioinformatics-related problems
Howard *et al*., 2007	Faculty perceptions of students' increased awareness		Faculty members perceived an increased awareness of the applications of bioinformatics among the students in their courses
Krilowicz *et al*., 2007	Instructor and student self-reported required prior knowledge and skills		Identified skills and knowledge from the fields of computer science, biology, and mathematics that are critical for students considering bioinformatics research
Lim *et al*., 2003	Student perceptions		The course was rated as informative, interactive, and effective for distance learning. Participants expressed that the course content was useful and well presented with good technical support
Lim *et al*., 2009	Student perceptions		Identified a positive response regarding the usefulness of an e-learning tool in guiding the learning and discussion process involved in problem-based learning and enhanced the learning experience by breaking down PBL activities into a sequential workflow
Machluf *et al*., 2013	Teachers' design of an assessment tool as a means of probing their knowledge and beliefs in adopting contemporary scientific research into their classroom		The analysis of the assessment tool revealed that teachers perceived research as combining laboratory experiments and bioinformatics approaches. Thus, the assessment tool represented characteristics of authentic modern scientific research and the teachers' appropriation of the new bioinformatics curriculum by extending its roots into the traditional curriculum
Medin and Nolin, 2011	Student self-assessment of their learning gains		Students reflected that the design aspect of the experiments increased their understanding and retention of molecular biology
Obom and Cummings, 2009	Compared student onsite and online learning and satisfaction	Course examinations	Perceived similar levels of satisfaction between most online and on-site student responses, obtained similar performance in grades earned by students in online and on-site courses, and perceived more rigorous course load and more opportunities for participation in online environment
Robertson and Phillips, 2008	Learning goals and assessments of student performance and perceptions	Pretest and posttest assessments, with instructor rubric to report perceived student learning	Students were more poised to troubleshoot problems that arose in real experiments. Students were receptive to the new materials and the majority achieved the learning goals

(*Continued*)

Table 7. Continued

Reference	Focus of evaluation	Learning assessment	Result
Shachak *et al.*, 2005	Faculty curriculum design activities		Identified that Gagne's conditions of learning instructional design theory provides a useful framework for developing bioinformatics training, but may not be optimal as a method for teaching it
Van Mulligen *et al.*, 2008	Faculty curriculum design activities		Participants indicated that the training challenge experience had contributed to their understanding and appreciation of multidisciplinary teamwork
Wefer and Sheppard, 2008	Science standards as related to bioinformatics		Identified a generally low representation of bioinformatics-related content in science standards
Yang *et al.*, 2008	Student stimulation to learn		Increased stimulation on students' activities in bioinformatics learning based on proper application-oriented bioinformatics curriculum and student-centered instructional strategy

As for assessment, findings from Table 7 show that the main purpose of these has been to assess curricular change. Their primary focus has been on identifying student perceptions and attitudes, with the secondary focus being on learning gains. These findings are consistent with the focus of assessment in genomics and bioinformatics reported by Campbell and Nehm (2013). Campbell and Nehm (2013) also performed a critical analysis of the quality of these assessments in which they raised concerns about the validity and reliability of these instruments and thus of the evidence derived from them.

Some of the assessment reported in this literature review is fragmented and superficial. It is fragmented in the sense that is not thorough and in depth. It is superficial in the sense that it is focused on perceptions and motivation and, in very few instances, on learning. This trend is understandable, because biology faculty members specifically, or science, technology, engineering, and mathematics faculty members in general, usually do not have formal training in educational research methods. However, in the same way faculty members seek interdisciplinary collaborations to complement their technical research agendas (e.g., biologists working with computer scientists), they can seek similar interdisciplinary collaborations with educational researchers to support their scholarship of teaching and learning. Furthermore, the National Science Foundation has called for discipline-based education research enterprises combining expertise of scientists providing disciplinary priorities, worldviews, knowledge, and practices, with expertise of educational researchers providing knowledge, theories, and methods that explain learning and cognition (Singer *et al.*, 2012). Having identified the appropriate learning outcomes and evidence of the learning, the last component of the "understanding by design" is to determine the pedagogical method to introduce the concepts and skills. Through this review, it was determined that bioinformatics education has a tremendous potential to be integrated through inquiry-based learning due to the scientific nature of the field. It can also be integrated through face-to-face and online delivery mechanisms such as computing tools and services that are open to the public.

CONCLUSIONS

In this study, we have investigated the state of undergraduate and graduate bioinformatics education as described in the published literature. In particular, this study emphasizes the opportunities for and challenges to the integration of computing and biology earlier in the curriculum. Opportunities include the enormous potential to integrate both scientific thinking and computational thinking (Wing, 2006) through bioinformatics. Bioinformatics offers the practical and technological infrastructure to introduce computing principles and practices in an applied and scientific way. In the same way, learners can have the opportunity to obtain computing knowledge and skills by using or creating meaningful applications in biology. Challenges, on the other hand, include the need to move beyond a basic application of the tools of bioinformatics to a deeper conceptual understanding of the field. It also suggests the need for training the future workforce not only as *consumers* of tools and services but also as future professionals who will be *producers* of tools and resources. This study also revealed the increased importance of preparing professionals in this field at earlier stages. That is, we need to develop the pipeline for workforce in this area starting at or even before the high school level. As a result, existing biology education communities of practice (Wenger, 2000) need to be expanded to support teachers and faculty as they adopt and adapt potential learning modules.

Bioinformatics education is an emerging field that requires attention from educators at all levels as well as from educational researchers. The results from this study also reveal the need for a better identification of learning outcomes and a better integration of assessment and pedagogical methods. Furthermore, the appropriate integration of these three components can be disseminated and validated through a more scholarly based integration and development of learning experiences ranging from K–12 to graduate levels. Such integration also calls for involvement from investigators in the social sciences who can help integrate educational research into bioinformatics education, representing an opportunity for educational researchers to study an emerging interdisciplinary field that integrates scientific thinking with computational thinking.

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