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Research Article

Bioinformatics: An Effective Teaching Resource in Biological Sciences

Samir Terdalkar
Associate Professor,
Department of Zoology, Fergusson College (autonomous), Pune
samir@fergusson.edu

Abstract

The world is strongly moving towards technological innovation and every field is undergoing revolutionary changes. Recent years have witnessed emergence of bioinformatics and data science as a necessity in almost all fields including biological science. If we look at the course structure of basic science, bioinformatics teaching hardly finds place in the programme structure specifically at the undergraduate levels. However, bioinformatics can be one of the courses at undergraduate level and it can be used for regular teaching as well. Bioinformatics envisages processing, storing and retrieving biological data. This has been very well supported by the development of algorithms for analysing biological data. Teaching basic bioinformatics as an interdisciplinary course at undergraduate level and making its use in teaching specific topics like genetics and molecular biology will enhance the competency of young graduates. The present paper provides a review of use of biological data and its applications to gain insights in core concepts of biological sciences. It also proves to be a valuable tool in performing sequence alignments, annotation and establishing relationships between different genomes/ species. All these tools taught will help graduates in their academic progression.

Keywords: bioinformatics, biological databases, genomics, sequence alignment

Introduction

Quantitation and quantitative tools are indispensable tools in modern biology and most of teaching and research now needs some type of mathematical, statistical and computational tool for assessing data and getting meaningful outcome from it. Introducing such kind of subjects which can create a good interface of biology and computers has become a necessity of today's undergraduate and post graduate education. The term 'Bioinformatics" was used to refer to the combination of computing, technology and molecular biology. According to Hagen (2000), bioinformatics has risen due to three important factors viz., exponential increase in the amount of amino acid sequences, and the idea that macromolecules carry biological information; and, researchers' access to high-speed computers developed during World War II. The present biological data sets used are derived from the Human Genome Project, which groups this area into three sub-areas: (1) genomics, which includes DNA sequences; (2) proteomics, which includes the function, shape and interaction of proteins; and (3) biological systems, which includes the analysis of the role of the interaction between proteins and DNA in the function of cells, tissues and organisms. Courses like Biochemistry, Genetics and Molecular Biology are essential part of undergraduate and post graduate syllabi. Bioinformatics can provide a wide angle to all these courses and can become an effective tool specifically for Genetics and Molecular Biology.

There has been a high demand for people with expertise in bioinformatics world over. Keeping in mind this demand/ need of bioinformatics experts or graduates with some knowledge of bioinformatics tools, we need to proactively incorporate bioinformatics in our syllabi and teaching. Similarly, taking into consideration of present scenario of higher education, we need to shift from conventional teaching pedagogies to more computer intensive / computer interface teaching-learning of pure and applied sciences. Some of the examples where bioinformatics can be brought into regular teaching could be use of online databases/ tools, Similarity Analysis, Sequence Alignments and genomes in general. This will give a better understanding of concepts regarding gene and gene expression.

However, there are few requisites, one should learn before making actual use of bioinformatics in their teaching-learning process. These are as follows:

Basic Computer Competencies required

1. Knowledge of the fundamentals of computer operation.
2. NCBI (GenBank), Ensembl, DDBJ to find sequences for proteins and genes.
3. BLAST to search genomes and proteomes for genes and proteins.
4. PDB to visualise 3D protein structures.
5. An awareness of and ability to make use of data bases and information databases.

Let us have an overview of basic framework, on how bioinformatics can be used in teaching with the help of few examples.

Conceptual Framework

1. Use of online literature sources- The first step in bioinformatics education is teaching students how to navigate online scientific databases, more over literature databases and the type of information stored in them. Platforms like PubMed, Google Scholar, OMIM etc., can be introduced to the students, allowing them to visualize the information stored in them, typically categorization of genes and journal articles. This skill improves their ability to access information but also teach them how to evaluate and synthesize scientific data. Tools like Science Citation Index also helps them to know research articles are interconnected with citations thereby promoting

importance of Citations in Science. Online literature can be very useful for teaching variety of topics in genetics.

2. Use of Databases- As students' progress towards higher education, they are encouraged to work with primary data (problem solving), steps involved in approaching databases and retrieving meaningful information. Databases can be of immense help in teaching genomes/ genomics, proteomics and taxonomy. Some other examples are Protein Data Bank, Gene Sequence Databases like Genbank. These databases allow students to work with real data, giving hands on experience in studying databases. This also helps in understanding the diversity of zoological organisms and their molecular characteristics.
3. Problem Solving- Problem solving using online resources in bioinformatics happens to be one of the important steps in using bioinformatics tools. This can be taken as an exercise, practical component in syllabi. Online problem solving resources can be used for this. Some of the problems could be as follows:
   (a) Use web browser to retrieve a protein sequence of lambda repressor from Swiss PROT/ UNIPROT. Enter "Lambda repressor" as key word in the query window and list out the references/ publications related to "lambda repressor"- Try to interpret the output with reference to different organisms/ animals
   (b) In the same data base, search more sequences for human MAP kinase inhibitor, "human catalase", and coli DNA polymerase"," HIV CCR5 receptor "and" cholera dehydrogenase". Record your findings and study the annotations-the output could be - A GO annotation is a way of describing the biological properties of a gene product using terms from the Gene Ontology (GO). The GO is a standardized vocabulary that covers three aspects of biology: molecular function, biological process, and cellular component. A GO annotation consists of a GO term, a gene product identifier, and an evidence code that indicates how the association was made. GO annotations can be used to compare genes from different species, to analyze gene expression data, and to discover new biological insights.
4. Similarity analysis module**-** The inference of structure and function based on biological sequence similarity is a fundamental concept in bioinformatics, and represents a good example of a bridging module. The Dot-plot method is a particularly informative way to do similarity analysis between two sequences. However, although the method is conceptually simple, it can be difficult for non-biology students to understand the biological significance. Conversely biology students may be confused by the mechanisms used to reduce noise in the plot. In this case we bridge an abstract visualization strategy directly to its biological basis to illustrate insertion/deletion/duplication, etc. This bridge provides a strong foundation so that all students can understand gene evolution. This is crucial if students are later to use or even develop sophisticated software to explore whole genome scale events.

5. Sequence Analysis- Phage Φ-X174 was sequenced in 1977, the DNA sequences of thousands of organisms have been decoded and stored in databases. This sequence information is analyzed to determine genes that encode polypeptides (proteins), RNA genes, regulatory sequences, structural motifs, and repetitive sequences. Comparing these sequences can give an insight to similarities between protein functions. A programme like BLAST will prove to be of great help, if learnt by a student.
6. Molecular Modeling- Bioinformatics tools, such as PyMOL and Chimera, can be used to visualize and analyze the 3D structure of biomolecules. This helps students understand the relationship between molecular structure and function.
7. Evolutionary Biology- Bioinformatics has added a new edge for this study. A student can study the origin and descent of species and changes over time.

Teaching and learning Bioinformatics at undergraduate level will benefit students in several ways, like enhancement in their knowledge base and also help in pursuit of their academic progression. Further, following skill sets could be developed in students.

Core Themes Main Topics

Core Themes	**Regular Teaching Topics**
Bioinformatics Resources	The relationships of pure / core sciences with bioinformatics, genomics and proteomics. Computational Tools (use of statistics) Use of PubMed/ NCBI
Biological Databases	Stored Information Understanding the stored information Retrieval of information Types
Similarity Analysis- Structure and Function	Comparison of sequences Searching of information in databases Local and global alignments- relevance with evolution
OMIM	Understanding Mendelian inheritance Correlation with present day research

Recent technologies

1. Programming Proficiency: Languages like Python, R, and Perl remain foundational for data manipulation and analysis.
2. Skills in SQL and NoSQL databases are vital for managing large-scale datasets.
3. Data Analysis and Visualization: Expertise in tools like ggplot2, Tableau, and Shiny enhances the ability to present findings effectively.
4. Statistical analysis using R or SAS is critical for extracting meaningful patterns from data.

5. Machine Learning and Artificial Intelligence: Proficiency in machine learning frameworks like TensorFlow and scikit-learn will be essential for predictive modeling.AI-driven bioinformatics is revolutionizing drug discovery and functional annotation.
6. Knowledge of Biological Databases: Mastery of databases such as NCBI, UniProt, and KEGG enables researchers to access and interpret relevant biological information.

Bioinformatics provides an edge in understanding the concepts in molecular biology and genetics and it will certainly help to improve learning abilities of students in following ways:

1. Problem Solving Ability: Solving problems in Bioinformatics would require students to think critically about biological databases/ biological data and find probable solutions to it. This improves their understanding of core subjects like Molecular Biology and Genetics.
2. Development of Computational Skills: It gives an idea to students regarding different tolls used in Bioinformatics typically in combination of using statistical tools and now using ‘R” software and Python programming. This widens their career options and provides them with a basic idea of data analysis.
3. Gateway for Advanced Research: Learning Bioinformatics will provide a gateway to students for embarking on advanced research areas like drug discovery, genomics and health care.

Conclusion

The trend of learning outcomes of bioinformatics learning at undergraduate level is to increase cognitive or knowledge in core subjects like Molecular Biology and Genetics. Once these are used in regular teaching assessment of Learning Outcomes would get enhanced and provide students with practical platform for understanding and learning the concepts. By incorporating bioinformatics into zoology teaching, educators can provide students with hands-on experience in analyzing and interpreting complex biological data. This can help students develop a deeper understanding of zoological concepts and their applications in real-world scenarios.

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