

Integrative Bioinformatics: A Branch of Bioinformatics that Focuses on Problems of Data Integration

Myron R Szewczuk*

Department of Biomedical and Molecular Sciences, Queen's University, Quebec, Canada

ABSTRACT

Integrative bioinformatics is a branch of bioinformatics concerned with data integration issues in the biological sciences. The amount of data collected has increased exponentially as a result of the emergence of high-throughput (HTP) technology in the life sciences, particularly in molecular biology. Furthermore, the data is dispersed throughout a variety of public and private repositories, and it is kept in a variety of forms. This circumstance makes it tough to search for these data and execute the necessary analysis to extract new knowledge from the entire set of available data. By giving unified access to life science data, integrative bioinformatics seeks to address this issue.

Keywords: Integrative bioinformatics; Molecular biology; Transcriptomics; Interactomics

DESCRIPTION

Approaches

Semantic web approaches: Data from multiple websites or databases is searched using metadata in the Semantic Web approach. Metadata is machine-readable code that defines the contents of a page for a programme, allowing for more precise comparisons between data and search queries. As a result, the number of irrelevant or useless results is reduced. Some meta-data exists in the form of ontologies, which can be tagged by users or programmes and help to simplify searches by allowing users to find and return data using key terms or phrases. The quality of the data in searches is often improved with this method, and with correct tagging, ontologies can uncover entries that may not clearly declare the search phrase but are nonetheless relevant. One disadvantage of this strategy is that the returned results are in the format of the database from which they came, making direct comparisons difficult. Another issue is that the terms used in tagging and searching can be unclear at times, which can lead to misunderstanding in the results. Furthermore, the semantic web approach is still considered an emerging technology and is not now in widespread use, current uses of ontology-based search in the biomedical sciences. Ontologies are also used in databases like SwissProt, Ensembl, and TrEMBL, which use this technology to search through

collections of human proteome-related data for tags that match the search phrase [1-4].

Data warehousing approaches: Data from several sources is extracted and consolidated in a single database as part of the data warehousing strategy. Various 'omics' datasets could be used to provide biological insights into biological systems. Data from genomes, transcriptomics, proteomics, interactomics, and metabolomics are examples. Changes in these sources should ideally be synchronized with the integrated database on a regular basis. The information is delivered to the users in a standardized format. Many programmers targeted at assisting in the building of such warehouses are meant to be highly adaptable so that they can be used in a variety of research initiatives. One advantage of this technique is that data may be analyzed in a single location with a consistent structure. One downside is that the databases are frequently large and difficult to maintain.

CONCLUSION

Integrative Bioinformatics Analysis is a computational approach that increases understanding of drug mechanisms related to cancer treatment in a timely manner and can be used to explain drug-disease interaction concepts. Due to the impact of groups like the Proteomics Standards Initiative, standardized formats for various types of data are increasingly emerging. Data submission in one of these new forms is even required in some data

Correspondence to: Myron R Szewczuk, Department of Biomedical and Molecular Sciences, Queen's University, Quebec, Canada, E-mail: szewczuk@23queensu.ca

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warehousing initiatives. Data mining is the process of looking for patterns in existing data using statistical methods. Currently, some scientists are focusing on combining existing data mining techniques with novel pattern analysis approaches that yield a few findings with a high possibility of relevance rather than spending time looking over each pattern detected by the first program. This method has the significant advantage of allowing for the production of fresh hypotheses to test.

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