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Editorial

EDITORIAL NOTE ON BIOINFORMATICS

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EDITORIAL

Bioinformatics, as a new emerging discipline, combines mathematics, information science, and biology and helps answer biological questions. The word 'bioinformatics' was first used in 1968 and its definition was first given in 1978. Bioinformatics has also been referred to as 'computational biology'. However, strictly speaking, computational biology deals mainly with modeling of biological systems. The main components of bioinformatics are given below:

1. The development of software tools and algorithms
2. The analysis and interpretation of biological data by using a variety of software tools and particular algorithms.

Approaches in the search for natural products are a combination of molecular and chemical techniques. Important criteria of molecular approaches include phylogenetic resolution and potential to a large-scale screening. Application of comparative genome sequence analysis is essential for a better understanding of the genetic and epigenetic components of different bacterial taxa. With the increased numbers of fully sequenced microbial genomes, including those of well-known bacterial producers of natural products, it has become clear that the genomic and metabolic capacity of these microorganisms is much higher than initially anticipated. This is due to the discovery of 'silent' or 'cryptic' secondary metabolite gene clusters that encode the production of additional, unidentified compounds.

Recent examination of massive sequencing (metagenomics) approaches to analyze the composition of bacterial communities of complex milieu including sea water, provide an

abundant source of molecular sequence data for analysis. These data are useful in comparative genome analyses to identify genes directly involved, for example, in nonribosomal peptide synthesis (peptide synthetase), modifying enzymes, or other genes coding the production of certain natural products. Often, the complete set of specific genes involved in the synthesis of a particular natural product is contained in a single operon. For example, as the presence of conserved sequence motifs and a modular organization of nonribosomal peptide synthetases often assembled into single bacterial operons, a specific sequence search algorithm can be developed to screen public database resources. This enables a detailed analysis of evolutionary, structural, and functional aspect of natural products production based on the comparison of molecular sequences, molecular modeling, and simulation. For example, the situation of genomic colinearity of modular synthetase components might also facilitate the identification of the molecular components of natural products production as well as the reconstruction of natural products synthesis pathways. This will permit to clarify the details of natural production systems and may allow the simulation of these pathways to explore possible strategies for the optimization or engineering of natural product production systems.

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