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Editorial:

OMICS AND BIOINFORMATICS TECHNOLOGIES FOR BIOMEDICAL RESEARCH

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Version española

Advances in bioinformatics, together with development of the high-throughput biological methods, have led to the advance of the 'omics'. Under the name of 'omics' disciplines¹⁻² are included a wide range of fields, which now range from genomics (study of the genome), proteomics (the study of the structure, function, location and interaction of proteins), transcriptomics (the mRNA and gene expression), metabolomics (metabolites and metabolic networks), the pharmacogenomics (the quantitative study of how genetics affects drug treatment), the physiomics (physiological studies) and nutrigenomics (effects of foods and food constituents on gene expression), etc

The development of these disciplines involves the use of omics technologies, which require the use of high throughput methods (microarrays, NMR, HTS, HPLC-MS ...) allowing it handle complex biological samples in large quantities with high sensitivity and specificity. As a result, it generates large amounts of data needed to understand the interrelationships between different molecular components.

The study and analysis of this vast amount of data is possible by bioinformatics³. Bioinformatics is a discipline that uses information technology to organize, analyze and distribute information on biomolecules in order to answer complex questions. Free access to the Internet allows all information is accessible to everyone. This arise as a need for make sense of the amount of biological data generated in recent decades, and to the increase of techniques capable of detecting a large number of alterations in different molecular components (gen, proteins, metabolites, etc)⁴.

In biomedicine, the 'omics' technologies facilitate the development of new biomarkers for early diagnosis and prognosis of various diseases, which is essential for the implementation of treatments⁵. In this sense the "omics" technologies allow the identification of signaling molecules associated with growth and cell death, which facilitates the monitoring of functional changes, molecular, cellular damage and the study of drug response. Thus, proteomics has shown its potential in the search for gene expression biomarkers for use both for diagnosis and prognosis of many diseases (cancer, cardiovascular...). Metabolomics allow the identification of biomarkers for diseases diagnosis, drug research, nutritional studies related to metabolism and metabolic disorders. Pharmacogenomics, allows knowing which are the genetic factors that affect for absorption, metabolism and drug action mechanisms. These techniques allow a better understanding and identification of molecular alterations and the development of biomarkers for diagnosis, prognosis and prediction of response to treatment⁶⁻⁸.

In summary, the impressive progress that the 'omics' technologies are experiencing in recent years favors the development of new therapeutic and diagnostic methods in the world of biomedicine.

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