EMERGING RESEARCH FRONTS - 2010

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Joaquín Dopazo talks with *ScienceWatch.com* and answers a few questions about this month's Emerging Research Front Paper in the field of Computer Science.

Article: FatiGO: a web tool for finding significant associations of Gene Ontology terms with groups of genes
Authors: Al-Shahrour, F;Diaz-Uriarte, R;**Dopazo, J**
Journal: BIOINFORMATICS, 20 (4): 578-580 MAR 1 2004
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SW: Why do you think your paper is highly cited?

The paper describes a web-based bioinformatic software that helps one to understand the functional implications of the genes selected in a genomic experiment. Since its publication, there has been a continuous growth in the demand for these type of tools. In the particular case of FatiGO, this functionality was offered in a very straightforward manner within a rigorous statistical framework.

Actually, the universe of web-based bioinformatics tools exhibits a peculiar Darwinian dynamic. To be user-friendly and quick in its calculations, as well as staying up and running permanently, constitutes a real competitive advantage for any tool. These facts, along with its timely publication in a moment in which there was a growing interest for the functional profiling of genomic data in the field are, most probably, the primary reasons for its popularity.

SW: Does it describe a new discovery, methodology, or synthesis of knowledge?

This paper describes a testing methodology, nowadays known under the generic name of "enrichment analysis" that provides information on the functional roles carried out by a group of pre-selected genes (or proteins). Perhaps, the most innovative aspect included in the publication was the introduction of the concept of

multiple testing in the framework of statistical contrast, which allowed us to eliminate a considerable number of false positives in the analysis.

"...the development of diagnostic or prognostic tools based in DNA microarrays is among the aspects with more social projection derived from our research. "

SW: Would you summarize the significance of your paper in layman's terms?

The method presented in the paper allows the conversion of the lists of uninformative codes of gene identifiers obtained in genomic experiments into their corresponding shared functional roles. In this way, a researcher can quickly have a pretty clear idea of the functionalities of the cell affected by an experiment and easily relate them to the experimental condition studied (i.e., disease, drug administration, etc.).

SW: How did you become involved in this research and were any particular problems encountered along the way?

My main interest has revolved around systems biology problems. The definition of the sets of functionally-related genes altered by an experiment constitutes the first step in the knowledge of the relationships among the genes that ultimately outline the cell functionality.

There is a cultural problem, still extended among many researchers, that prevents them from understanding that genes do not operate alone, but in a complex network of interactions.

The reductionist view of genes in isolation, related to functions, has been demonstrated to be an oversimplification of the reality which cannot any longer be maintained. This view, unfortunately, constitutes a particular burden for the advancement of several fields in which systems biology should play an eminent role.

SW: Where do you see your research leading in the future?

In line with the systems' perspective, my interests are pursuant to understanding the relationships among genes that define the functional modules (e.g., pathways) in the cell, as well as the high-level relationships among such modules. A correct understanding of the assembly and relationships among the pieces of the system will pave the way toward achieving an operation over its functionality and reverting perturbations, such as diseased states, etc.

SW: Do you foresee any social or political implications for your research?

Although my work is quite far away from a translational use in biomedicine, some aspects are of immediate application. For example, the development of diagnostic or prognostic tools based on DNA microarrays derived from our research is among the aspects offering more social projection.

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Web

KEYWORDS: FatiGO; FALSE DISCOVERY RATE; EXPRESSION DATA-ANALYSIS.

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