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Editorial

High-Throughput Data Analysis for Chronic Diseases Investigation

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Abstract

Large-scale genome analysis, proteomics, clinical biostatistics and bioinformatics, pathophysiology and clinical and molecular epidemiology are today complementary disciplines applied daily for the discovery of new pharmaceutical targets or the understanding of molecular interactions laying behind the development of rare and chronic diseases. During the past years we have worked on different projects involving advanced technologies which purpose was to improve the understanding and treatment of chronic diseases mainly cancer, alzheimer and cardiovascular diseases that I am describing in this Editorial.

Large-Scale Genome Analysis

In a first work, we could find specific gene networks (oxidative stress genes, renin-angiotensin system) responsible of the pathophysiological alteration in "hypertrophy/hypertension" by analyzing microarrays gene expression data [1]. Currently, we are finishing a statistical analysis where we have used the CGH arrays data to identify breakpoints and chromosome aberrations implicated in the breast cancer in the light of the evolutionary mutational sites of the genome [2].

Proteomics

Another work in evolutionary proteomics [3], showed that the same protein could have different functions according to its structure in different organisms. The aim objective of this work was to adapt and apply a new clustering/alignment method on topoisomerase type IA protein sequences of representative organisms from the three domains of life in order to find conserved and non-conserved motifs. Such tools are very useful today for the finding of new chimers/drugs, the understanding of molecular structure-function relation and the study of molecular evolution.

Pathophysiology and Epidemiology

In an epidemiological work, the impact of the metabolic syndrome (MS) on arterial stiffness was different between young and elderly untreated hypertensive independently of age and blood pressure, two cardiovascular risk factors [4]. This revealed the time evolution of arterial stiffness in MS patients which could not be detected in younger MS patients and may be due to a late under/over-expression of some genes. This assumption is actually the main work of basic cardiovascular research labs [5].

Clinical Research and Antihypertensives

Medicine and biology are converging progressively towards a personal prognosis, diagnosis, and treatment according to patient's pathophysiology and risk factors. Thus, the quality of clinical markers like blood pressure (BP) signals should be tested in order to establish a good diagnosis especially in populations where it's difficult to measure the BP signals like in obese patients [6]. Other markers such arterial stiffness should be investigated in cardiovascular complications before prescribing a drug [7]. In case of negative diagnosis, the anti-hypertensive treatment should be efficient depending on the pathophysiology of the population especially in diabetic hypertensive patients. A meta-analysis [8] has shown that candesartan cilexetil controls hypertension independently of glycemia level in French diabetic hypertensive patients compared to their control, which was not the case of other drugs. Therefore, predictive methods based on clinical meta-analysis and statistical inference could deeply help physicians to prevent the disease before its occurrence or to offer an adequate treatment when the diagnosis is established. Finally, the pharmaceutical industry was a strong link between fundamental and clinical research, currently all the laboratories are fully equipped with advanced high throughtput analysis platforms able to analyse thousands of biological samples in order to find specific molecular targets and their corresponding drugs.

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