Endocrinología, Diabetes y Nutrición

2 - MAKING SENSE OF METABOLOMIC DATA: COMPREHENSIVE ANALYSIS OF ALTERED METABOLIC PATHWAYS IN DIABETES AND OBESITY

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Resumen

Bioinformatic analysis and visualization techniques for `omics' data are key tools for understanding complex biological systems. They reduce the complexity of data and allow generating hypotheses and searching for disease biomarkers. The aim of this work is to analyse the suitability of bioinformatic tools to interpret metabolomics datasets of a range of diseases including type 1 and 2 diabetes and obesity. We examined several disease datasets from metabolomics studies through different bioinformatic approaches: metabolic pathways, networks and disease-/functional-based analyses. Then we have analysed the accuracy of these tools to identify several traits of the datasets and their suitability to perform enrichment analyses. The analysis of metabolic pathways, small-scale systems of biochemical reactions and events of regulation and signalling, proved to be the most appropriate approach to analyse metabolomics datasets. Tools based on KEGG metabolic pathways were the most suitable ones as they allowed us examining metabolic alterations in type 1 and 2 diabetes and obesity and formulating hypotheses about the physiopathology of these diseases. For instance, alterations in the metabolism of amino acids, nitrogen, glutathione, sphingolipids and primary bile acids were revealed in diseased conditions. The study of altered metabolic pathways allowed us interpreting data from metabolomics studies and extracting very valuable information from them that might help identifying disease biomarkers and possible metabolic alterations related to diseases. This information could be translated to the clinical practice to predict metabolic alterations before the onset of diseases.