SORS: Understanding disease with omic data

Objectives

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Abstract: Omic data is big data in biology. Acquired at different biological domains, omic data is highly structured and rich, as biological processes leave their imprint across different biological levels. I will argue that decoding omic data in relation to a given process offers understanding which can be translated into specific hypotheses relating human health. I will thus present six examples of how to decode genomic, transciptomic and methylomic data to gain insights into the biology of inversion polymorphisms, epistasis, recombination, co-splicing networks and the mosaic loss of chromosome Y. I will discuss how the insights gained into these processes allow us to make specific recommendations on cancer and Alzheimer's disease treatments, explain the comorbidity of asthma and obesity and offer a biological clue into why women live longer than men. I will also present further questions that can be answered using other types of omic data.

Short bio: Alejandro Cáceres is a senior statistician at Institute for Global Health in Barcelona (ISGlobal) where he conducts research in genetic epidemiology. He was a postdoc at the Maudsley hospital in King's College London and holds a PhD in theoretical physics from the University of Cambridge. He works in the development of methods to analyze omic data that can lead to the understanding of the underlying mechanisms of disease. He has published methods, available in public repositories, that include detection of inversion polymoprhisism, epistasis, co-splicing networks and transcriptomic signatures of disease.

Barcelona Supercomputing Center - Centro Nacional de Supercomputación

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