

Multi-scale data integration of biological complexity: Towards rational drug design and systems-based medicine

Sergio E. Baranzini

University of California, USA

The public availability of high throughput datasets from a variety of biological sources has prompted the creation of a multitude of databases that significantly facilitate biomedical research. However, although each individual experiment may successfully address a focused set of hypotheses, a more comprehensive understanding of biological processes may emerge by integrating results from multiple datasets into a coherent framework. Furthermore, knowledge about higher-order, more clinically relevant aspects of any complex disease may be only achieved by these kind of analyses. Unfortunately, such integrative approaches to complex diseases have not been yet realized in part due to the lack of a theoretical framework and appropriate analytical tools to implement them.

We recently developed iCTNet, a Cytoscape plugin to create and analyze human complex traits networks that assembles and integrates information from genome-wide association studies, protein-protein and protein-DNA interactions, tissue expression, and drug target. iCTNet integrates close to 15,000 nodes (of 4 types) and more than 95,000 interactions (of 5 types). I will present examples of how this kind of integrative approaches enable identification of system-level properties at different level of biological complexity. This new knowledge can lead to a new way of thinking about therapeutic drug design, and human disease management.

Biography

Dr Baranzini received his PhD in human molecular genetics from the University of Buenos Aires in 1997. Shortly after, he pursued postdoctoral training at UCSF Department of Neurology where he specialized in neurogenetics and his research focused on multiple sclerosis. His training included genetics, immunology, neuroscience, and molecular biology, with an emphasis in gene expression analysis and bioinformatics. Dr Baranzini also trained in mathematical modeling and complexity, which provided him a solid foundation to approach the research of complex diseases from a systems biology perspective. He joined the Faculty at UCSF in 2003 and is currently Associate Professor of Neurology.