RA-map: building a state-of-the-art interactive knowledge base for rheumatoid arthritis

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Abstract

Rheumatoid arthritis (RA) is a progressive, inflammatory autoimmune disease of unknown aetiology. The complex mechanism of aetiopathogenesis, progress and chronicity of the disease involves genetic, epigenetic and environmental factors. To understand the molecular mechanisms underlying disease phenotypes, one has to place implicated factors in their functional context. However, integration and organization of such data in a systematic manner remains a challenging task. Molecular maps are widely used in biology to provide a useful and intuitive way of depicting a variety of biological processes and disease mechanisms. Recent large-scale collaborative efforts such as the Disease Maps Project demonstrate the utility of such maps as versatile tools to organize and formalize disease-specific knowledge in a comprehensive way, both human and machine-readable.

We present a systematic effort to construct a fully annotated, expert validated, state-of-the-art knowledge base for RA in the form of a molecular map using the software CellDesigner. The RA map illustrates critical molecular and signaling pathways implicated in the disease. Signal transduction is depicted from receptors to the nucleus using the Systems Biology Graphical Notation (SBGN) standard representation. The knowledgebase interfaces with various other databases for content annotation and enrichment and can also serve as a template for omic data visualization. Furthermore, topological analysis of the underlying biological network can help reveal structural hubs while functional enrichment analysis can highlight possible disease comorbidities.

The RA map is available online at ramap.elixir-luxembourg.org

References and useful liks

Funahashi, Akira, et al. "CellDesigner: a modeling tool for biochemical networks." *Proceedings of the 2006 Winter Simulation Conference*. IEEE, 2006.
Gawron, Piotr, et al. "MINERVA—a platform for visualization and curation of molecular interaction networks." *NPJ systems biology and applications* 2.1 (2016): 1-6.