Adapted Boolean network models for extracellular matrix formation.

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Abstract

Due to the rapid data accumulation on pathogenesis and progression of chronic inflammation, there is an increasing demand for approaches to analyse the underlying regulatory networks. For example, rheumatoid arthritis (RA) is a chronic inflammatory disease, characterised by joint destruction and perpetuated by activated synovial fibroblasts (SFB). These abnormally express and/or secrete pro-inflammatory cytokines, collagens causing joint fibrosis, or tissue-degrading enzymes resulting in destruction of the extra-cellular matrix (ECM).We applied three methods to analyse ECM regulation: data discretisation to filter out noise and to reduce complexity, Boolean network construction to implement logic relationships, and formal concept analysis (FCA) for the formation of minimal, but complete rule sets from the data.

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