Different stimuli for inference of gene regulatory network in rheumatoid arthritis

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Abstract

Since genetic and epigenetic factors are known to be involved in the pathogenesis of rheumatoid arthritis the
search for key players in this disease is one of the most important challenges. For this purpose gene regulatory
networks are one possibility to reveal underlying interactions for different stimuli. In this study we analyzed
the cellular response of synovial fibroblasts to 4 different stimuli. We infered a gene regulatory network that
is able to explain the observed data for stimulation by TNF-a, TGF-b1, IL-1 and PDGF-D simultaneously.

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