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Fuzzy modelling of biological systems and its application to the analysis of MAPK signalling pathway

ABSTRACT

Signalling pathways are one of the fundamental topics of research in systems biology as they are involved in extracellular communication and regulate various cellular processes. Their analysis is difficult due to two factors: the first presents significant differences in temporal responses of different proteins, and the second presents the fact that they are interleaved through both common stimuli and cases when different stimuli trigger the transmission of the same information. Therefore, computational models play an important role in exploring the connections between different components of the signalling pathways.

A wide spectrum of methods with various applications is available for analysing and understanding of signalling pathways. Some methods require a complex understanding of the problem's biochemical background and result in highly accurate models, while with others, our knowledge may be more limited, which then results in less accurate predictions of the model.

Methods that represent a compromise between the two approaches are recently becoming prevalent. These include fuzzy logic methods, on which we focus in this work. For each such method we describe its advantages and disadvantages and then apply it to the MAP kinase signalling pathway.

Key words: fuzzy logic, computational biology, modelling and simulation, signalling networks, MAP kinase