

# A New Simulation Framework for the Modeling of Signal Transduction Pathways: P Systems

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*The secret of life, the well spring of reproduction, is not to be found in the beauty of Watson-Crick pairing (DNA), but in the achievement of collective catalytic closure. The roots are deeper than the double helix and are based in chemistry itself.*

*(S. Kauffman, 1995)*

Understanding the Biosignaling pathways is very essential for designing effective therapeutic approaches. With many Pathways unraveled, each one with its own unique complexity, there is a need to model the Biosignaling pathways for understanding them.

A typical group of Biosignaling pathways is known as Apoptosis (also known as programmed cell death). These pathways have immense significance in designing cancer therapies. Apoptosis is a mechanism which helps the unwanted, injured, or improperly developed cells to commit suicide playing a key role in nature. Aberrations in apoptotic responses to death signals contribute to cancer development, resistance to treatment, and autoimmune diseases. One major mechanism for inducing the apoptosis is through the activation of death receptors. Among the death receptors the signaling pathways for FAS induced apoptosis are best characterized. Modeling the FAS induced Apoptosis pathway will help in understanding the complex signaling behavior of this pathway.

Modeling FAS induced Apoptosis (any Biosignaling pathway) can be done in many ways and the most traditional approach is using differential equations. We use a computing device called P system using membrane computing framework to model the FAS induced Apoptosis. Membrane computing, a non-deterministic model of computation starts from the assumption that the processes taking place in the compartmental structure of a living cell can be interpreted as computations. P system focuses on the compartmental structure also along with other parameters for modeling. P systems consider the quantity of components in the cascade to be discrete i.e. the individual chemical reactions are asynchronous and occur discretely at random interval length of time. In P systems expansion of existing model is done by adding rules and new membranes whenever possible. The membrane structure of P systems representing the heterogeneity of the structural organization of the cell and its easy extendibility makes them an alternative to classical approaches like ODEs.