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Modelling a signalling module

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The NF-κB transcription factor plays a critical role in regulating cell growth, cell survival and the response to stress. The activity of NF-κB is controlled by three inhibitory IκB isoforms (IκBα, -β, and -ε) that regulate NF-κB cellular localization. In the November 8 Science, Hoffmann *et al.* describe a computational modelling approach to understanding NF-κB regulation (*Science* 2002, **298:**1241-1245). They constructed a computational model that incorporates multiple control parameters including the rate of synthesis of each IκB isoform, the formation and stability of binary and tertiary protein complexes, cellular localization and transport rates. The model predicts an oscillatory NF-κB activation profile created by negative feedback regulation loops. Analysis of mouse fibroblasts lacking combinations of IκB genes revealed that the different isoforms function to modulate fast and slow responses to inflammatory stimuli and are responsible for distinct gene expression programs.

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