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In this paper I will try to describe my understanding of my work with Dr. Lun thus far in a top-down manner…

A gene regulatory network can be described as a system of equations in which any gene , where is a set of all genes in the network, arbitrarily depends on in which for non-self-regulating genes. As such, the expression level of directly affects the expression level of . These expression levels can be described as a set of functions, so for clarity is a function .

A steady state of any such network that is strictly a linear system of equations can be expressed as a dot product between an dependency matrix in which , and , so that , where is a nonzero vector and . For clarity, a nonzero value in indicates that depends on . The following linear algebra can be performed to find .

Moreover, if the dependency matrix is unknown for the linear system of equations for , one can be calculated by performing perturbations onto . To do this, we use an matrix where is the initial steady state and is the steady state after perturbing .

For nonlinear networks however, linear algebra is not sufficient enough to find the steady-state of and new methods must be used. The following set of nonlinear functions will be used to described the steady state for .

Where is a set of indices of all nonzero values of row of the dependency matrix , is the power set of , is the relative activation of , and , where K is an uniformly generated [0,1] matrix, and N is an constant matrix. Their values correspond to the dissociation constants and Hill coefficients, respectively (as per the research paper). For this nonlinear system, a steady state can be found by using the property: where where has the function layout of (as shown initially) and is an initial state of an arbitrary vector. This way, will converge toward with each successive iteration.