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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 matrix multiplication between an dependency matrix in which , and gene vector such 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 constant [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 the steady state with each successive iteration. Since the network is nonlinear, performing the matrix recovery as with the linear case by performing perturbations onto to find the nonzeros of may not be completely precise.

For the next part, a Gaussian random function can be used for both the linear and nonlinear networks to emulate a level of molecular noise. For the nonlinear case,

Where is a factor of the noise. This will cause fluctuations in which, in turn, will cause yield an altered matrix . For the nonlinear case, the noise can be performed on the converged vector so that . More precision will be lost during the recovery process when using for the perturbations to generate due to the noise as well as it being a nonlinear system.