A. Lane

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 gene where for non-self-regulating genes. As such, the expression level of gene (denoted as ) directly affects the expression level of gene . These expression levels can be described as a set of functions, so for clarity is a function of all

A steady state of such a network that is strictly a linear system of equations can be expressed as a matrix multiplication between an matrix , and gene expression vector such that , where , is a nonzero vector, and is the expression level for gene . For clarity, a nonzero value in indicates that the expression level for gene depends on gene . The following linear algebra can be induced to find the steady state .

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 gene .

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 of a nonlinear network.

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 starting with an initial arbitrary vector and converging toward by using the property: where where has the function layout of (as shown above) with the exception that . converges toward the steady state with each iteration. Finding the matrix that describes the dependencies of all genes can be estimated by performing perturbations as with the linear case. For the next part, a Gaussian random function can be used to emulate a level of molecular noise. For the nonlinear case,

Where is a factor of noise that conforms to Gaussian random variables and is the steady state after perturbing gene . This will cause fluctuations in to yield which, in turn, will yield an altered matrix . As such, more precision will be lost due to the noise in the process of recovering in addition to the loss of precision due to the function’s nonlinear nature.