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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 is unknown, 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 . M can then be recovered using the following linear algebra. For the following equation, we’ll use the notation for matrices: , and .

For linear systems of equations, can be recovered by using equation:

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 .

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.

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.