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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 a network, arbitrarily depends on gene such that for non-self-regulating genes. As such, a matrix can be used to describe the set of dependencies of all of the genes. The dependency matrix will be defined as such:

We will denote as the gene expression level of gene , where is a function of all . Furthermore, a steady state of a network can be described as a set of functions. The structure of these functions correspond to the nonzero elements of matrix . The steady state of said network, when expressed strictly as a system of linear equations, can be described via matrix multiplication. We’ll denote an matrix , and gene expression vector such that , where is a nonzero vector. For clarity, a nonzero value in indicates that the expression level for gene depends on gene by a factor of . The following proof can be induced to find the steady state .

However, for most purposes (and thus ) is unknown. Perturbations must be performed onto and the new steady states observed to estimate and . To do this, we use an matrix where is the initial steady state and is the steady state after perturbing gene . Both and can then be recovered. The following notation will be used for the upcoming proof:

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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 denotes a set of indices of all nonzero values of row of matrix , denotes the power set of , denotes the relative activation of and is within the domain , and , where K and N are matrices who’s nonzero elements correspond to the nonzero elements of matrix . The values of and are the dissociation constants and Hill coefficients, respectively. Here, a steady state can be found by converging an initial arbitrary vector 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.