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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 interdependencies between the sets of genes. This such matrix will be denoted as , with dimensions and is 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 regulatory network corresponding to can be described as a set of functions. The steady state of said network, when expressed strictly as a system of linear equations, can be described as matrix multiplication. We’ll denote matrix with same dimensions as , with (where ), 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 and implies . The following proof can be induced to find the steady state .

However, for many purposes the regulatory network is unknown and thus must be found. One such way of finding is through a series of perturbations unto. Doing so will yield new steady states which can be observed to estimate . For the case of linear systems of equations, can also be found (or, if noise is present, estimated). 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:

can be recovered by using the 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 variable can be applied to emulate a level of molecular noise.

Where represents a factor of noise and is a Gassian random variable of a normal distribution with expected value of 0 and a standard deviation of 1, and represents 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.