

# Sparse Grids and the Master Equation for Gene Regulatory Networks

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**Abstract:** An important driver of the dynamics of gene regulatory networks is noise which is generated by the random interactions of genes with their products and regulators. As relatively small numbers of molecules of each substrate are involved such systems are best described by stochastic models, i.e., the stochastic master equations which provide probability distributions over the state space. Here the state is a discrete vector of the form  $(n_1, \dots, n_k)$  where the  $n_i$  include the amounts of the different proteins, RNA, dimers and polymers and the state of the DNA etc. As in some cases hundreds of components can be involved in a gene regulatory network the approximation of the probability distribution has to address the curse of dimensionality. The traditional approach uses stochastic simulation techniques which effectively address the curse. However, many (thousands of) repeated simulations are required to provide precise information about stationary points, bifurcation phenomena and other properties of the stochastic processes due to the  $O(N^{-1/2})$  sampling error where  $N$  is the number of simulations. An alternative way to address the curse of dimensionality is provided by sparse grid approximations and the direct solution of the master equations. The sparse grid methodology is applied and the application demonstrated to work efficiently for up to 10 proteins and we are currently developing techniques which can deal with 100s of proteins. The sparse grid methodology is generalised to the case of integer variables  $n_i$  and a multiresolution technique for this case is presented. Error bounds are provided which confirm the effectiveness of sparse grid approximations for “smooth” high-dimensional probability distributions.

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