

Parameter estimation in genetic networks using a constrained stochastic space search method

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1 Abstract

Numerous stochastic search methods have been applied in parameter estimation problems in genetic network identification. In this work, a constrained stochastic space search (CSSS) method for parameter estimation is proposed and used to optimize the goal function for the difference between measured and estimated gene expression time series data. Both linear and nonlinear model formalism were used. The performance of the proposed optimization method was compared to another robust stochastic algorithm (ICRS/DS), which is a modification of the ICRS algorithm [1].

Even though, the ICRS/DS method was shown to be robust, the problem with using it is that this method requires making heuristic guesses of various tuning parameters for initialization. The ICRS/DS also takes a long time to achieve convergence to optimum solutions. To address these problems an alternative method (the CSSS) is introduced, a method uses a technique of variance scaling on the parameters. This avoids the necessity to make heuristic guesses and speeds up the optimization process. The CSSS algorithm is fast and efficient when applied to less noisy time series data sets from small-sized genetic networks.

2 Introduction

Parameter estimation is an important and integral aspect of genetic network identification. Understanding such complexities is useful in gaining useful information from biological systems. This highlights the need to develop efficient algorithms for parameter estimation from time series data. Systems theory, statistical and mathematical models offer tools used in modeling genetical networks. These tools aid investigations into network dynamics and help unravel the complexities commonly found in biological networks. Proper model choice and parametrization are crucial for successful identification. This is reflected in the model fit to data using the CSSS method. Using the CSSS optimization technique requires a balance to be made between the algorithms' speed of convergence, accuracy and precision of parameter estimates.

3 Results

A comparison of the CSSS algorithm to the ICRS/DS stochastic optimization algorithm by Carrasco and Banga [2] was made and the results show the CSSS method outperforms the ICRS/DS method. The CSSS method strikes a balance between parameter accuracy and speed of algorithm convergence. Independent experimental replicates were run and identification performed. The results show that for the same initialization conditions, the CSSS converged faster than the ICRS/DS and had on average smaller relative mean errors. Relative error analysis was performed with noise-free data and the results indicated that the standard deviations on the parameters are again lower for identification with the CSSS as compared to the ICRS/DS method.

4 Conclusion

In modeling biological networks, obtaining good identification requires careful constraint specification on the parameters - irrespective of the optimization method used. This ensures that only biologically meaningful parameters are obtained. Since the CSSS does not require making heuristic guesses on numerous initialization parameters, it is suitable for application in network identification problems - particularly for parameter estimation problems in small-sized biological networks. The CSSS optimization method for both the linear and nonlinear model representation outperformed the ICRS/DS in numerous aspects.

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References

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