

Model order reduction of deterministic and stochastic gene regulatory networks.

Altwasser R, Guthke R, Vlaic S, Emmett MR, Conrad CA, Meyer-Baese A (2013) Model order reduction of deterministic and stochastic gene regulatory networks. In: Hamid R. Arabnia, Quoc-Nam Tran (eds.) Proceedings of the International Conference on Bioinformatics and Computational Biology BIOCAMP'13 13th Int. Conf. Bioinformatics and Computational Biology, Las Vegas/USA, 09/16/2012-09/19/2012, pp. 487-496. CSREA Press, USA. ISBN: 1-60132-234-8.

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Abstract

The complexity of gene regulatory networks in terms of both large-scale description as well as nonlinear models is often an obstacle for analysis purposes. Therefore, the development of effective model reduction techniques is of paramount importance in the field of systems biology. In this paper, we apply Carleman bilinearization for model reduction for gene regulatory networks based only on gramian computations. The method is based on the bilinear representation of weakly nonlinear systems and Taylor's series expansion. Thus, we obtain a computationally simple solution and identify parameters that are relevant to the behavior of the system. The theoretical results are elucidated in an illustrative example and thus shown how they can be applied to reverse engineering design.

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