ON IMPROVING ADAPTIVE ERROR-DRIVEN AGGREGATION OF MARKOV CHAINS

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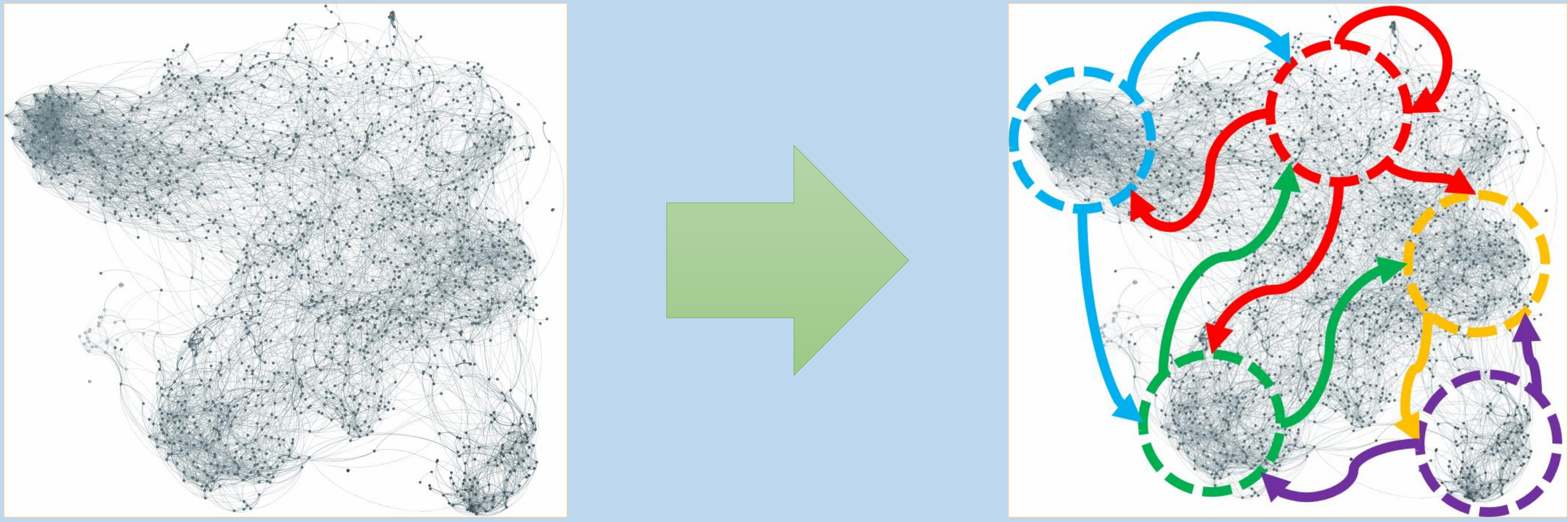
48

Motivation

Markov models are widely used in many areas of science and engineering in order to evaluate the probability of certain events of interest. Quantitative analysis of such models suffers from the state space explosion problem. In order to handle larger state spaces, several approximation techniques have been proposed. For various systems, level of precision affects the soundness of verification results, so accurate quantification of the approximation error is crucial.



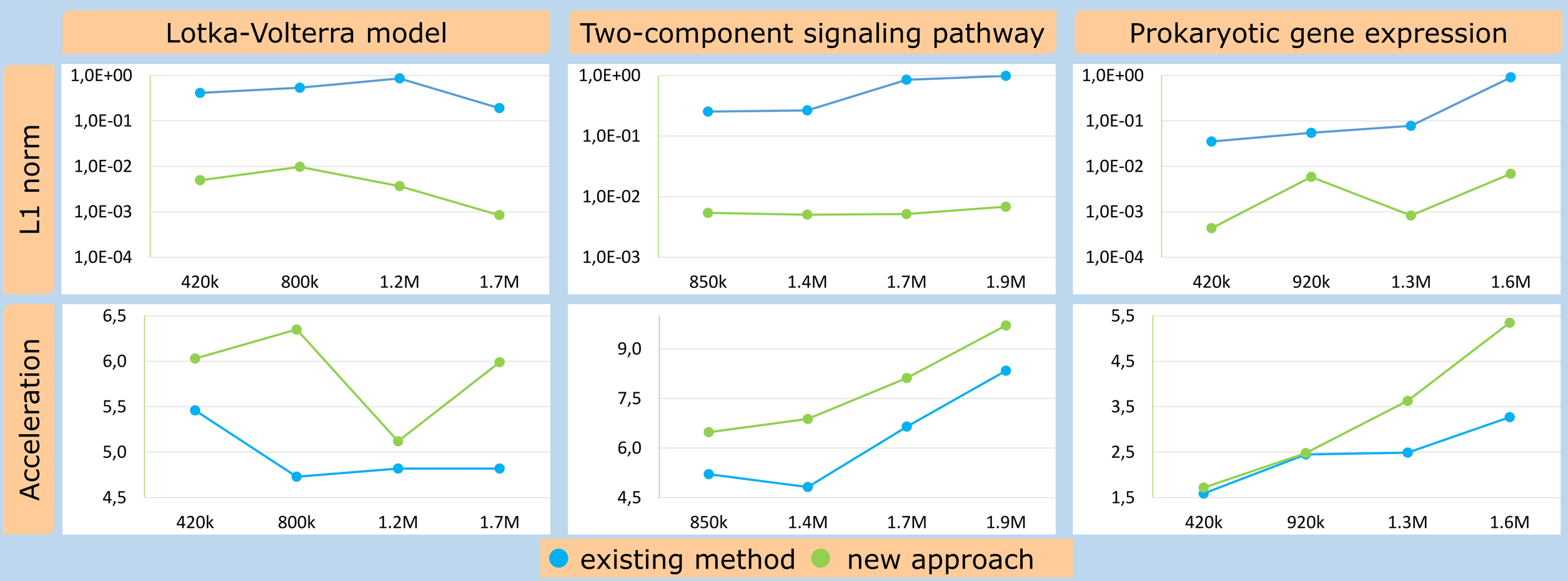
Key contributions

We consider adaptive aggregation method for discrete-time Markov chains presented in [1]. The basic idea behind this technique is clustering the state space sequentially in time, with the quality of each aggregation being quantified and used to derive explicit error bounds.

In this work we focus on key performance aspects of adaptive aggregation technique. Based on this analysis, we improve existing method by introducing more efficient approach to model abstraction and derive theoretical error bounds on this approximation. Compared to [1], our technique makes use of average outgoing probabilities between clusters to define abstract transition matrix, which preserves system dynamics to a higher degree.

Experimental evaluation

We evaluate both methods on three case studies: the *Lotka-Volterra model*, *two-component signaling pathway* and *prokaryotic gene expression*. We compare both acceleration and precision of theoretical bounds (**L1 norm**) acquired, the x-axis represents the size of a model. From all twelve experiments we inspect accuracy improvement by up to three orders magnitude along with considerable performance increase.



References

[1] Alessandro Abate, Luboš Brim, Milan Češka and Marta Kwiatkowska. *Adaptive Aggregation of Markov Chains: Quantitative Analysis of Chemical Reaction Networks*, pages 195-213. Springer International Publishing, Cham, 2015.