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Improved Predictive Models for the IRMA Network Using Nonlinear Optimisation

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Abstract : Cellular complexity stems from the interactions among thousands of different molecular species. Thanks to the emerging fields of systems and synthetic biology, scientists are beginning to unravel these regulatory, signaling, and metabolic interactions and to understand their coordinated action. Reverse engineering of biological networks has has several benefits but a poor quality of data combined with the difficulty in reproducing it limits the applicability of these methods. A few years back, many of the commonly used predictive algorithms were tested on a network constructed in the yeast Saccharomyces cerevisiae (S. cerevisiae) to resolve this issue. The network was a synthetic network of five genes regulating each other for the so-called in vivo reverse-engineering and modeling assessment (IRMA). The network was constructed in S. cereviase since it is a simple and well characterized organism. The synthetic network included a variety of regulatory interactions, thus capturing the behaviour of larger eukaryotic gene networks on a smaller scale. We derive a new set of algorithms by solving a nonlinear optimization problem and show how these algorithms outperform other algorithms on these datasets.

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