

Boolean networks provide a powerful yet simple modeling framework, and are commonly used to model both signalling and regulatory processes in cells. Previously, Boolean networks have been used to predict the effects of drugs using signalling models, model differentiation and carcinogenesis using regulatory models, and predict drug targets for cancer and other conditions. Despite their usefulness, the reconstruction of Boolean networks from data is still a challenging task, with many model reconstructions done manually and spanning small subsystems. Existing methods for automatic reconstruction of Boolean networks use heuristics and approximations or consider a limited family of possible models. Further, the Boolean networks are inferred on a node-by-node basis, forgoing any network-wide objectives. In this work, we focus on the reconstruction of Boolean models from binary time-series data using a reference network topology. We introduce novel Integer Linear Programming (ILP) formulations for model reconstruction from time-series data. Our approach is capable of reconstructing arbitrary models, performs optimization on a network level, and guarantees optimal agreement with the given data. Our approach also allows the incorporation of a prior-knowledge interaction network to guide the reconstruction. We demonstrate via simulations that our method is able to faithfully reconstruct the underlying model given data and a prior-knowledge network. We then analyze the robustness of our method to noise and incorrect prior-knowledge of the network and its performance on scarce data.