# Preliminary Results on Predicting Robustness of Biochemical Pathways through Machine Learning on Graphs

Pasquale Bove, Alessio Micheli, Paolo Milazzo, and Marco Podda

Department of Computer Science, University of Pisa, Italy
{bovepas,micheli,milazzo,marco.podda}@di.unipi.it

## Abstract

Biochemical pathways are complex dynamical systems in which molecules interact with each other in order to carry out cell functions. Interactions are based on chemical reactions, in which molecules can take different roles: reactants, products, promoters and inhibitors.

Pathways can be modeled and analyzed in several ways. For example, chemical kinetics laws, such as the law of mass action, make it possible to describe and analyse the dynamics of a set of chemical reactions through Ordinary Differential Equations (ODEs). Moreover, stochastic modeling and simulation approaches are also very common, typically based on of the many variants of Gillespie's stochastic simulation algorithm [1].

Graphical representations of biochemical pathways are also very common (see e.g., [2, 5, 4]) since they can provide a quite natural visual representation of the involved reactions. These representations enable network and structural analysis methods for the investigation of properties of the pathway as a whole. Moreover, they can usually be translated into ODEs or stochastic models in order to apply also standard numerical simulation techniques.

Models of biochemical pathways are typically used to investigate dynamical properties of these systems such as the reachability of steady states, the occurrence of oscillatory behaviors, causalities between species, and robustness. In particular, robustness (i.e. the maintenance of some concentration levels against the perturbation of parameters or initial conditions) is a key property of may pathways. Unfortunately, its assessment often requires the execution of a huge number of simulations in order to extensively explore the parameter space.

Our proposal is to use Machine Learning methods specifically designed for the application on graphs in order to predict robustness properties on the basis of the structure of the pathway graph only. This would make it possible, after the model has been trained on a set of classified graphs examples, to avoid the burden of performing a huge number of simulations. To this aim, we have conducted an essay in which Graph Neural Networks [6] have been applied on a dataset of pathway graphs obtained from the BioModels database [3]. The results of the essay are promising both in terms of accuracy in the prediction of robustness of new pathways, and in terms of performances in the prediction phase, whose

execution time is negligible compared to the time required to perform numerical or stochastic simulations.

## References


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