
Gene network inference for the prediction of silencing experiment in cancer cells

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Abstract

In mathematics as in biology, the interactions between genes are usually depicted as an oriented graph, where the vertices represent the different genes and the edges indicate a dependance relationship between two nodes. A lot of technics have been recently developed in order to infer this network from temporel genomic data. Graphical gaussian models, penalized linear models or random forests can be cited as examples.

Given a graph, which was infered from a model and temporal data, we aim to model a biological experiment known as *silencing*. This involves reducing the level of expression of a group of genes in order to observe an impact on another set of genes, known as "targets". These experiments are a hope for doctors to reduce the cell proliferation which occurs in cancer cells. We would like to develop and compare two methods to mathematically simulate the phenomenon of silencing. These methods will take into account the specificities due to the lack of medical data and the structure of the graph. Their performance will then be tested numerically on temporal data simulated by a standard linear model.

Keywords: gene network, silencing modelling, numerical simulations

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