Cascade: a $R$-package to study, predict and simulate the diffusion of a signal through a temporal gene network.

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Temporal gene interactions, in response to environmental stress, is a complex system that can be efficiently described using gene regulatory networks (GRN): a GRN allows to highlight the more influential genes and to spot some targets for biological intervention experiments. Despite that many reverse-engineering tools have been designed, the Cascade package is an integrated solution adding several new and original key features such as the ability to predict changes in gene expressions after a biological perturbation in the network and graphical outputs that allow monitoring the spread of a signal through the network.

Since the emergence of high-throughput technologies, many tools have been developed to learn gene expression profiles and reverse-engineer their underlying GRN [1,2]. These tools are either based on static co-expression methods or, if the biological phenomenon shows any temporality, time dependent methods. While the former relies on the assumption that co-expressed genes share some biological characteristics, the latter infers a directed network with temporal dependencies. In this last case, another important distinction should be made between exogenous stress (e.g., growth response) and endogenous phenomenon (e.g., cell cycle) [3,4]. This leads to different network topologies: in exogenous stress, networks’ topologies seem to have larger hubs and shorter paths through temporal dependent transcriptional waves [3]. This results in a quick response to environmental modifications [3]. The Cascade package is designed to model such “cascade networks” taking advantage of the assignment of genes to temporal clusters which are then used to enforce temporal causality in the network.


