

# NetBuilder'

## A tool for modeling and simulation of genetic regulatory networks

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Genetic regulatory networks (GRNs) describe e.g. how gene expression and cell-cell signalling are integrated and regulated. These networks may contain non-linear interactions such as feedback or feed-forward loops which can add to their often considerable complexity. Further complexity is introduced by the fact that regulators such as transcription factors may act synergistically in a combinatorial manner. Such combinatorial interactions often exhibit highly specific regulatory effects, and may only be present at specific developmental stages. In order to assist the study of GRNs we have developed NetBuilder', a new software tool for the construction, logical modeling, simulation, evolution and analysis of these networks.

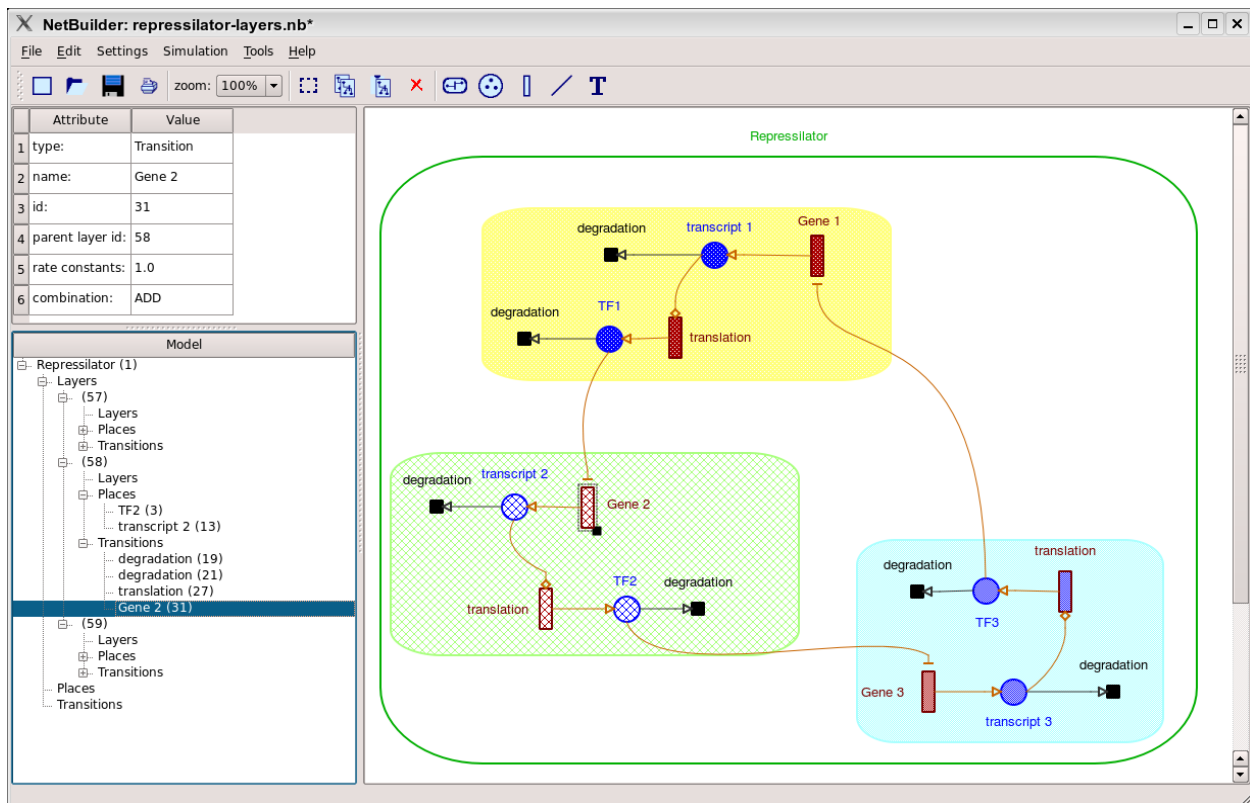


Figure 1: Screen shot of NetBuilder'. The window is split into three parts. On the right there is the drawing area and on the left top the table of attributes of an selected object and on the bottom the hierarchical tree of the current model showing which place or transition belongs to which layer.

NetBuilder' uses a Petri-net formalism to represent the components of a GRN and their respective interactions. In this representation, places represent components of the network and transitions represent processes acting upon them. Additionally, the user can create layers to represent compartments or to combine places and transitions to form a module.

NetBuilder' consists of an easy-to-use graphical user interface for drawing and specifying the connectivity of a network model. Alternatively, a model can also be constructed by coding the appropriate commands in a Python driver module. If the model does not contain any kinetic information for the simulation, the mathematical description will be automatically generated with the parameters set to default values which can be adjusted at any time. Stochastic, continuous and hybrid simulation engines are available for simulating the dynamics of the created model along with functionality for recording and plotting the resulting trajectories. Regulatory inputs can be grouped and integrated in flexible ways to allow the modeling of modular cis-regulatory genes and the combinatorial action of their regulatory inputs.

In future versions we will intend to integrate an evolutionary algorithm to allow the automated generation of networks with specific output behaviors. We also plan to include an algorithm for reducing the complexity of generated networks.

More information about NetBuilder' and the link for the download can be found on our web page: <http://strc.herts.ac.uk/bio/maria/Apostrophe/index.htm>.

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