# **The NetBuilder' project**

# Development of a tool for constructing, simulating, evolving, and analysing complex regulatory networks

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NetBuilder' uses the **Petri Net** formalism to aid modelling and analysis processes for complex regulatory networks, and to support understanding of the network structure and the role of the various elements. The tool is separated into a graphical user interface, the model designer, an analysis and a simulation engine.

#### **Network construction:**

**Simulation engine:** 

**Interoperability:** 

Graphical model designer:

- create layers, places, and transitions with selfdefined sizes, colors, fonts or use images.
- create arcs as lines or bezier curves (supported arc types: activation, inhibition, input, and output)

Or write a Python driver module

Deterministic:

- LSODA (via SciPy)
- simple forward Euler method with fixed step sizes

Stochastic:

- Gillespie/Gibson & Bruck

#### *Hybrid* (under delopment)

- print model
- save model as JPG
- read & save model in SBML (Systems Biology Markup Lang)

### Further developments:

- read & save model in PNML (Petri Net Markup Language)
- connection to **SBW** (Systems Biology Workbench)

Drawing area:

- copy objects

- delete objects

- move objects

- rotate objects

- scale objects



## **Evolution:**

# **Analysis:**

- reducing the **complexity** of networks
- finding **network motifs**
- adjusting dynamic behaviour

We have developed a (genetic) algorithm to evolve genetic regulatory networks that show a specific output behaviour on the basis of a given input function. We are currently attempting to generalize the procedures, and make them suitable for the integration into NetBuilder'. The screen shot shows an example of an evolved biological clock [1].

The tool will be **open-source** and **freely** available when the test phase is completed. Beta tester welcome. Just write us an email. Check our web page for latest information:

http://strc.herts.ac.uk/bio/maria/Apostrophe/index.htm

