

Systems biology

# MaBoSS 2.0: an environment for stochastic Boolean modeling

Gautier Stoll<sup>1,2,3,4,\*</sup>, Barthélémy Caron<sup>5</sup>, Eric Viara<sup>6</sup>, Aurélien Dugourd<sup>5</sup>,  
Andrei Zinovyev<sup>5</sup>, Aurélien Naldi<sup>7</sup>, Guido Kroemer<sup>1,2,3,4,8,9,10</sup>,  
Emmanuel Barillot<sup>5</sup> and Laurence Calzone<sup>5,\*</sup>

<sup>1</sup>Université Paris Descartes/Paris V, Sorbonne Paris Cité, Paris F-75006, France, <sup>2</sup>Gustave Roussy Cancer Campus, Villejuif F-94800, France, <sup>3</sup>INSERM, U1138, Paris F-75006, France, <sup>4</sup>Equipe 11 labellisée par la Ligue Nationale contre le Cancer, Centre de Recherche des Cordeliers, Paris F-75006, France, <sup>5</sup>Institut Curie, PSL Research University, INSERM, U900, Mines Paris Tech, Paris F-75005, France, <sup>6</sup>Sysra, Yerres 91330, France, <sup>7</sup>DIMNP UMR CNRS 5235, University of Montpellier, Montpellier F-34090, France, <sup>8</sup>Metabolomics and Cell Biology Platforms, Gustave Roussy Cancer Campus, Villejuif F-94800, France, <sup>9</sup>Pôle de Biologie, Hôpital Européen Georges Pompidou, AP-HP, Paris F-75015, France and <sup>10</sup>Department of Women's and Children's Health, Karolinska Institute, Karolinska University Hospital, Stockholm S-171 76, Sweden

\*To whom correspondence should be addressed.

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## Abstract

**Motivation:** Modeling of signaling pathways is an important step towards the understanding and the treatment of diseases such as cancers, HIV or auto-immune diseases. MaBoSS is a software that allows to simulate populations of cells and to model stochastically the intracellular mechanisms that are deregulated in diseases. MaBoSS provides an output of a Boolean model in the form of time-dependent probabilities, for all biological entities (genes, proteins, phenotypes, etc.) of the model.

**Results:** We present a new version of MaBoSS (2.0), including an updated version of the core software and an environment. With this environment, the needs for modeling signaling pathways are facilitated, including model construction, visualization, simulations of mutations, drug treatments and sensitivity analyses. It offers a framework for automated production of theoretical predictions.

**Availability and Implementation:** MaBoSS software can be found at <https://maboss.curie.fr>, including tutorials on existing models and examples of models.

**Contact:** gautier.stoll@upmc.fr or laurence.calzone@curie.fr

**Supplementary information:** Supplementary data are available at *Bioinformatics* online.

## 1 Introduction

Chemical kinetics and logical formalism have already been extensively used for modeling signaling pathways that are implicated in pathologies such as cancer, HIV, or auto-immune diseases. On one hand, models using chemical kinetics are more precise as they can output the variation of gene or protein concentrations over time, but to do so, speed of reactions and relative entity concentrations need to be known a priori. On the other hand, logical models can include

a high number of variables at the expense of precision. Many tools and algorithms have been developed for logical modeling; and a community effort has been made to facilitate the exchange and the comparison of models among these tools (<http://www.colomoto.org/>; Naldi *et al.*, 2015). With the framework of MaBoSS, we are able to describe temporal behaviors of these signaling pathways while maintaining the simple description inherent to Boolean models (Stoll *et al.*, 2012). Since MaBoSS provides probabilistic results of

all model entities (e.g. gene/protein/phenotype), theoretical results can be confronted to many types of experiments, including single-cell behaviors. MaBoSS has already proved its efficiency in biological interpretation of cancer-related models (Calzone *et al.*, 2015; Cohen *et al.*, 2015; Remy *et al.*, 2015; Verlingue *et al.*, 2016) and is constantly evolving.

In addition to the initial core C++ script (MaBoSS 1.2.2), the new version of MaBoSS (2.0) includes an environment that facilitates the elaboration of a project in MaBoSS, in particular: model construction, visualization of solutions, simulations of mutations, drug treatments and sensitivity analyses (Fig. 1). The environment is accessible through separated scripts in Perl and Python, or in an integrated library at <https://maboss.curie.fr/>. A tutorial offers an example of the practical use of the functionalities presented here (Supplementary Material and <https://maboss.curie.fr/>).

## 2 Constructing a Boolean model using MaBoSS

MaBoSS is a simulation software for continuous time Boolean modeling. The model is described by a network, where nodes have Boolean states. Transitions between the node states are governed by logical equations, with an associated rate (a real number  $\in [0, \infty]$ ). The model is written in a specific language and saved in a '.bnd' file (for Boolean Network Description). Modeling parameters, including initial conditions, maximum time, etc. are gathered in a '.cfg' file (for ConFiGuration file). The idea is to have a single.bnd file, and several.cfg files that account for different experimental situations (initial conditions, mutations, drug treatments, etc.). That way, 'external variables', noted by the name of the variable with a preceding \$ and representing real numbers, are defined in the.bnd file and can be set and modified in the associated.cfg file.

Writing a MaBoSS model can be facilitated by creating and exporting it using the user-friendly tool GINsim (Naldi *et al.*, 2009) (from <http://ginsim.org/dev/>). This export results in the creation of

a.bnd file and a.cfg file with default parameters. Thus, any model in SBML qual standard format (Chaouiya *et al.*, 2013) (including multi-valued models), can be exported in MaBoSS format. Similarly, it is possible to export a MaBoSS model (.bnd and .cfg files) into a set of logical rules written in a text format. The output is a text format that is supported by the library bioLQM (available at <https://github.com/colomoto/bioLQM>), which allows the export in SBML qual or other formats for other modelling tools such BoolNet (<http://www.colomoto.org/software/boolnet.html>; Müssel *et al.*, 2010). Note that with a minor modification (a change of, into,), the output format can be imported directly in BoolNet.

One important asset of MaBoSS 2.0 is the possibility of using any probability distribution as an initial condition. For instance, for a set of 2 genes ( $A, B$ ), the following probabilities can be assigned:  $p[(A, B) = (0, 0)] = 0.7$  and  $p[(A, B) = (1, 0)] = 0.3$ , thus offering the possibility to characterize an heterogeneous cell population where each probability of network state corresponds to a subpopulation.

## 3 Running MaBoSS and processing the output files

MaBoSS core script is accessible through command line. It estimates time dependent probabilities of 'network states', a network state is a vector of Boolean values associated to node states. The outputs of MaBoSS contain three files: a file for time dependent probabilities of network states (probtraj.csv file), a file for asymptotic probability decomposition in 'indecomposable stationary distribution' (stat-dist.csv file) and a file for the fixed points and their associated probability (fp.csv file). This latter file allows to quickly verify the existence of a limit cycle: when the sum of all fixed point probabilities is less than 1, it can be concluded that there exists at least one limit cycle that cannot be computed exactly but remains to be characterized.

### 3.1 Formatting of results

The outputs of MaBoSS are compact text files that are difficult to exploit as such. With practice, we have developed a script that extract specific information from these files: *MBSS\_FormatTable* runs MaBoSS in a specific subfolder, and generates formatted tables for the trajectories, easily manageable in a spreadsheet.

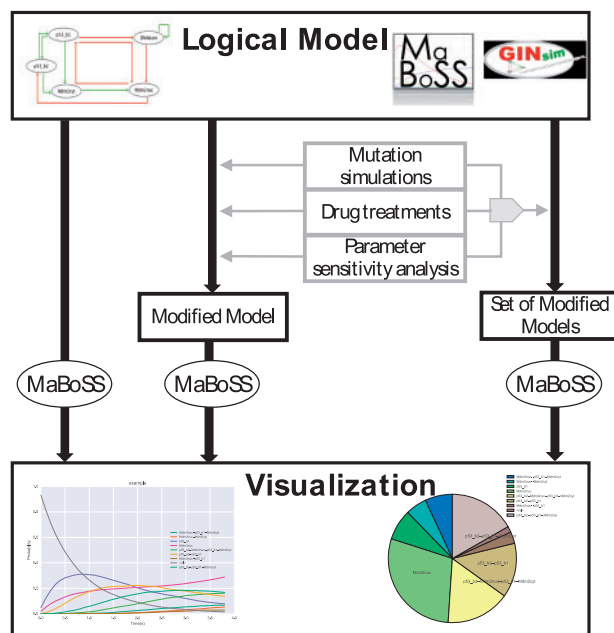
### 3.2 Visualization of results

The script *MBSS\_TrajectoryFig* can be used for plotting trajectories, and *MBSS\_PieChart* exports the asymptotic distribution in the form of a pie chart.

## 4 Modifications of a master model

One purpose of mathematical modeling is to predict the effect of specific perturbations (e.g. losses or gains of function, or combinations thereof). For instance, cancers can be considered as mutants of a model in normal conditions, which we refer to as 'master model'. To do so, some of the following scripts create new 'external variables' and vary them according to the task the modeler wishes to perform. Recall that external variables of MaBoSS correspond to parameters in the.bnd file that can be modified in the.cfg file (see reference card).

**Mutant simulations.** Simulating gene alterations can be done by over-writing the rules of the corresponding components. The script *MBSS\_MutBnd* allows the use of a single.bnd file for all different model variants (including wild type and mutant conditions). The



**Fig. 1.** Pipeline of the use of MaBoSS 2.0 functionalities. A logical model can be simulated directly, modified by mutations, drug treatments or sensitivity analyses and all modifications can be gathered into a single command and simulated at once

script adds two external variables to each gene that the user wishes to mutate: the first one representing a possible deletion or a loss of function, the other reproducing amplifications or gains of function. These external variables can then be modified and set as desired in specific.cfg files. Once several.cfg files have been constructed, the use of *FormatTable* is particularly suited, because it generates a folder with the name of the.cfg file in order to keep track of each mutant simulation.

**Parameter sensitivity analysis.** The transition rates for each node can be varied to assess their importance in some outputs. For that, it is important to control their value through external variables. The script *MBSS\_SensitivityAnalysis* allows to vary the value of external variables separately by creating a.cfg file per modification. Then, a shell script is automatically created and can run the simulations for all the newly created.cfg files.

**Drug treatments.** For the simulation of drug treatments, the script *MBSS\_DrugSim* generates new nodes that will be used as drugs. They act as inhibitors of the specified targets. The strength of the inhibitor can be modulated to account for intermediate drug dosages. Also, in the course of a simulation, a drug treatment can be applied and removed after a certain time. For that, we have developed a script, *MBSS\_InitCondFromTrajectory*, with which one can select the final probability distribution of a simulation and use it as the initial condition for another simulation of the model with the new drug condition.

## 5 Automation of multiple simulations

In order to optimize Boolean model analyses, *MBSS\_MultipleSim* offers the possibility to generate multiple.cfg files and run the simulations at once with a single command.

## 6 Integrated functionalities

In order to run a complete project including all needed perturbations into a single command, *MBSS\_PrepareProjectFile* prepares a folder containing all.cfg files corresponding to all the modifications without launching the simulations. In addition, it creates a shell script for running MaBoSS for all possible.cfg files and processing the outputs files. For running multiple simulations on a server, the folder can be imported and the shell script can be adapted to the server environment. Note that the definition of multiple runs is more straightforward in *MBSS\_MultipleSim*, but is more flexible in *MBSS\_PrepareProjectFile*.

## 7 Conclusion

MaBoSS 2.0 and its associated environment have been developed to answer specific needs of modelers. They can be combined and used into the following pipeline (see Supplementary Material for an example): (i) Construct a logical model, by writing directly the.bnd and.cfg files or by exporting them from GINsim; (ii) Run the model,

analyze the results within a spreadsheet, and visualize the results; (iii) Test parameter sensitivity; (iv) Confront the model to known experimental observations: mutations, drug effects and (v) Set up a protocol for comparing experiments to model results for new biological insights.

In the future, we plan to construct a library version of MaBoSS in Python and in R to facilitate its implementation in these environments. We welcome the contribution of all future users to extend MaBoSS applications.

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## References

- Calzone,L. *et al.* (2015) Predicting genetic interactions from Boolean models of biological networks. *Integr. Biol.*, 921–929.
- Chaouiya,C. *et al.* (2013) SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modeling formalisms and tools. *BMC Syst. Biol.*, 7, 135.
- Cohen,D.P. *et al.* (2015) Mathematical modelling of molecular pathways enabling tumour cell invasion and migration. *PLoS Comput. Biol.*, 11, e1004571.
- Müssel,C. *et al.* (2010) BoolNet – an R package for generation, reconstruction and analysis of Boolean networks. *Bioinformatics*, 26, 1378–1380.
- Naldi,A. *et al.* (2009) Logical modelling of regulatory networks with GINsim 2.3. *Biosystems*, 97, 134–139.
- Naldi,A. *et al.* (2015) Cooperative development of logical modelling standards and tools with CoLoMoTo. *Bioinformatics*, 31, 1154–1159.
- Remy,E. *et al.* (2015) A modeling approach to explain mutually exclusive and co-occurring genetic alterations in bladder tumorigenesis. *Cancer Res.*, 75, 4042–4052.
- Stoll,G. *et al.* (2012) Continuous time Boolean modeling for biological signaling: application of Gillespie algorithm. *BMC Syst. Biol.*, 6, 116.
- Verlingue,L. *et al.* (2016) A comprehensive approach to the molecular determinants of lifespan using a Boolean model of geroconversion. *Aging Cell*. doi:10.1111/accel.12504.