

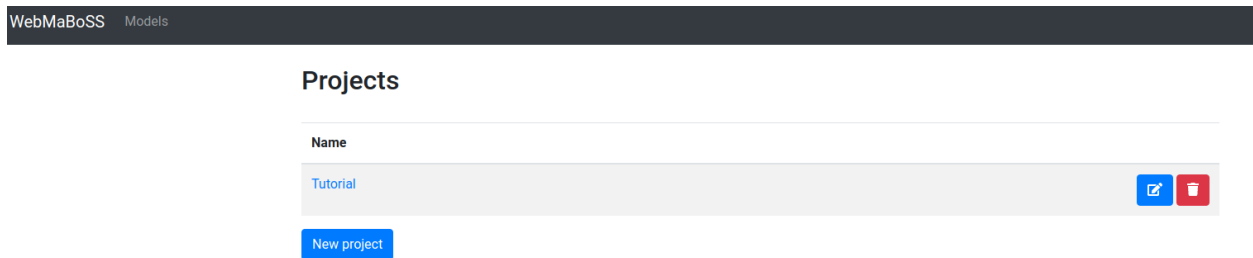
WebMaBoSS Tutorial

Here we propose a tutorial to give the user a total overview about the WebMaBoSS functionality.

It is possible to get access through browser at <https://maboss.curie.fr/webmaboss/>

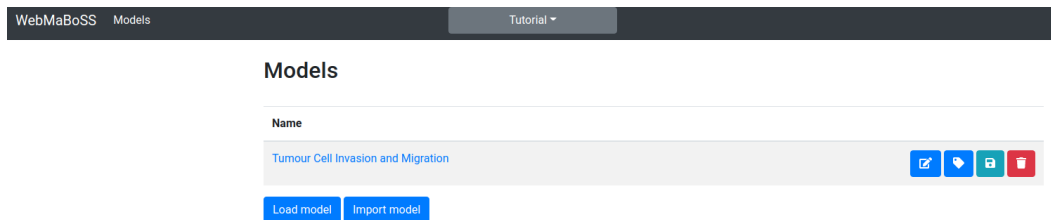
Starting a Project:

WebMaBoSS allows the user to organize the models inside Projects folder.



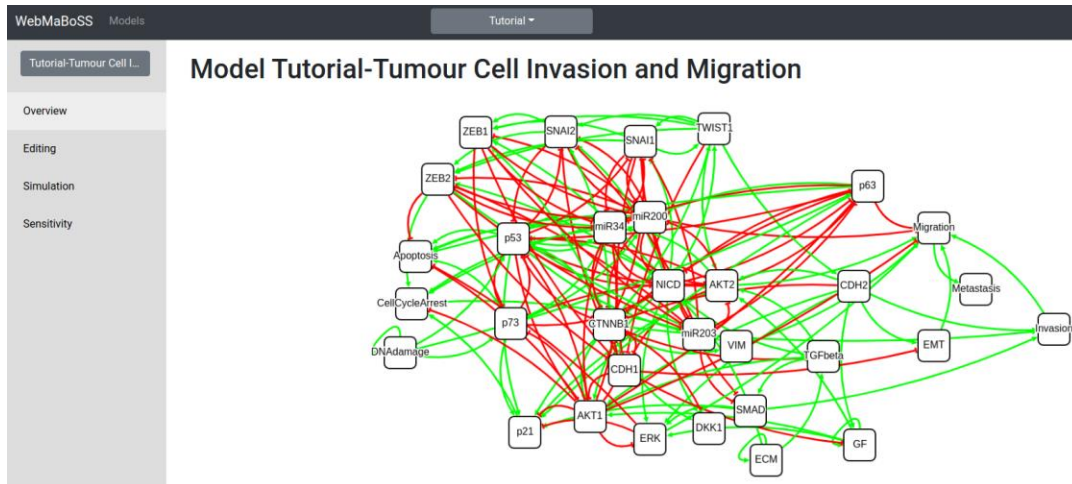
In the Projects folder the users can upload their own model in Z-GINML, SBMLqual or MaBoSS format or import a model from BioModels and Cell Collective.

For this tutorial we will use a model of Tumour Cell Invasion and Migration from [Cohen DP et al.](#) imported from Cell Collective.



Overview Tab

Once imported the model, it can be visualized in the Overview tab.



This particular model is composed by 32 nodes, describing the intercourse of different transcription factors involved in the invasion process; to acquire the ability to migrate Epithelial to Mesenchymal Transition (EMT) is needed to gain motility. that is induced loss of E-cadherin (*CDH1*) and by gene expression of N-cadherin (*CDH2*), this last one is up-regulated by activation of *ZEB1/2* *SNAI1/2* and *TWIST1*. In order to activate the Metastasis phenotype, EMT is needed as well as the activation of Migration and Invasion.

Editing tab

Models exported in MaBoSS are characterized by two file, model.bnd and model.cfg.

The .bnd file contains the logic equation for each node of the network, while the .cfg file contains the parameters for the MaBoSS simulation.

On WebMaBoSS the .cfg file is summarized in the editing tab. The user can visualize the logical equation for each node and editing the formula using the buttons on the right of the corresponding nodes or insert a new node in the network.

EMT		
rateUp	@logic ? \$L_EMT : 0	
rateDown	@logic ? 0 : \$d_EMT	
logic	(CDH2 & !CDH1)	

MaBoSS computes the trajectories over time and the probable states of the model associating an initial states for each node, that by default is set to 0. The user can change the initial state of each node of the network in order to simulate different initial conditions. This can be done as shown in the figure below:

Rates	Initial values	Outputs	Parameters	Settings
DNADamage	<input type="checkbox"/>	50%	Random	
ECM	<input type="checkbox"/>	81%	Random	
p63	<input type="checkbox"/>	0%	Random	
miR200	<input type="checkbox"/>	32%	Random	
VIM	<input type="checkbox"/>	0%	Random	
p53	<input type="checkbox"/>	0%	Random	
miR203	<input type="checkbox"/>	77%	Random	

In order to reduce the computational time of the simulation, the user should reduce the number of output nodes that will be displayed in next results (**less than 10 output nodes to avoid longer computational time**).

Model Tutorial-Tumour Cell Invasion and Migration

Output Node	Status
DNADamage	On
ECM	On
p63	Off
miR200	Off
VIM	Off
p53	Off
miR203	Off
ZEB2	Off
CTNNB1	Off
DKK1	Off
SNAI2	Off
p21	Off
CellCycleArrest	On
SNAI1	Off
GF	Off
TWIST1	Off

Simulation tab

Once edited the parameters, the user can launch a simulation through the Simulation tab. The previously modified parameters will be kept and will be shown a recap of the simulation before to submit.

WebMaBoSS Models

Tutorial-Tumour Cell L... Model Tutorial-Tumour Cell

Overview

Editing

Simulation

Sensitivity

New simulation

Create new simulation

General Initial states Output Mutations

Name Tutorial

Max time 1000

Time tick 0,5

Sample count 1000

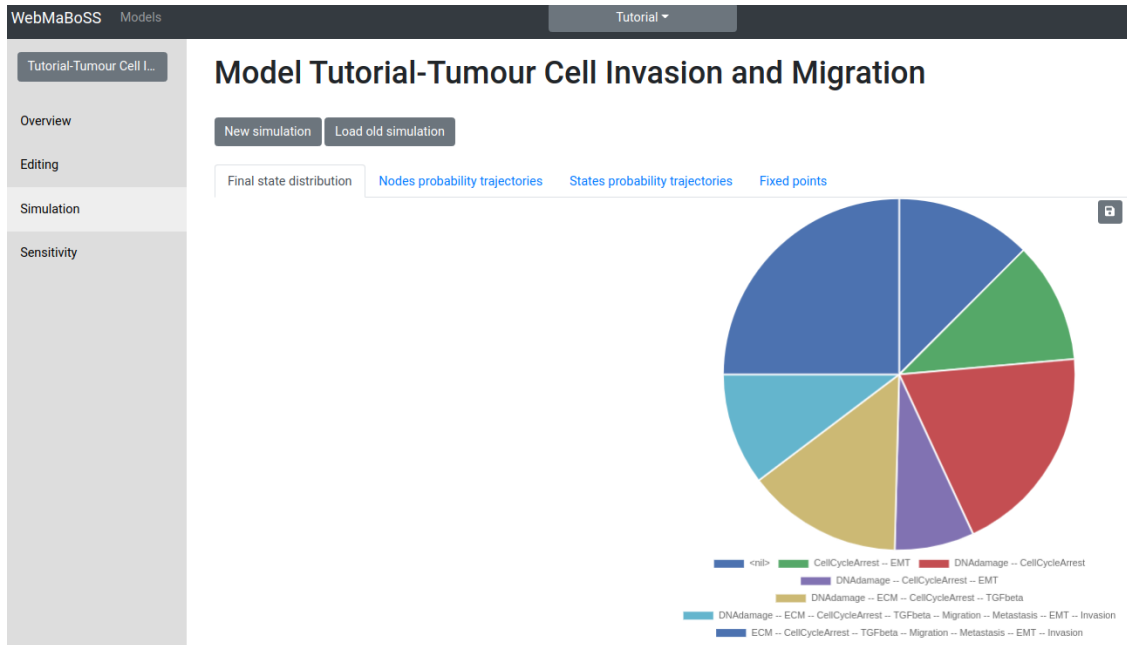
Thread count 6

Discrete time

Close Submit

Below we are showing the results of a simulation of **wild type** model with random initial conditions.

WebMaBoSS will automatically generate a plot for the *final state distribution*:



Nodes probability trajectories plot:

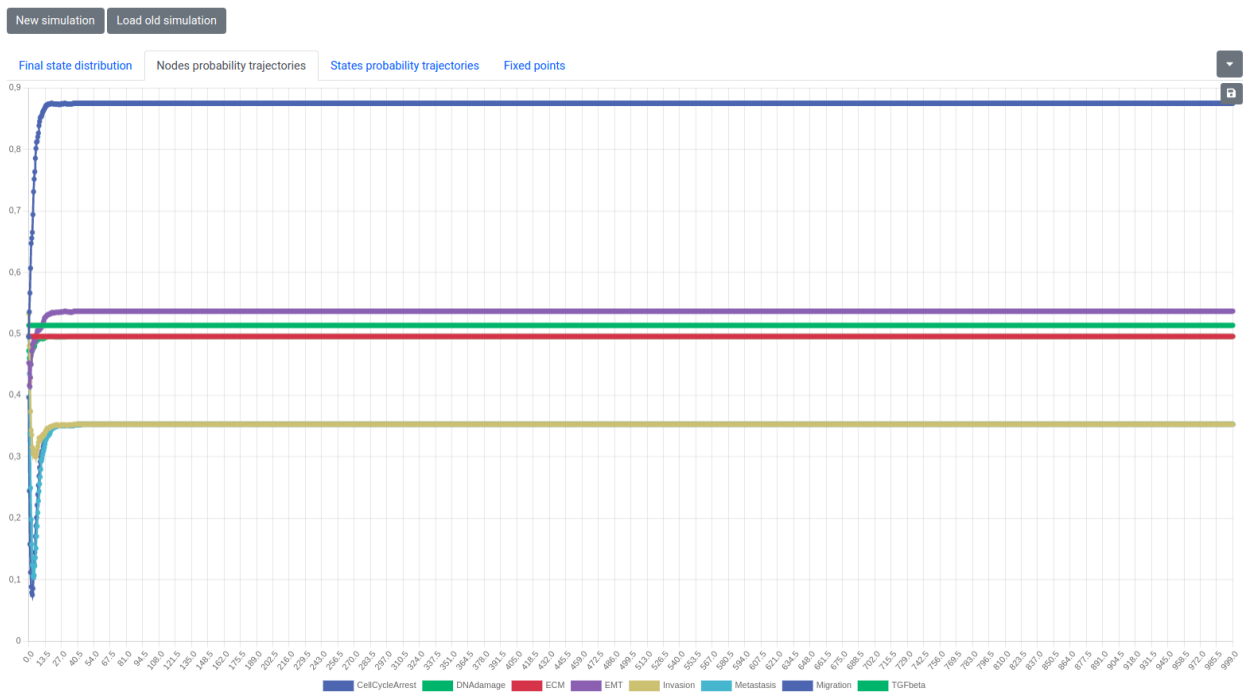
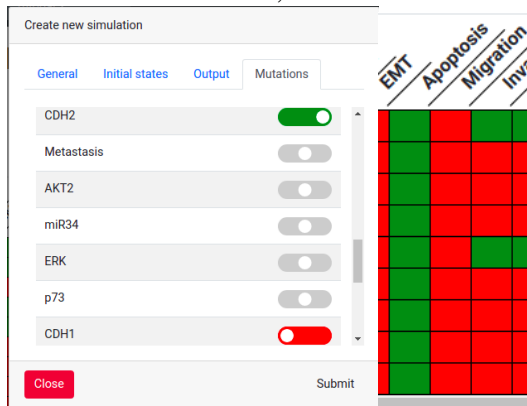


Table of the fixed points:

In the **Mutations** tab, the user can force the up/down regulation of certain nodes.



This is useful to understand what the influence of a gene or transcription factor is and the impact of a node on the possible network states.

As example, we simulated a loss of function of E-cadherin (CDH1) while forcing the activation of N-cadherin (CDH2). This leads to the activation of EMT, confirming that down-regulation of CDH1 and up-regulation of CDH2 is necessary in order to induce Epithelial to Mesenchymal Transition.

