

# Hands On : Using MaBoSS with WebMaBoSS

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PerMedCoE summer school  
*from pathway modelling tools to cell-level simulations*

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# Using MaBoSS with WebMaBoSS

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WebMaBoSS Tutorials About

Demo Sign in Register



## WebMaBoSS

A web tool for simulating Boolean models

Click [here](#) to login if you already have an account, otherwise you can quickly create one [here](#).

If you want to quickly test WebMaBoSS, you can have a look at our [demo project](#).

### Model analysis

WebMaBoSS allows simulations, and multiple outputs for results. It also allows sensitivity analysis by performing single and double mutations.

### Compatibility

WebMaBoSS is able to import models in MaBoSS format (bnd, cfg files), BoolNet format, SBML-qual format, or in GINsim format. It also allows to export models in any of these three formats.

### Public databases

WebMaBoSS allows to browse models from CellCollective and BioModels, and import them.

WebMaBoSS was created and is maintained by the team [Computational System Biology of Cancer](#) at [Institut Curie](#).


It is open-source and available on [GitHub](#), where you can also find instructions to run it locally and tutorials.

# Using MaBoSS with WebMaBoSS

## › Create an account

WebMaBoSS   Tutorials   About   Demo   Sign in   Register

Register to WebMaBoSS



Username

E-mail (optional)

Password

Confirm password


[Register](#)

# Using MaBoSS with WebMaBoSS

## › Logging in



Sign in



Username

Password

Sign in

# Using MaBoSS with WebMaBoSS

## › List of projects

[WebMaBoSS](#) [Tutorials](#) [About](#) [Profile](#) [Logout](#)

### Projects

Name	
<a href="#">Cell Cycle</a>	<a href="#">✎</a> <a href="#">✖</a>
<a href="#">Metastasis</a>	<a href="#">✎</a> <a href="#">✖</a>
<a href="#">Cell Fate</a>	<a href="#">✎</a> <a href="#">✖</a>
<a href="#">Tutorial</a>	<a href="#">✎</a> <a href="#">✖</a>
<a href="#">Cancer models</a>	<a href="#">✎</a> <a href="#">✖</a>

[New project](#)

# Using MaBoSS with WebMaBoSS

## › Creating a project

The screenshot displays the WebMaBoSS web application. At the top, a dark navigation bar contains the text 'WebMaBoSS' followed by links for 'Tutorials' and 'About' on the left, and 'Profile' and 'Logout' on the right. The main content area has a dark grey background. On the left, a 'Projects' sidebar lists several categories: 'Name', 'Cell Cycle', 'Metastasis', 'Cell Fate', 'Tutorial', and 'Cancer models'. A 'New project' button is located at the bottom of this sidebar. In the center, a white modal window titled 'Add new project' is open. It contains a 'Name' input field with the text 'Invasion models' and a 'Description' text area with the text 'Models describing invasion'. At the bottom of the modal are two buttons: a red 'Close' button and a blue 'Create project' button. On the right side of the main content area, there is a list of existing projects, each represented by a blue icon, a text label, and a red trash can icon for deletion.

# Using MaBoSS with WebMaBoSS




## › List of models

[WebMaBoSS](#) [Models](#) [Tutorials](#) [About](#) [Cancer models ▾](#) [Profile](#) [Logout](#)

### Models

**Name**

Montagud 2021 Prostate Cancer

[Load model](#) [Import model](#)

# Using MaBoSS with WebMaBoSS

## › Loading a model

The screenshot shows the WebMaBoSS interface with a 'Load model' dialog box open. The background interface includes a top navigation bar with 'WebMaBoSS', 'Models', 'Tutorials', and 'About'. On the right, there are links for 'Profile' and 'Logout'. The main content area is titled 'Models' and shows a table with one entry: 'Montagud 2021 Prostate Cancer'. Below the table are two buttons: 'Load model' and 'Import model'. The 'Load model' dialog box is a white modal with a title bar 'Load model'. It contains the following fields: 'Name' with the text 'Cohen 2015 Invasion model'; 'Type' with a dropdown menu showing 'MaBoSS'; 'BND file' with the text 'metastasis.bnd' and a 'Browse' button; and 'CFG file' with the text 'metastasis.cfg' and a 'Browse' button. At the bottom of the dialog are two buttons: a red 'Close' button and a blue 'Load model' button.

WebMaBoSS Models Tutorials About Profile Logout

### Models

Name
Montagud 2021 Prostate Cancer

Load model Import model

#### Load model

Name  
Cohen 2015 Invasion model

Type  
MaBoSS

BND file  
metastasis.bnd Browse

CFG file  
metastasis.cfg Browse

Close Load model



# Using MaBoSS with WebMaBoSS

## › Importing a model

The screenshot shows the 'Import model' dialog box in the WebMaBoSS application. The dialog has two tabs: 'BioModels' and 'CellCollective'. The 'BioModels' tab is active, displaying a table of models. The table has two columns: 'Name' and 'Author'. The models listed are:

Name	Author
Traynard2016 - Mammalian cell cycle regulation - Logical Model	Pauline Traynard
Cacace2020 - Logical model of the regulatory network controlling...	Denis Thieffry
Howell2020- Compartmental Logical model of mitotic exit	Rowan Howell
Terfve2012 - Signalling in liver cancer - logical model	Vijayalakshmi Chelliah
Floc&#39;hay2020 - SeaUrchin_model_ginsim	Denis Thieffry
Mbodj2016 - Mesoderm specification during Drosophila develop...	Denis Thieffry
Rodriguez-Jorge2019 - Boolean model of TCR signaling for CD4 +...	Denis Thieffry
Rodriguez-Jorge2019 - Boolean model of combined TCR and TLR...	Denis Thieffry
Afenya2018 - peripheral blood dynamics in the disease state	Szeyi Ng

At the bottom of the dialog, there is a toggle switch for 'Use SBML names' which is currently turned on, and a red 'Close' button.

# Using MaBoSS with WebMaBoSS

## › Model interaction graph



# Using MaBoSS with WebMaBoSS

## › Creating a new simulation : General settings

The screenshot displays the WebMaBoSS web application. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. The left sidebar shows a menu with 'Cohen 2015 Invasion' selected, and sub-items: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and contains a 'New simulation' button. A modal dialog box titled 'Create new simulation' is open, showing the 'General' tab. The dialog contains the following fields and controls:

- Name:** A text input field with the placeholder 'Name of the simulation'.
- Max time:** A numeric input field with the value '40'.
- Sample count:** A numeric input field with the value '1000'.
- Discrete time:** A toggle switch, currently turned off.
- Use physical random generator:** A toggle switch, currently turned off.
- Pseudorandom seed:** A numeric input field with the value '0'.

At the bottom of the dialog, there is a red 'Close' button and a 'Submit' button.

# Using MaBoSS with WebMaBoSS

## › Creating a new simulation : Initial states

The screenshot displays the WebMaBoSS web application interface. On the left, a sidebar contains navigation links: Overview, Editing, Simulation, and Sensitivity. The main content area shows the 'Model Cohen 2015 Invasion' with a 'New simulation' button. A modal dialog box titled 'Create new simulation' is open, featuring four tabs: General, Initial states (selected), Output, and Mutations. The 'Initial states' tab lists several parameters with sliders and percentage values:

Parameter	Value
CTNNB1	0 %
CellCycleArrest	0 %
DKK1	0 %
DNA damage	50 %
ECMicroenv	50 %
EMT	0 %

At the bottom of the dialog, there are 'Close' and 'Submit' buttons.

# Using MaBoSS with WebMaBoSS

## › Creating a new simulation : Output nodes

The screenshot displays the WebMaBoSS web application interface. At the top, there is a navigation bar with links for 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. On the left side, a sidebar menu lists 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area shows the 'Model Cohen 2015 Invasion' with a 'New simulation' button. A modal dialog box titled 'Create new simulation' is open, featuring four tabs: 'General', 'Initial states', 'Output', and 'Mutations'. The 'Output' tab is selected, showing a list of nodes with toggle switches: AKT1 (off), AKT2 (off), Apoptosis (on), CDH1 (off), CDH2 (off), CTNNB1 (off), and CellCycleArrest (on). At the bottom of the dialog, there are 'Close' and 'Submit' buttons.

# Using MaBoSS with WebMaBoSS

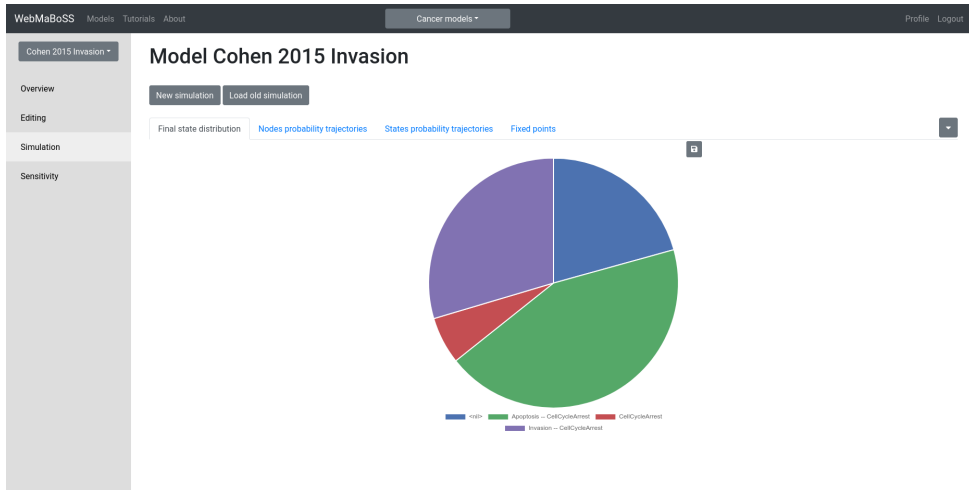
## › Creating a new simulation : Mutants

The screenshot displays the WebMaBoSS web application. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. The left sidebar contains a dropdown menu for 'Cohen 2015 Invasion' and a list of options: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area shows the title 'Model Cohen 2015 Invasion' and a 'New simulation' button. A modal dialog box titled 'Create new simulation' is open, featuring four tabs: 'General', 'Initial states', 'Output', and 'Mutations'. The 'Mutations' tab is active, showing a list of genes with toggle switches: AKT1 (checked), AKT2, Apoptosis, CDH1, CDH2, CTNNB1, and CellPulseArrest. At the bottom of the dialog are 'Close' and 'Submit' buttons.

Gene	Status
AKT1	On
AKT2	Off
Apoptosis	Off
CDH1	Off
CDH2	Off
CTNNB1	Off
CellPulseArrest	Off

# Using MaBoSS with WebMaBoSS

## › Simulation results : Final states



# Using MaBoSS with WebMaBoSS

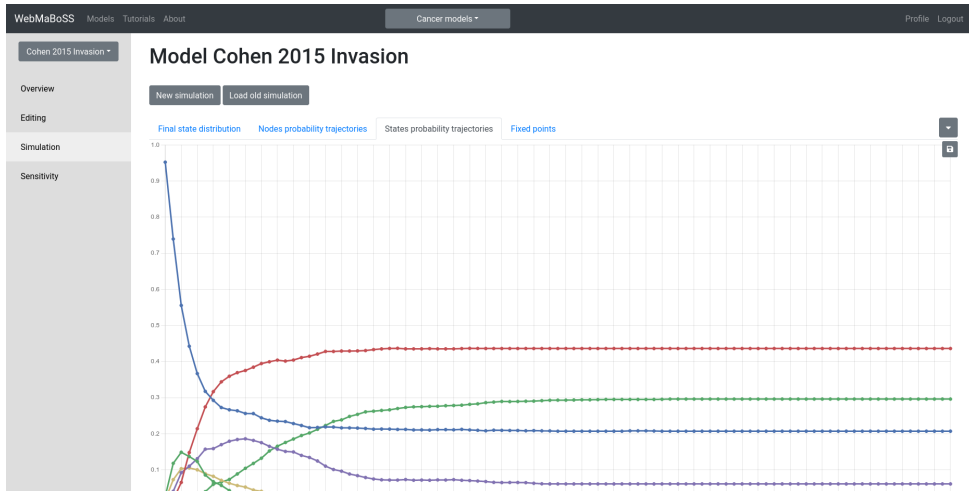
## › Simulation results : Node trajectories





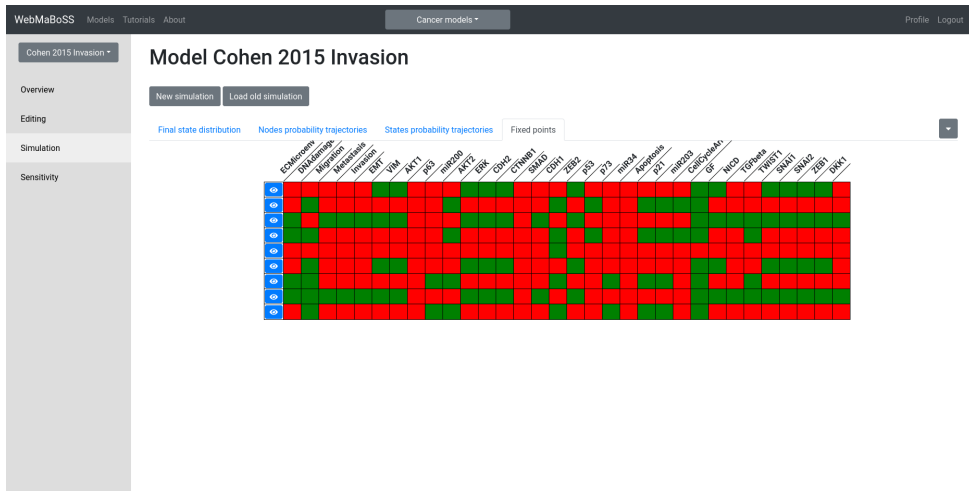
# Using MaBoSS with WebMaBoSS

## › Simulation results : State trajectories



# Using MaBoSS with WebMaBoSS

## › Simulation results : Fixed points



- Model editing : (in)activation rules

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# Using MaBoSS with WebMaBoSS

## › Model editing : (in)activation rules

The screenshot displays the WebMaBoSS web application interface. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', and 'Profile Logout'. The left sidebar contains a dropdown menu for 'Cohen 2015 Invasion' and a list of tabs: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and features a sub-tabbed interface with 'Rates', 'Initial values', 'Outputs', and 'Parameters'. The 'Rates' tab is active, showing a list of biological processes and their associated logic rules. A modal dialog box titled 'Editing formula' is open, allowing the user to edit the logic for the 'logic' rate. The dialog has fields for 'Name' (containing 'logic') and 'Formula' (containing a complex logic expression involving variables like 'p21', 'I2EB2', 'IAKT1', 'ImiR200', 'ImiR203', and 'miR34'). The dialog includes 'Close' and 'Submit' buttons. The background table lists various biological processes such as AKT1, AKT2, Apoptosis, CDH1, CDH2, CTNNB1, CellCycleArrest, rateUp, rateDown, logic, DKK1, DNAdamage, ECMicroenv, EMT, ERK, GF, Invasion, Metastasis, Migration, NICD, SMAD, and SNAI1, each with a corresponding logic rule and a set of control buttons (arrows and a square icon).

WebMaBoSS Models Tutorials About

Cohen 2015 Invasion

Overview Editing Simulation Sensitivity

Model Cohen 2015 Invasion

Rates Initial values Outputs Parameters

AKT1

AKT2

Apoptosis

CDH1

CDH2

CTNNB1

CellCycleArrest

rateUp @logic ? \$u\_CellCycleArrest : 0

rateDown @logic ? 0 : \$d\_CellCycleArrest

logic (p21 & I2EB2 & IAKT1 & ImiR200 & ImiR203 & miR34) | (p21 & I2EB2 & IAKT1 & ImiR200 & miR203) | (p21 & I2EB2 & IAKT1 & miR200) | (p21 & I2EB2 & IAKT1) | (p21 & IAKT1)

DKK1

DNAdamage

ECMicroenv

EMT

ERK

GF

Invasion

Metastasis

Migration

NICD

SMAD

SNAI1

Editing formula

Name logic

Formula (p21 & I2EB2 & IAKT1 & ImiR200 & ImiR203 & miR34) | (p21

Close Submit

# Using MaBoSS with WebMaBoSS

## › Model editing : Initial states

The screenshot shows the WebMaBoSS web application interface. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', a 'Cancer models' dropdown, and 'Profile' and 'Logout' links. The left sidebar contains a dropdown menu for 'Cohen 2015 Invasion' and a list of navigation options: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and has four tabs: 'Rates', 'Initial values' (which is active), 'Outputs', 'Parameters', and 'Settings'. Below the tabs, a list of biological processes is shown, each with a slider and a percentage value:

Biological Process	Initial Value (%)
AKT1	50%
AKT2	0%
Apoptosis	0%
CDH1	0%
CDH2	0%
CTNNB1	0%
CellCycleArrest	0%
DKK1	0%
DNA damage	50%
ECMicroenv	50%
EMT	0%
ERK	0%

# Using MaBoSS with WebMaBoSS

## › Model editing : Output nodes

The screenshot displays the WebMaBoSS web application interface. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Cancer models', 'Profile', and 'Logout'. The left sidebar contains a dropdown menu for 'Cohen 2015 Invasion' and a list of navigation options: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and features four tabs: 'Rates', 'Initial values', 'Outputs', and 'Parameters'. The 'Outputs' tab is currently selected, showing a list of output nodes with their respective toggle switches. The nodes and their states are as follows:

Output Node	Toggle State
AKT1	Off
AKT2	Off
Apoptosis	On
CDH1	Off
CDH2	Off
CTNNB1	Off
CellCycleArrest	On
DKK1	Off
DNA damage	Off
ECMicroenv	Off
EMT	Off
ERK	Off
GF	Off
Invasion	On

# Using MaBoSS with WebMaBoSS

## › Model editing : Parameters

WebMaBoSS

ModelsTutorialsAbout

Cancer models ▾

ProfileLogout

Cohen 2015 Invasion ▾

Overview

Editing

Simulation

Sensitivity

Model Cohen 2015 Invasion

RatesInitial valuesOutputsParametersSettings

\$d_AKT1	1		
\$d_AKT2	1		
\$d_Apoptosis	1		
\$d_CDH1	1		
\$d_CDH2	1		
\$d_CTNNB1	1		
\$d_CellCycleArrest	1		
\$d_DKK1	1		
\$d_DNADamage	1		
\$d_ECMicroenv	1		
\$d_EMT	1		
\$d_ERK	1		
\$d_GF	1		
\$d_Invasion	1		
\$d_Metastasis	1		
\$d_Migration	1		
\$d_NICD	1		
\$d_SMAD	1		
\$d_SNAI1	1		
\$d_SNAI2	1		
\$d_TGFbeta	1		

# Using MaBoSS with WebMaBoSS

## › Model editing : Settings

WebMaBoSS

Models

Tutorials

About

Cancer models ▾

Profile

Logout

Cohen 2015 Invasion ▾

Overview












Editing

Simulation

Sensitivity

### Model Cohen 2015 Invasion

[Rates](#)[Initial values](#)[Outputs](#)[Parameters](#)[Settings](#)

time_tick	0.5	
max_time	40	
sample_count	1000	
discrete_time	0	
use_physrandgen	0	
seed_pseudorandom	0	
display_traj	0	
statdist_traj_count	0	
statdist_cluster_threshold	1	
thread_count	6	
statdist_similarity_cache_max_size	20000	



# Using MaBoSS with WebMaBoSS

## › Sensitivity analysis : General settings

The screenshot displays the WebMaBoSS web application. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. The left sidebar contains a dropdown menu for 'Cohen 2015 Invasion' and a list of options: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and features a 'New sensitivity analysis' button. A modal dialog box titled 'New sensitivity analysis' is open, showing three tabs: 'General', 'Candidates', and 'Output'. The 'General' tab is active, containing a 'Name' field with the placeholder 'Name of the simulation', two toggle switches for 'Single mutations' and 'Double mutations' (both currently off), a 'Local' dropdown menu, a red 'Close' button, and a 'Submit' button.

# Using MaBoSS with WebMaBoSS

## › Sensitivity analysis : Mutant candidates

The screenshot displays the WebMaBoSS web application interface. At the top, there is a navigation bar with links for 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. The main content area is titled 'Model Cohen 2015 Invasion' and includes a sidebar with options like 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. A 'New sensitivity analysis' button is visible in the main area. A modal dialog box titled 'New sensitivity analysis' is open, featuring three tabs: 'General', 'Candidates', and 'Output'. The 'Candidates' tab is active, showing a list of parameters with toggle switches: ERK (on), GF (on), Invasion (off), Metastasis (off), Migration (off), and NICD (on). At the bottom of the dialog, there are 'Close' and 'Submit' buttons.

# Using MaBoSS with WebMaBoSS

## › Sensitivity analysis : Output nodes

The screenshot displays the WebMaBoSS web application interface. The top navigation bar includes 'WebMaBoSS', 'Models', 'Tutorials', 'About', 'Profile', and 'Logout'. The left sidebar shows a menu with 'Cohen 2015 Invasion' selected, and sub-items: 'Overview', 'Editing', 'Simulation', and 'Sensitivity'. The main content area is titled 'Model Cohen 2015 Invasion' and contains a 'New sensitivity analysis' button. A modal dialog box titled 'New sensitivity analysis' is open, showing three tabs: 'General', 'Candidates', and 'Output'. The 'Output' tab is active, displaying a list of nodes with toggle switches: 'AKT1', 'AKT2', 'Apoptosis' (checked), 'CDH1', 'CDH2', and 'CTNND1'. At the bottom of the dialog are 'Close' and 'Submit' buttons.

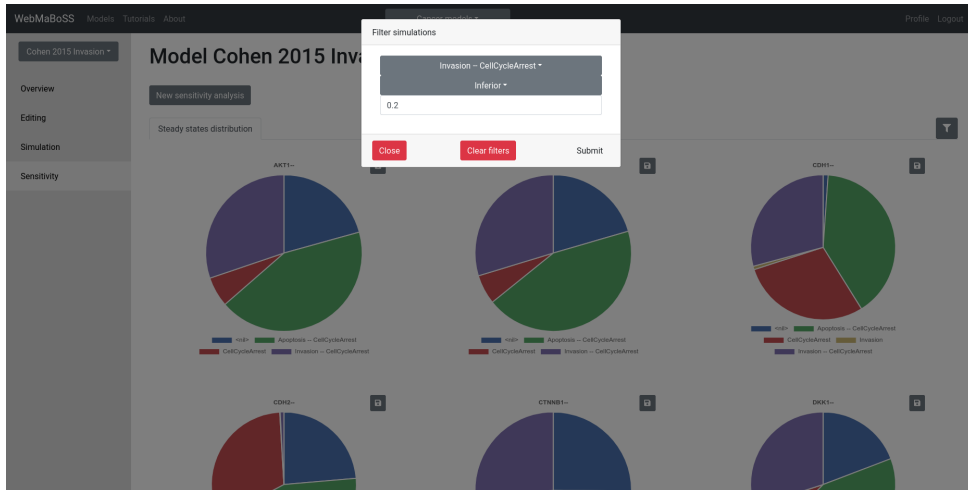
# Using MaBoSS with WebMaBoSS

## › Sensitivity analysis : Results



# Using MaBoSS with WebMaBoSS

## › Sensitivity analysis : Filtering results



# Using MaBoSS with WebMaBoSS

## › Sensitivity analysis : Filtered results



## Using MaBoSS with WebMaBoSS

- › Hands on
  - › Create a new project
  - › Load Cohen's model (bnd and cfg available in manuals/Modules/MaBoss/ folder)
  - › Perform default simulation
  - › Perform simulation with ECMicroenv and DNADamage on

## Using MaBoSS with WebMaBoSS

- › Hands on

- › Perform simulation with NICD++, p53– mutant
- › Perform sensitivity analysis on single mutants, testing only inhibitions
- › Filter mutants where state Invasion – CellCycleArrest is less than 20%