

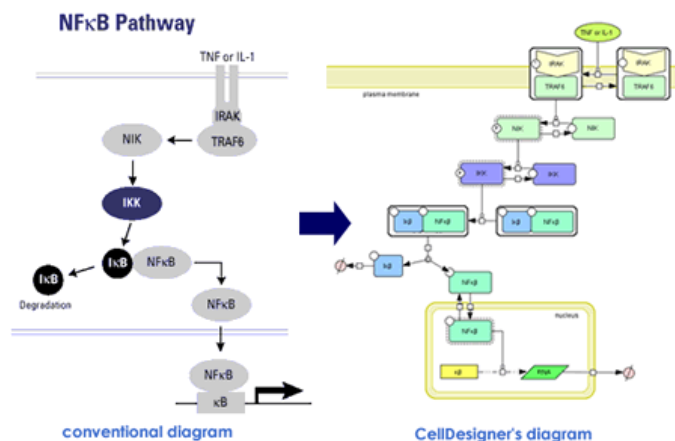
## **Wellcome Connecting Science: Computational Systems Biology – Tool Directory**

This document serves as a directory of the tools discussed and introduced in the Wellcome Connecting Science course on Computational Systems Biology.

### **Tools for Maps:**

Cell Designer (<https://www.celldesigner.org>)

Cell Designer is a tool for generating, building, and manipulating static maps.



Downloadable, not open source, graphical user interface.

Tutorial given: Monday morning.

### **Tool for Converting Maps to Models:**

CaSQ (<https://casq.readthedocs.io/en/stable/>)

CaSQ is a tool that can convert models from a static map to a dynamic model suitable for running in modelling tools such as MaBoSS, GinSim, and BioModelAnalyzer. It takes an .xml file generated by eg. Cell Designer, and converts it to an eg. .sbmlq



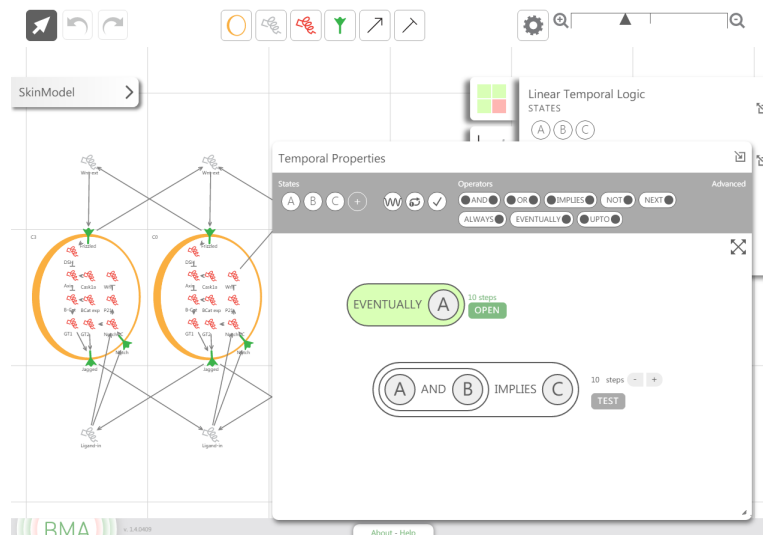
Downloadable, command line/python usage, open source.

Tutorial given: Tuesday morning.

## Tools for Dynamic Modelling:

### BioModelAnalyzer (<https://biomodelanalyzer.org>)

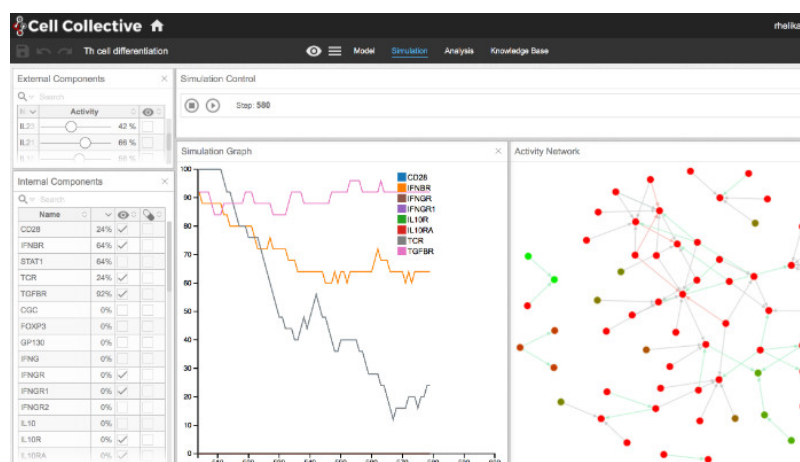
BioModelAnalyzer performs dynamic modelling of networks. It performs synchronous, deterministic modelling. It can perform stability analysis, simulation analysis, and linear temporal logic (logical query) analysis. It runs in a web browser with a click and drag interface. It reads files in .json format.



Web browser (and downloadable), open source, synchronous.  
Tutorial given: Thursday

### Cell Collective (<https://cellcollective.org/>)

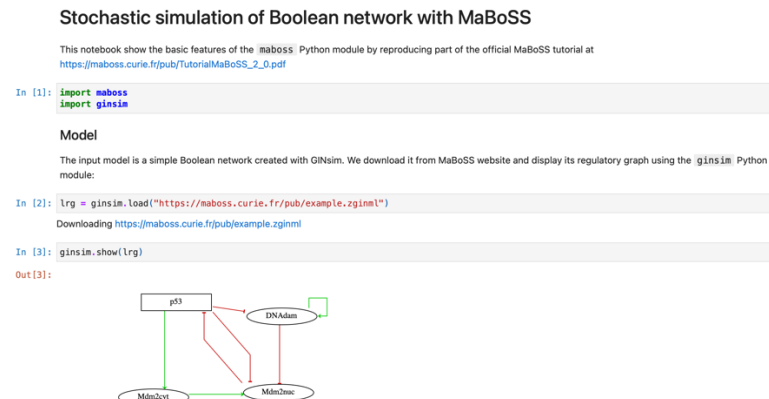
Cell Collective is a toolbox for simulating (and building) dynamic and logical models. It performs synchronous and stochastic modelling. It runs in a web browser with a login and click and drag interface.



Web browser, open source, synchronous, stochastic.  
Tutorial given: Tuesday afternoon

## CoLoMoTo Notebook (<https://colomoto.github.io/colomoto-docker/>)

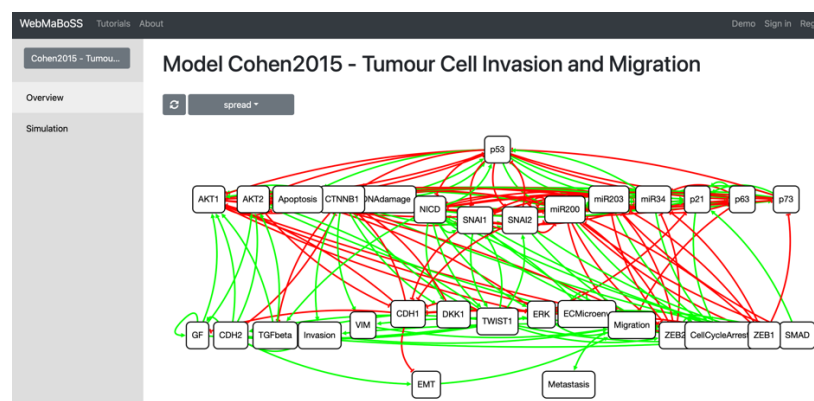
CoLoMoTo Notebooks are a tool for running analysis of Boolean/dynamic models in a jupyter notebook. These notebooks run in python and so can integrate with other tools (eg. Pandas, NetworkX, Matplotlib). Notebooks can be run in a web browser or the tool downloaded and run. It interfaces with many logical modelling tools such as GinSim, MaBoSS, and CellCollective.



Web browser, download, open source, dynamic modelling  
Training given: Thursday morning

## MaBoSS (<https://webmaboss.vincent-noel.fr/>)

MaBoSS performs analysis and simulation of Boolean networks. It runs in a web browser. MaBoSS performs stochastic modelling, and has tools for eg. sensitivity analysis



Web browser, open source, stochastic  
Training given: Wednesday

## Some Model Databases (Not extensive):

Biomodels (<https://www.ebi.ac.uk/biomodels/>)

Atlas of Cancer Signaling (<https://acsn.curie.fr/ACSN2/ACSN2.html>)

Panther Pathways (<https://www.pantherdb.org/pathway/>)