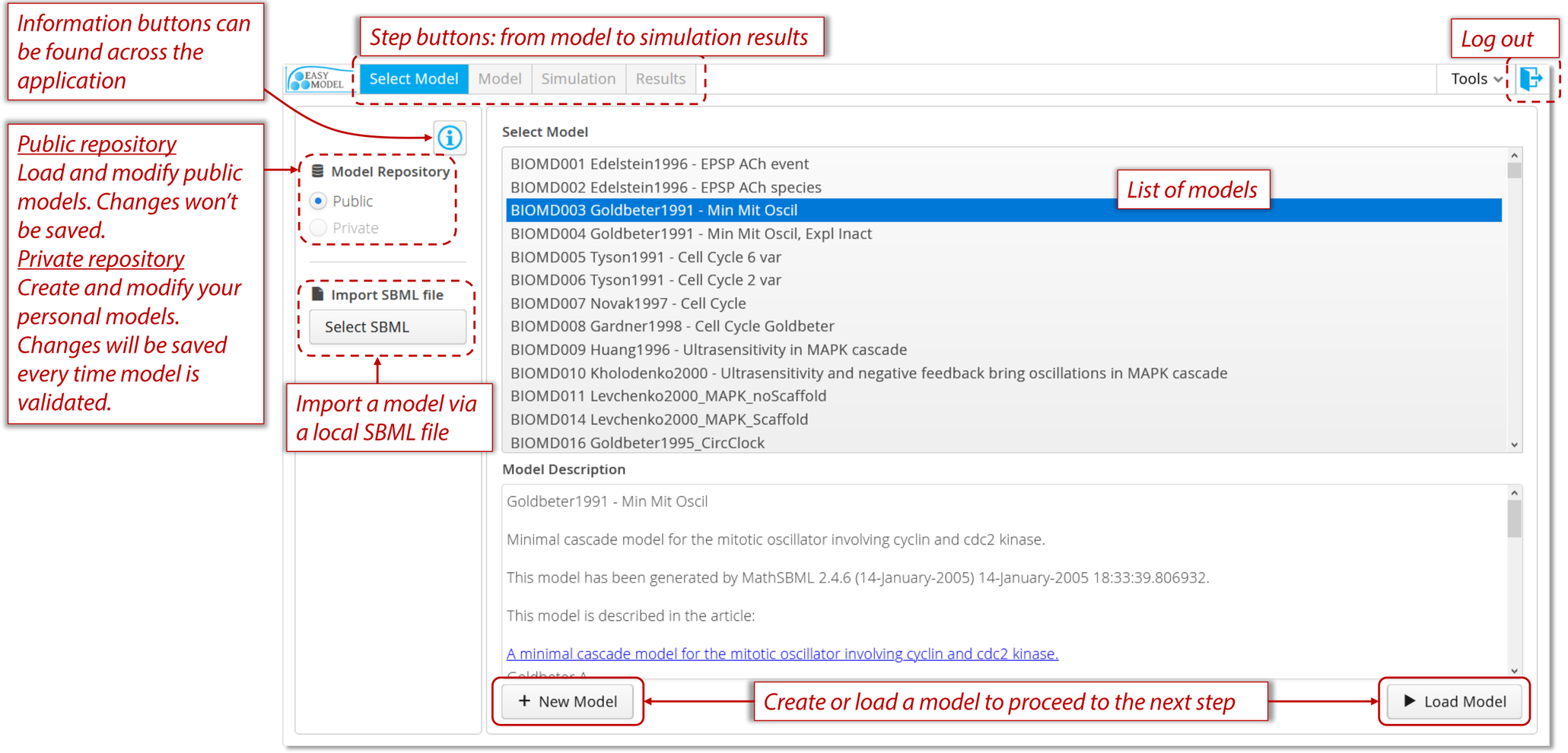
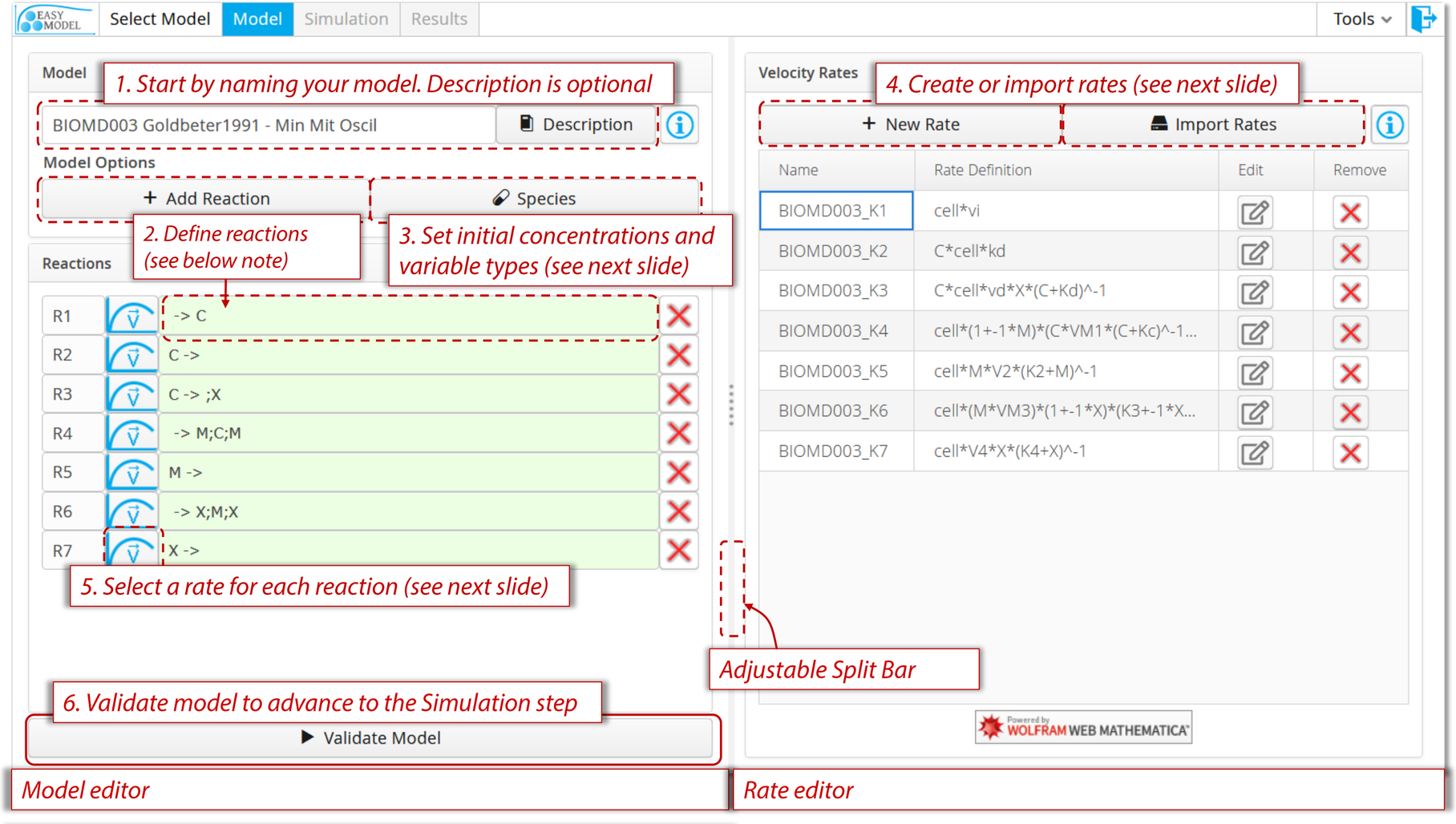
Welcome to EasyModel!

This tutorial will teach you how to model and simulate a systems biology model.

In each slide you will find annotations, indicating how you can use the user interface.

Press next to start the tutorial (or press skip to use EasyModel).


Information buttons can be found across the application
Step buttons: from model to simulation results
Log out
Select Model
Model
Simulation
Results
Tools
Public repository
Load and modify public models. Changes won't be saved.
Private repository
Create and modify your personal models. Changes will be saved every time model is validated.
Model Repository
Public
Private
Import SBML file
Select SBML
Import a model via a local SBML file
Select Model
BIOMD001 Edelstein1996 - EPSP ACh event
BIOMD002 Edelstein1996 - EPSP ACh species
BIOMD003 Goldbeter1991 - Min Mit Oscil
BIOMD004 Goldbeter1991 - Min Mit Oscil, Expl Inact
BIOMD005 Tyson1991 - Cell Cycle 6 var
BIOMD006 Tyson1991 - Cell Cycle 2 var
BIOMD007 Novak1997 - Cell Cycle
BIOMD008 Gardner1998 - Cell Cycle Goldbeter
BIOMD009 Huang1996 - Ultrasensitivity in MAPK cascade
BIOMD010 Kholodenko2000 - Ultrasensitivity and negative feedback bring oscillations in MAPK cascade
BIOMD011 Levchenko2000_MAPK_noScaffold
BIOMD014 Levchenko2000_MAPK_Scaffold
BIOMD016 Goldbeter1995_CircClock
List of models
Model Description
Goldbeter1991 - Min Mit Oscil
Minimal cascade model for the mitotic oscillator involving cyclin and cdc2 kinase.
This model has been generated by MathSBML 2.4.6 (14-January-2005) 14-January-2005 18:33:39.806932.
This model is described in the article:
A minimal cascade model for the mitotic oscillator involving cyclin and cdc2 kinase.
+ New Model
Create or load a model to proceed to the next step
Load Model



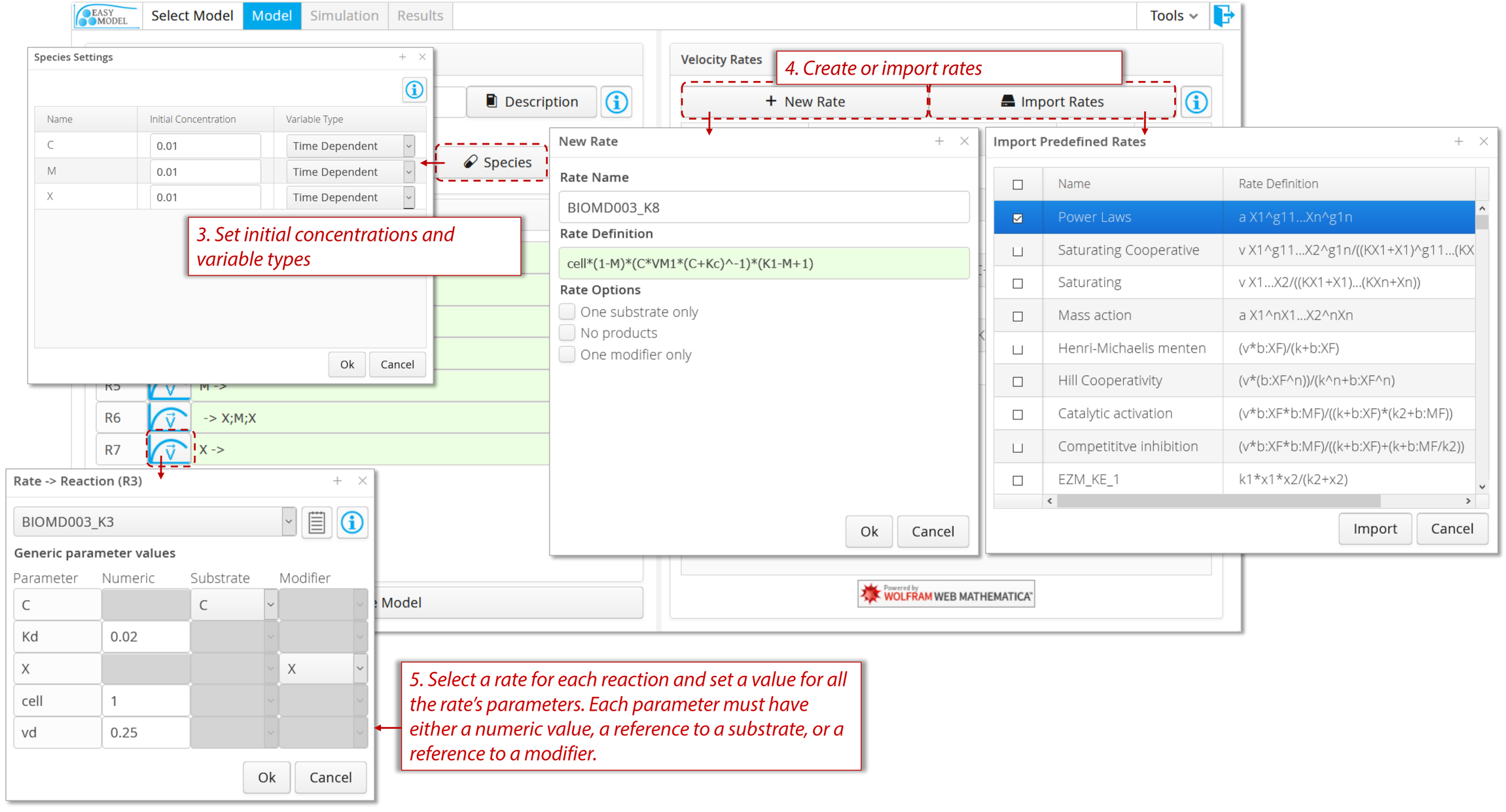
How to write reactions using Substrates, Products and Modifiers:

$n_1*S_1 + n_2*S_2 + \ldots \rightarrow m_1*P_1 + m_2*P_2 + \ldots ; M_1; M_2; \ldots$

n_i, m_i: *Stoichiometric coefficient.*

S_i, P_i: *Substrates and Products.*

M_i: *Modifiers that can activate or inhibit the reaction rate.*


Select Model
Model
Simulation
Results
Tools
Species Settings
Name
Initial Concentration
Variable Type
C
0.01
Time Dependent
M
0.01
Time Dependent
X
0.01
Time Dependent
Ok
Cancel
3. Set initial concentrations and variable types
Description
Species
Velocity Rates
4. Create or import rates
New Rate
Import Rates
New Rate
Rate Name
BIOMD003_K8
Rate Definition
cell*(1-M)*(C*VM1*(C+Kc)^-1)*(K1-M+1)
Rate Options
One substrate only
No products
One modifier only
Ok
Cancel
Import Predefined Rates
Name
Rate Definition
Power Laws
a X1^g11...Xn^g1n
Saturating Cooperative
v X1^g11...X2^g1n/((KX1+X1)^g11...(KX
Saturating
v X1...X2/((KX1+X1)...(KXn+Xn))
Mass action
a X1^nX1...X2^nXn
Henri-Michaelis menten
(v*b:XF)/(k+b:XF)
Hill Cooperativity
(v*(b:XF^n))/(k^n+b:XF^n)
Catalytic activation
(v*b:XF*b:MF)/((k+b:XF)*(k2+b:MF))
Competititve inhibition
(v*b:XF*b:MF)/((k+b:XF)+(k+b:MF/k2))
EZM_KE_1
k1*x1*x2/(k2+x2)
Import
Cancel
R5
M ->
R6
-> X;M;X
R7
X ->
Rate -> Reaction (R3)
BIOMD003_K3
Generic parameter values
Parameter
Numeric
Substrate
Modifier
C
C
Kd
0.02
X
X
cell
1
vd
0.25
Ok
Cancel
5. Select a rate for each reaction and set a value for all the rate's parameters. Each parameter must have either a numeric value, a reference to a substrate, or a reference to a modifier.
Model
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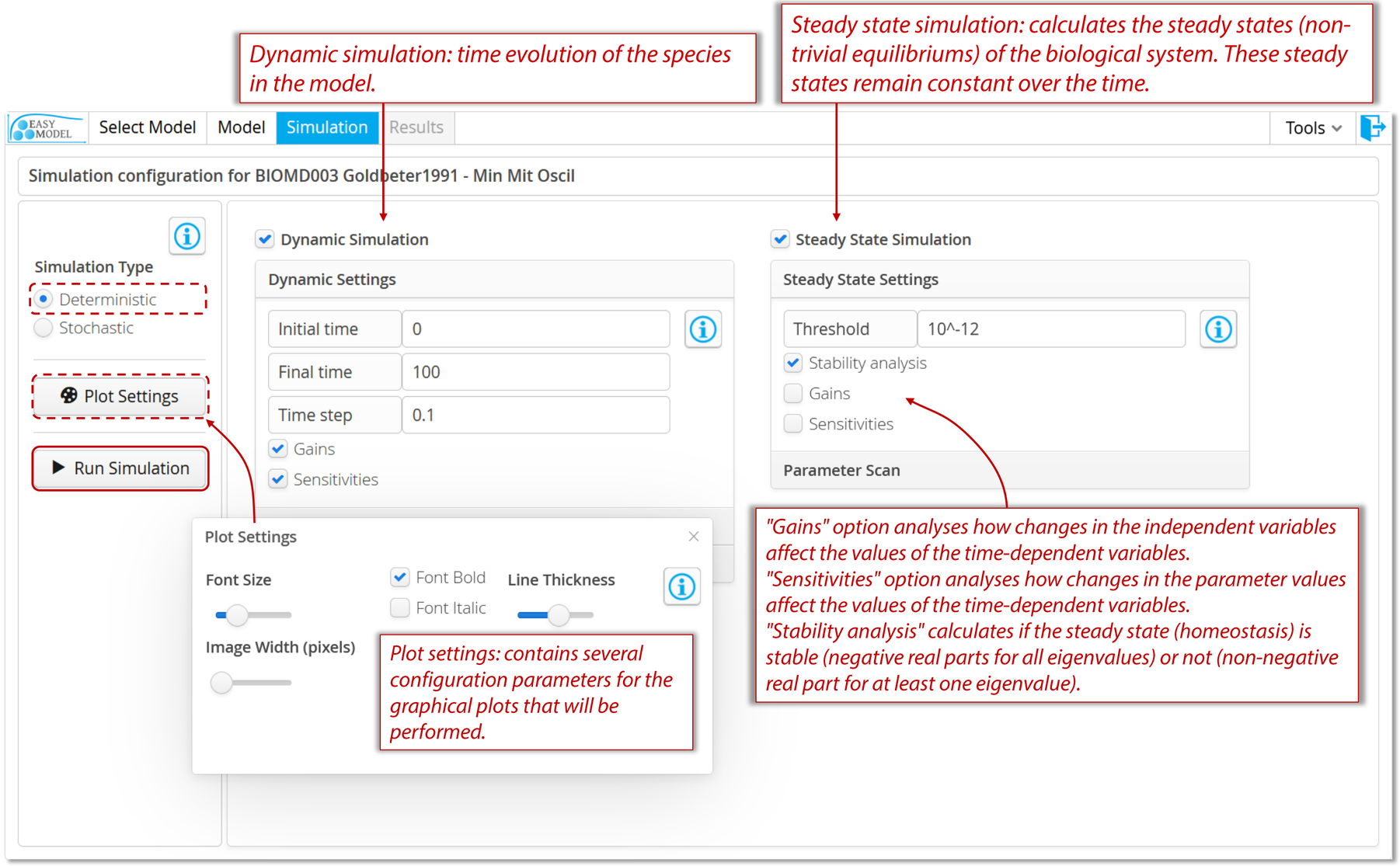
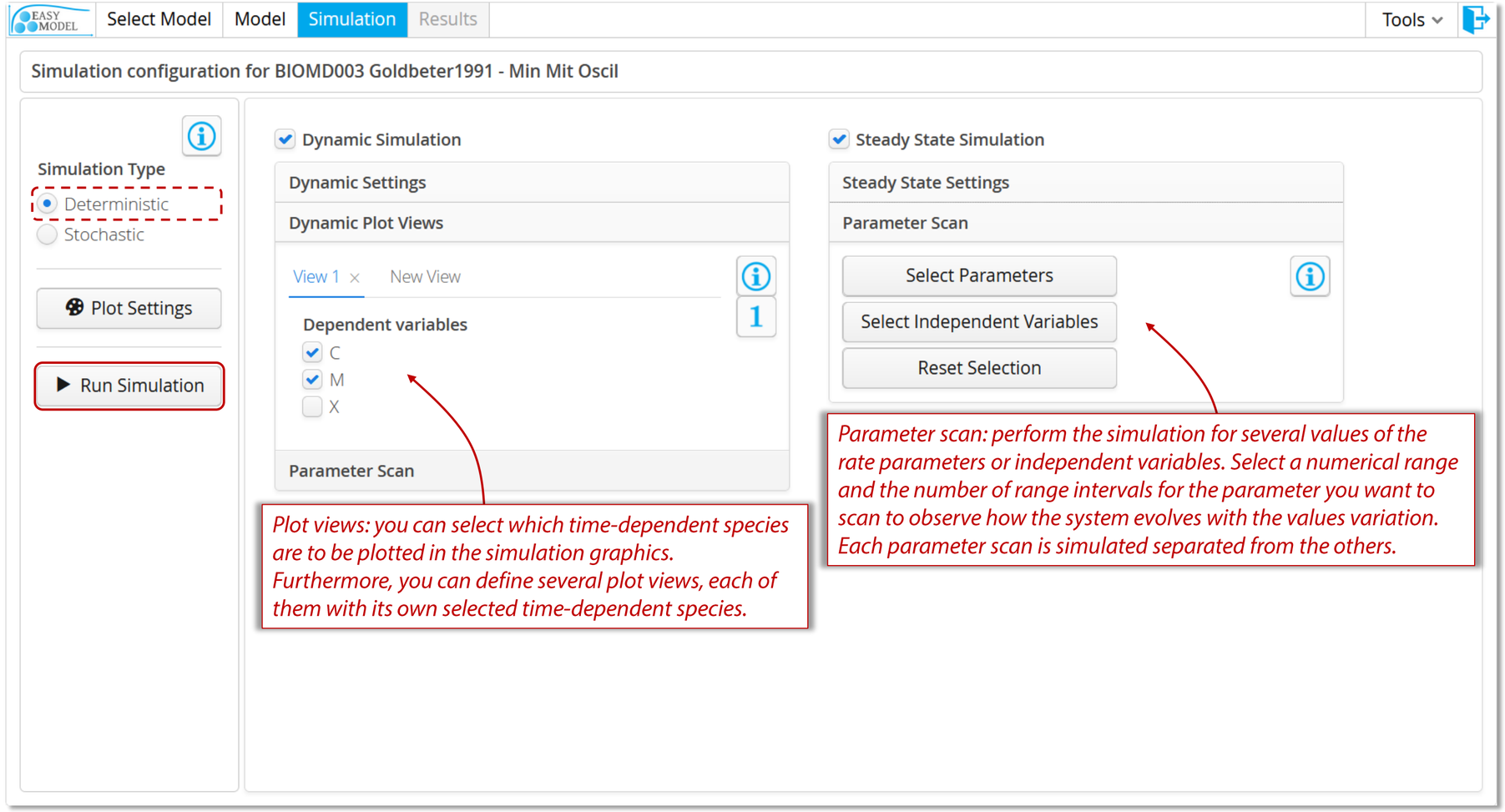
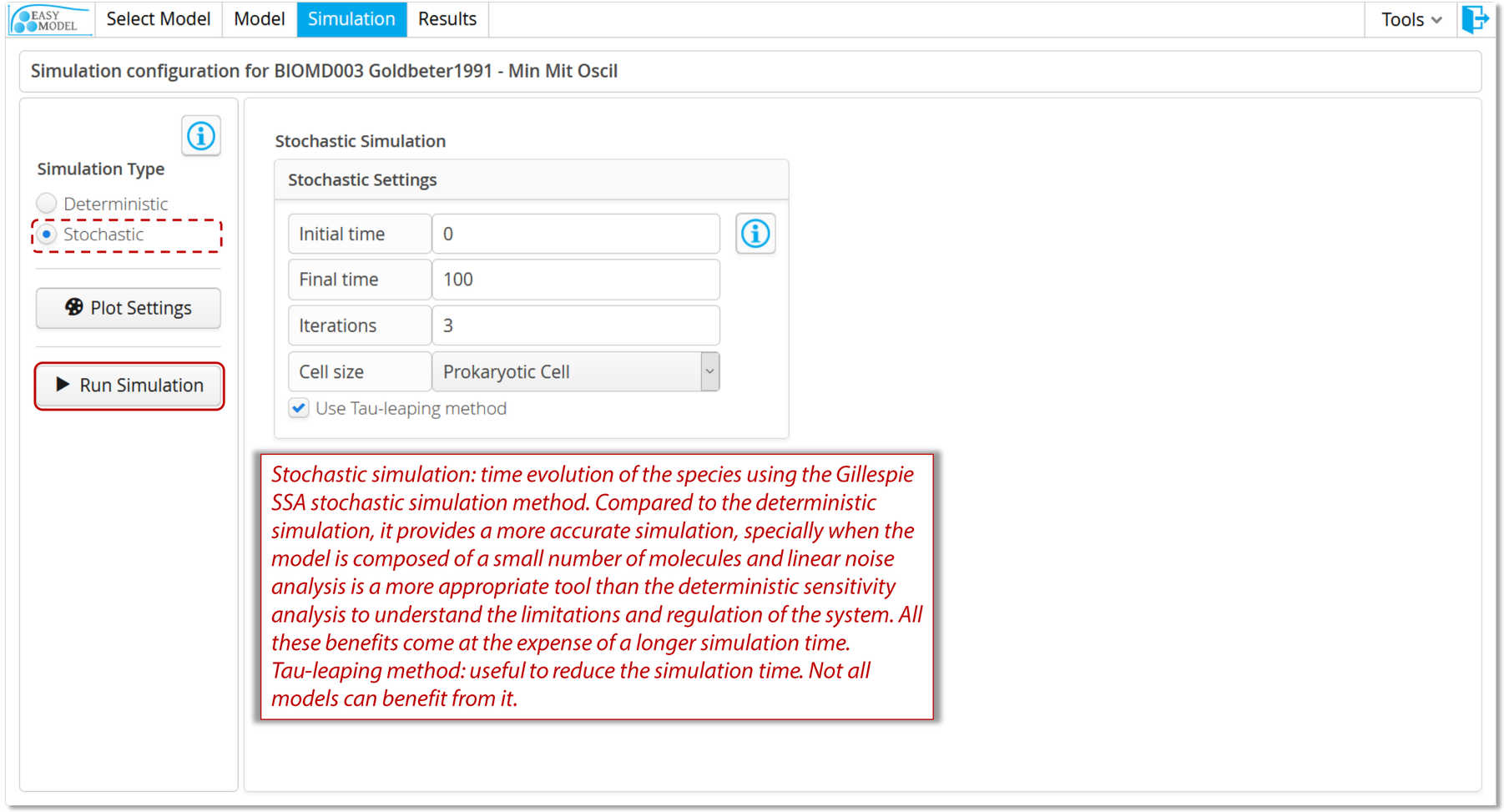

Dynamic simulation: time evolution of the species in the model.
Steady state simulation: calculates the steady states (non-trivial equilibriums) of the biological system. These steady states remain constant over the time.
EASY MODEL
Select Model
Model
Simulation
Results
Tools
Simulation configuration for BIOMD003 Goldbeter1991 - Min Mit Oscil
Simulation Type
Deterministic
Stochastic
Plot Settings
Run Simulation
Dynamic Simulation
Dynamic Settings
Initial time
0
Final time
100
Time step
0.1
Gains
Sensitivities
Steady State Simulation
Steady State Settings
Threshold
10^-12
Stability analysis
Gains
Sensitivities
Parameter Scan
Plot Settings
Font Size
Font Bold
Font Italic
Line Thickness
Image Width (pixels)
Plot settings: contains several configuration parameters for the graphical plots that will be performed.
"Gains" option analyses how changes in the independent variables affect the values of the time-dependent variables.
"Sensitivities" option analyses how changes in the parameter values affect the values of the time-dependent variables.
"Stability analysis" calculates if the steady state (homeostasis) is stable (negative real parts for all eigenvalues) or not (non-negative real part for at least one eigenvalue).

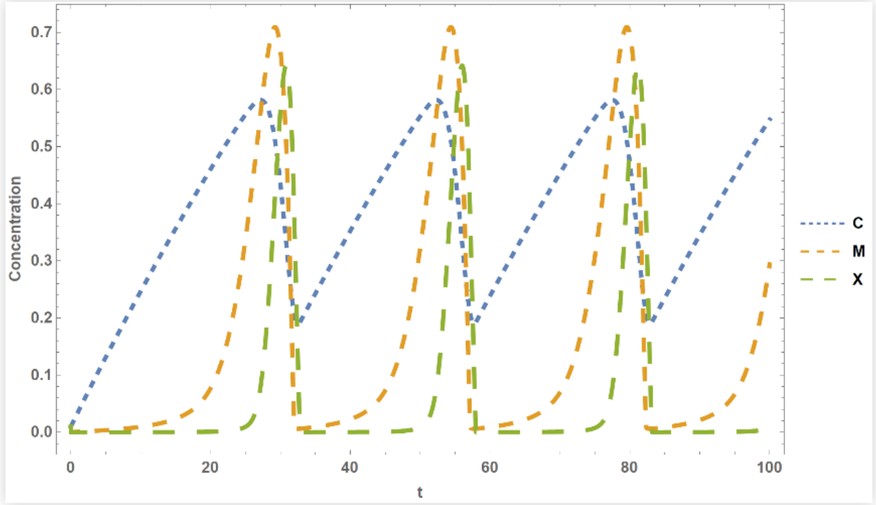

EASY MODEL
Select Model
Model
Simulation
Results
Tools
Simulation configuration for BIOMD003 Goldbeter1991 - Min Mit Oscil
Simulation Type
Deterministic
Stochastic
Plot Settings
Run Simulation
Dynamic Simulation
Dynamic Settings
Dynamic Plot Views
View 1
New View
Dependent variables
C
M
X
Parameter Scan
Steady State Simulation
Steady State Settings
Parameter Scan
Select Parameters
Select Independent Variables
Reset Selection
Plot views: you can select which time-dependent species are to be plotted in the simulation graphics. Furthermore, you can define several plot views, each of them with its own selected time-dependent species.
Parameter scan: perform the simulation for several values of the rate parameters or independent variables. Select a numerical range and the number of range intervals for the parameter you want to scan to observe how the system evolves with the values variation. Each parameter scan is simulated separated from the others.


EASY MODEL
Select Model
Model
Simulation
Results
Tools
Simulation configuration for BIOMD003 Goldbeter1991 - Min Mit Oscil
Simulation Type
Deterministic
Stochastic
Plot Settings
Run Simulation
Stochastic Simulation
Stochastic Settings
Initial time
0
Final time
100
Iterations
3
Cell size
Prokaryotic Cell
Use Tau-leaping method
Stochastic simulation: time evolution of the species using the Gillespie SSA stochastic simulation method. Compared to the deterministic simulation, it provides a more accurate simulation, specially when the model is composed of a small number of molecules and linear noise analysis is a more appropriate tool than the deterministic sensitivity analysis to understand the limitations and regulation of the system. All these benefits come at the expense of a longer simulation time.
Tau-leaping method: useful to reduce the simulation time. Not all models can benefit from it.

EASY MODEL | Select Model | Model | Simulation | Results | Tools

Results for BIOMD003 Goldbeter1991 - Min Mit Oscil

Dynamic Simulation



Download Dynamic Simulation Table

Generated Files

Mathematica Notebook | SBML

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The simulation results are displayed in the final step.
Clicking the cancel button aborts the simulation.

Left-click images for high-resolution copies.

You can download:
-Images.
-Results text files.
-Mathematica Notebook of the model and simulation.
-SBML file of your model.

Simulation finished

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You have completed the tutorial!

Press next to start using EasyModel.