

Building a treatment train

From Wswiki

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1 Introduction

Water companies have to focus on reduction of costs, improvement of product quality, better use of energy resources and reduction of environmental emissions. Automation of drinking water treatment plants results in such an improvement. Costs for chemicals can be decreased, when changes in flow rate automatically result in changes in operations.

Water quality models can be used for improvement of product quality, optimisation of chemical use and savings on energy costs. By combining flow prediction with quality modelling a more advanced control of a treatment plant is possible.

Stimela is an environment for standardised mathematical models of drinking water treatment processes. Stimela is developed by Delft University of Technology and DHV and is especially designed for water quality modelling in drinking water treatment. Stimela models of drinking water treatment processes calculate changes of the water quality parameters, such as pH, oxygen concentration, DOC concentration etc., with regard to design values and settings of operational parameters.

All Stimela models are made in a standard format with a standardised handling of the models' input and output. The standardisation enables the users to connect the models in serial or parallel order with an easy drag and drop action. The output of the first model is the input for the second model, thus simulating a complete drinking water treatment plant, starting with a raw water input block.

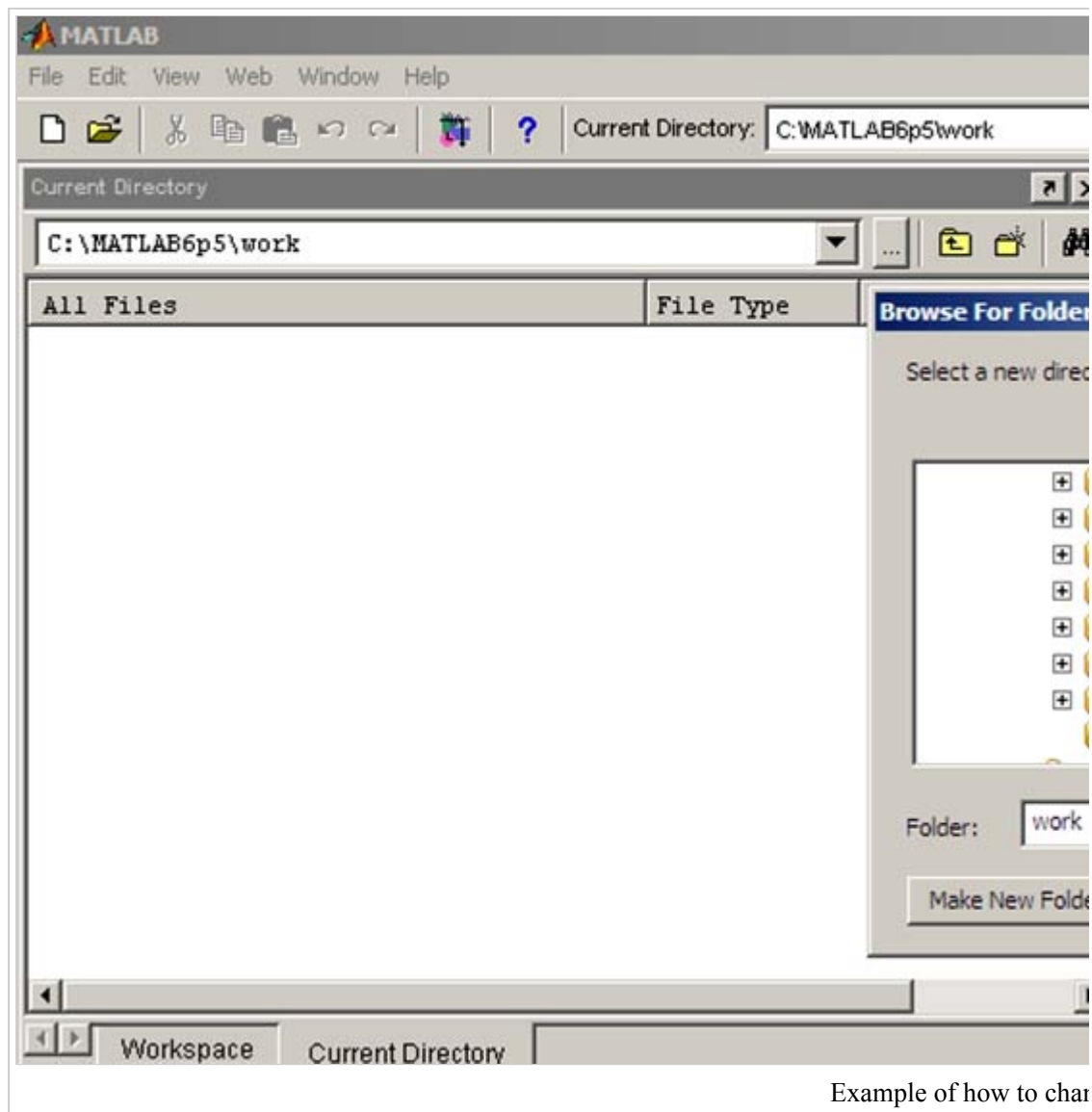
The Stimela environment is built within Matlab/Simulink[®] which is suitable for mathematical modelling. Stimela combines a user friendly interface with graphical visualisation of the results, without the necessity for users to learn Matlab[®] or Simulink[®]. Stimela can be used for a number of purposes, such as:

- optimisation of drinking water treatment processes
- design of drinking water plants
- education by increasing the insight in the parameters influencing the processes
- research

2 Getting started

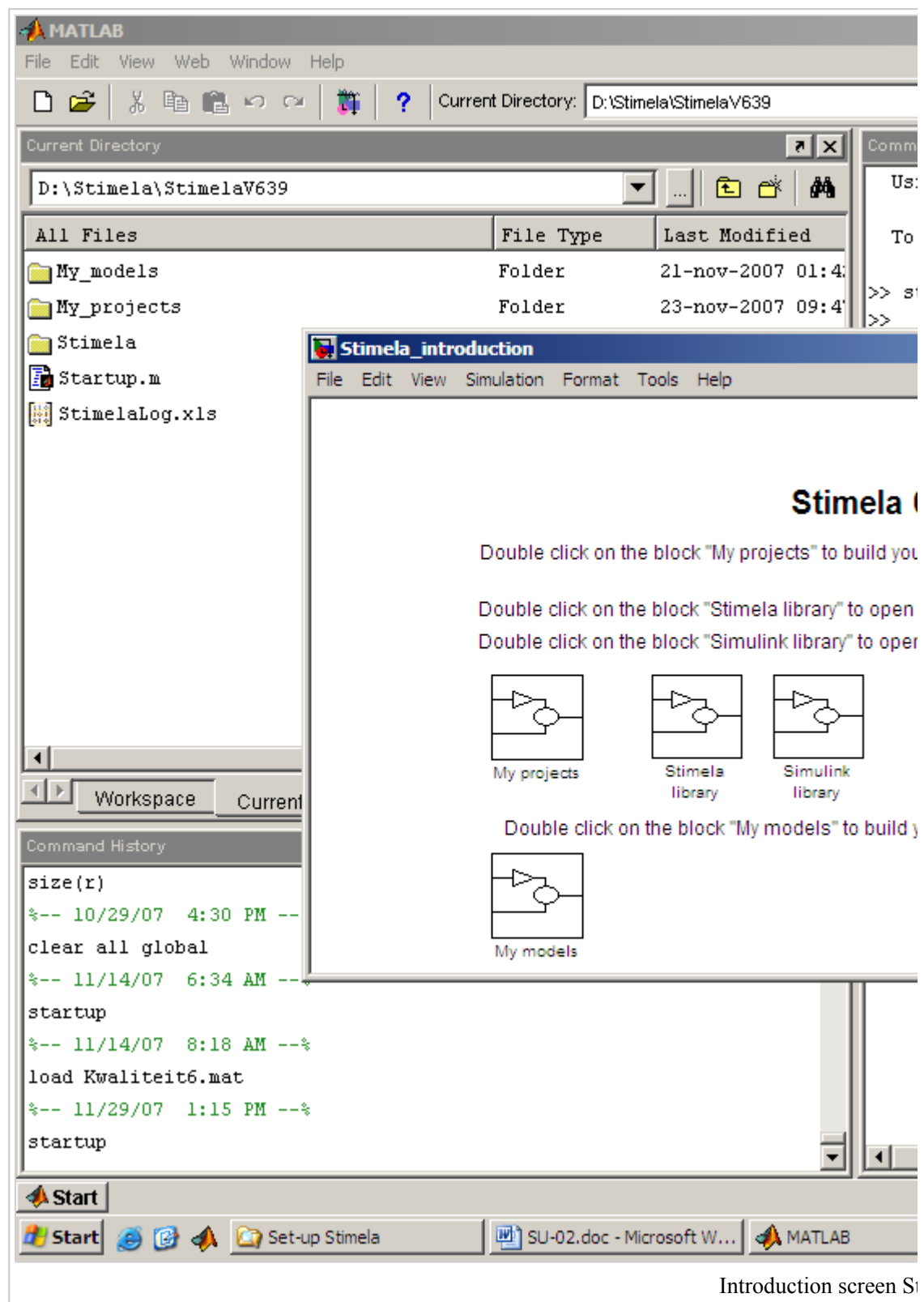
Stimela can be started as follows:

- First make sure you are in the Stimela directory in Matlab. How to change the directory in Matlab is indicated in the next figure.



- Then Stimela can be started by typing behind Matlab prompt: `>>Startup`

Stimela will start and the introduction screen will appear, see the figure below.



Introduction screen S

There now are four possibilities to proceed:

- My projects,

- My models,
- Stimela library,
- Simulink library.

My projects

My projects should be used when a calculation is needed of a of a treatment plant (project) consisting of one or more treatment steps without altering the equations of the models, but by changing the raw water influent parameters, the control parameters and the process parameters. How to build your own project is described in Chapter 8.

My models

My models is used when the user is not satisfied with the existing models and wants to make changes in the core of the models, such as the basic equations that describe the model. When the model is tested extensively it can be sent to the Stimela developers with a suggestion to add the new model to the basic Stimela models hence resulting in a new Stimela release. A detailed description of how to make your own model is described in Chapter 5.

Stimela library

The ‘Stimela library’ is a collection of the models that can be used for building your own project. In Chapter 6 the Stimela library is handled in more detailed.

Simulink library

The ‘Simulink library’ contains numerous building blocks, Simulink blocks, which can be used as extra tools while building models, see Chapter 7.

3 Basic concepts

Models and projects

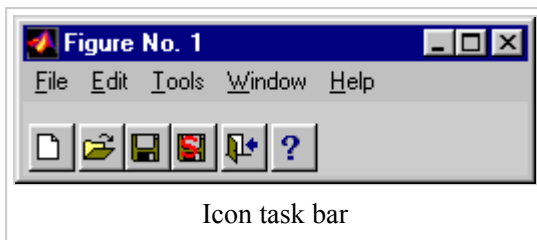
In Stimela the terms ‘Model’ and ‘Project’ are used. The term ‘Model’ indicates a treatment system from the Stimela library. A ‘Project’ consists of one or more models, and at least holds the basic module ‘Import raw water’. When working with a project, calculations can be performed ranging from a single treatment step to a complete water treatment system, defined by the user itself.

Simulation

Simulation is the execution of a calculation.

Icon task bar

In the next figure the icons are shown which occur when altering one of the editor screens.



Open file

When clicking the second icon an existing file can be opened.

Save

With the third icon the file can be saved.

Save as

The fourth icon can be used when a file is preferably saved under a new name.

Exit

The fifth icon is used to exit the screen.

Help

The sixth icon can be used to open a help file, if available.

Decimals

The decimal separator is a period(.), not a comma (,).

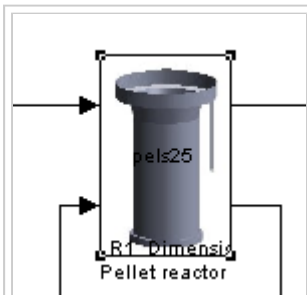
One project at a time

When a project is opened, the work directory in Matlab is automatically adjusted. It is possible that two projects are opened at the same time, however the current directory is the one of the project opened last. If after a simulation of the latest opened project a simulation of the formerly opened project is started error messages will probably pop-up. By closing this project and re-opening it the correct directory will be set, solving the error messages. These problems can be prevented by just opening one project at a time, and wait with opening a new project until the simulation of the former project was finished.

4 Setup of a Stimela model block

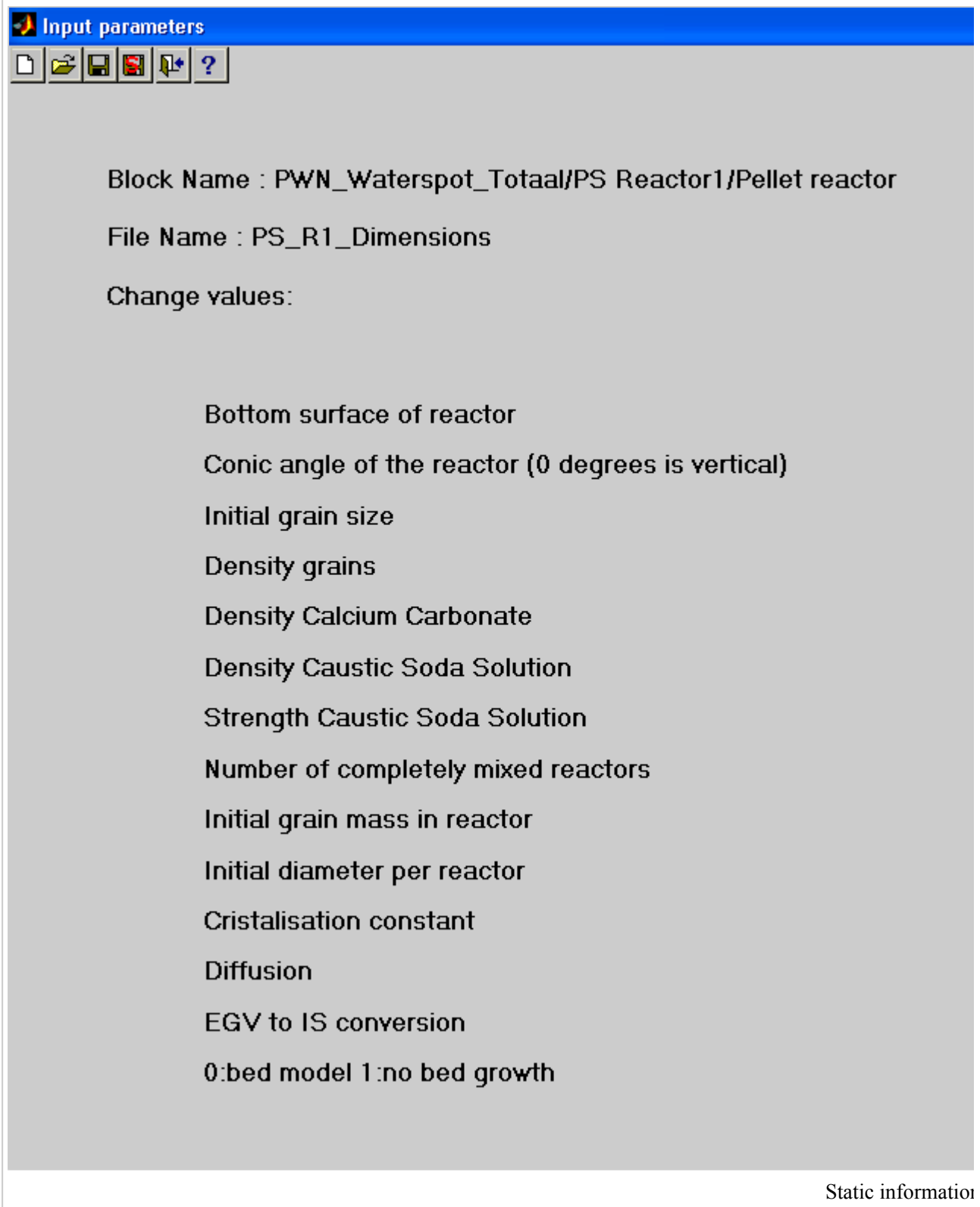
All Stimela models, including the standard models like 'pels25' for softening, 'cascad' for cascade aeration, and 'dubfil' for a dual media rapid sand filter, have a similar structure. From the outside, on the left side, each model has two arrows entering the model block, of which the lower one is

optional. The upper arrow is the input for the water quality and flow, the lower one contains extra control information. On the right side two lines leave the model block of which the lower one is optional. The upper line contains water quality and flow information of the outgoing water, the lower line contains extra measurements.



Each model block has two inputs and two outputs.

When double clicking the model block, the static information of the model is given, such as the dimensions.



Input parameters

Block Name : PWN_Waterspot_Totaal/PS Reactor1/Pellet reactor

File Name : PS_R1_Dimensions

Change values:

Bottom surface of reactor

Conic angle of the reactor (0 degrees is vertical)

Initial grain size

Density grains

Density Calcium Carbonate

Density Caustic Soda Solution

Strength Caustic Soda Solution

Number of completely mixed reactors

Initial grain mass in reactor

Initial diameter per reactor

Cristalisation constant

Diffusion

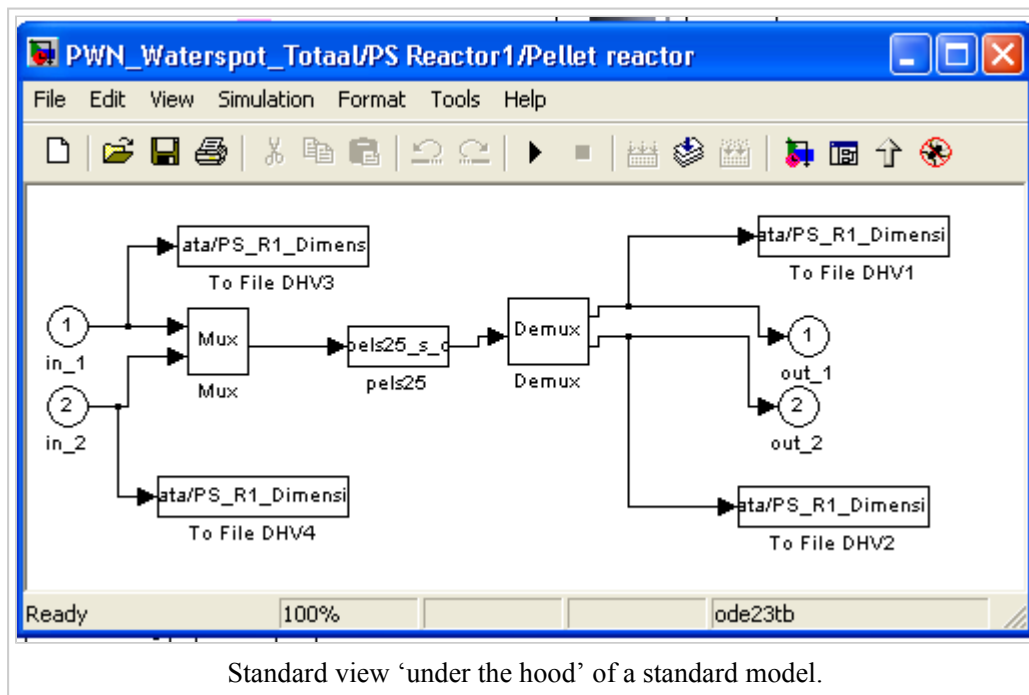
EGV to IS conversion

0:bed model 1:no bed growth

Static information

Notice that the first time when the static information form is opened, the file name is 'unknown'. When a model is used in a project (see chapter 7) use the save as button to save the file containing the static information. When save as is selected the Stimela data folder is opened, which is the right place to save the file. In the last figure, the chosen file name is 'PS_R1_dimensions'. After closing the file using the exit button the file name is shown in the model block too. For more explanation on the icons, see Chapter 2.

When we look ‘under the hood’ of the model block (right mouse menu), we see the standard model in the middle, in this example ‘pels25’.



Standard view ‘under the hood’ of a standard model.

The addition ‘_s’ means it is an s-function file, containing the code of the model. When we look in the folder containing this _s file, we see more models with the same file name apart from the extension. Each ‘_extension’ has a specific purpose (see table).

Meaning of extensions in the standard model folders

<u>d</u>	
<u>f</u>	
<u>g</u>	Graphics, to plot the results in graphs
<u>i</u>	
<u>m</u>	
<u>p</u>	
<u>s</u>	s function: the actual model code
<u>s_c</u>	s function, migrated to C++ code
<u>c</u>	

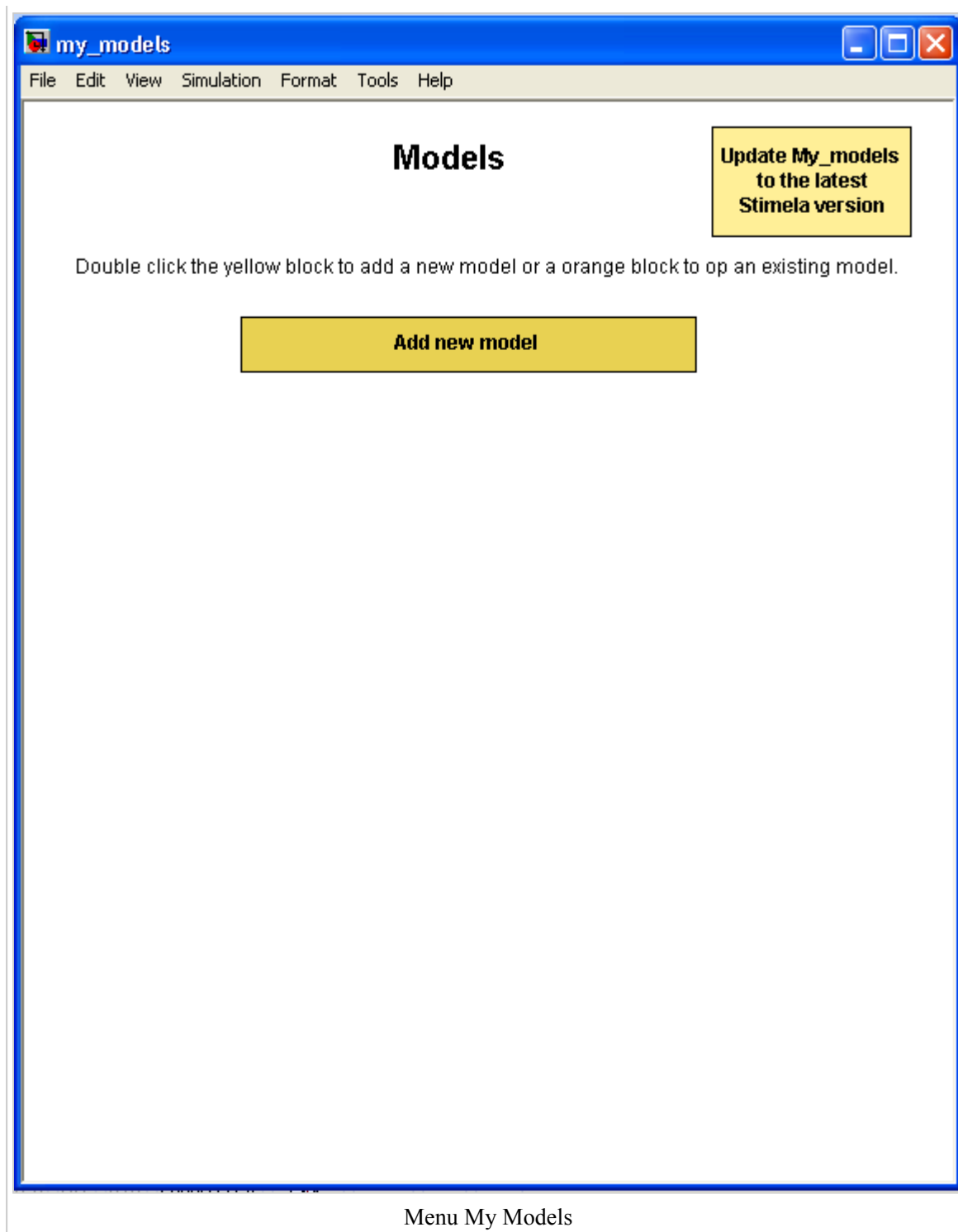
The ‘Mux’ block groups information, the ‘Demux’ block splits the information streams. The upper left arrow is the incoming water quality. This data is written to a .mat file named after the filename containing the static information of the model used in this place (in this example ‘PS_R1_Dimensions’) followed by _in.sti (in the example PS_R1_Dimensions_in.sti). Although the

extension is ‘.sti’ the file is a ‘.mat’ file. The optional control information, left under, is written to {file name}_ES.sti, the effluent water quality, right upper line, is written to {file name}_out.sti and the extra measurements are written to {file name}_EM.sti. All these files are stored in the Stimeladata folder of the project where they belong to:

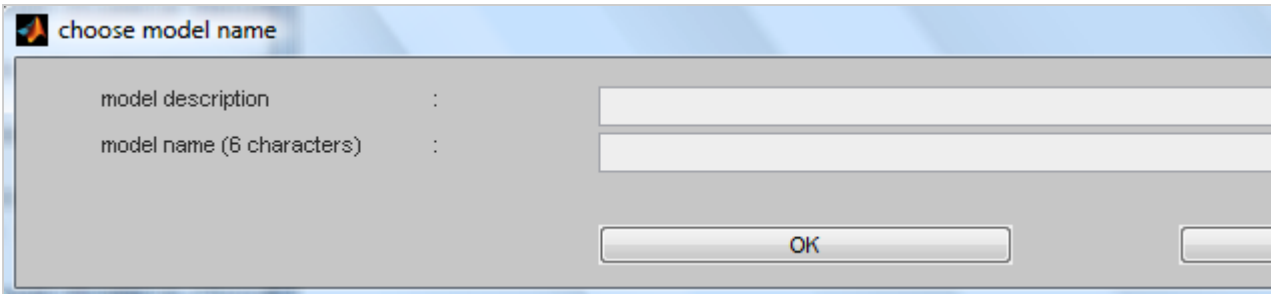
\StimelaV{Stimela_version_number}\My_projects\{project_name}\StimelaData.

5 Develop a new or improve an existing model

In the introduction screen of Stimela (see Chapter 2) the option ‘my Models’ is available. This is the part where you can start to develop a new model or improve an existing model. A model is a standard building block (typically one treatment step) in a project. If ‘my Models’ is double clicked, the next figure pops up.



By double clicking 'Add new project' a pop-up is generated in which the new project name should be typed, see the figure below.



choose model name

model description :

model name (6 characters) :

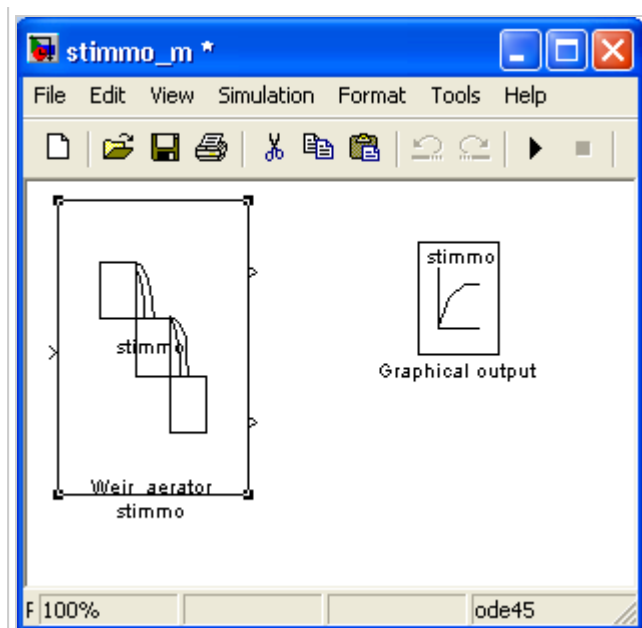
OK

Choose the new model name

By changing the name followed by <OK> a new screen appears in which the template for the new model can be selected. In this list all standard models available within Stimela are given.



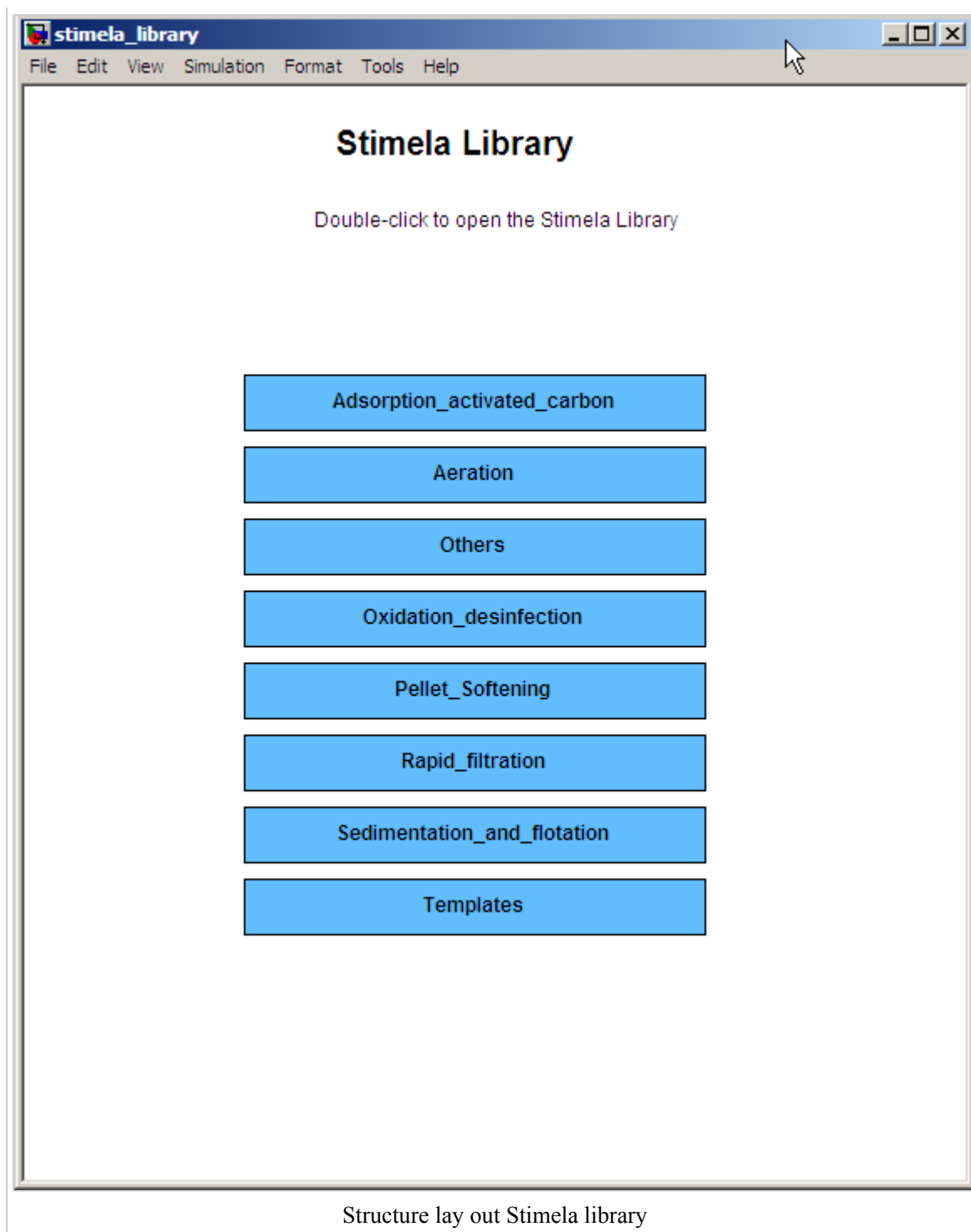
When the template for the new model is chosen this window is opened.



Example weir aerator as template for new model

6 Stimela library

Stimela uses so called libraries. The libraries are a collection of pre-programmed functions and models which can be used by building a new project. The libraries have different levels.



The Stimela library can be opened by double clicking the 'Stimela library' button in the Stimela introduction screen (see SU-02). As indicated by Figure 1 the Stimela library contains several libraries, such as Adsorption_activated_carbon, Aeration, Others, Oxidation_desinfection, Pellet_Softening, Rapid_filtration, Sedimentation_and_flotation and Templates. Each of these libraries contains one or more models regarding this topic. An overview of the library structure is given in the figure below.

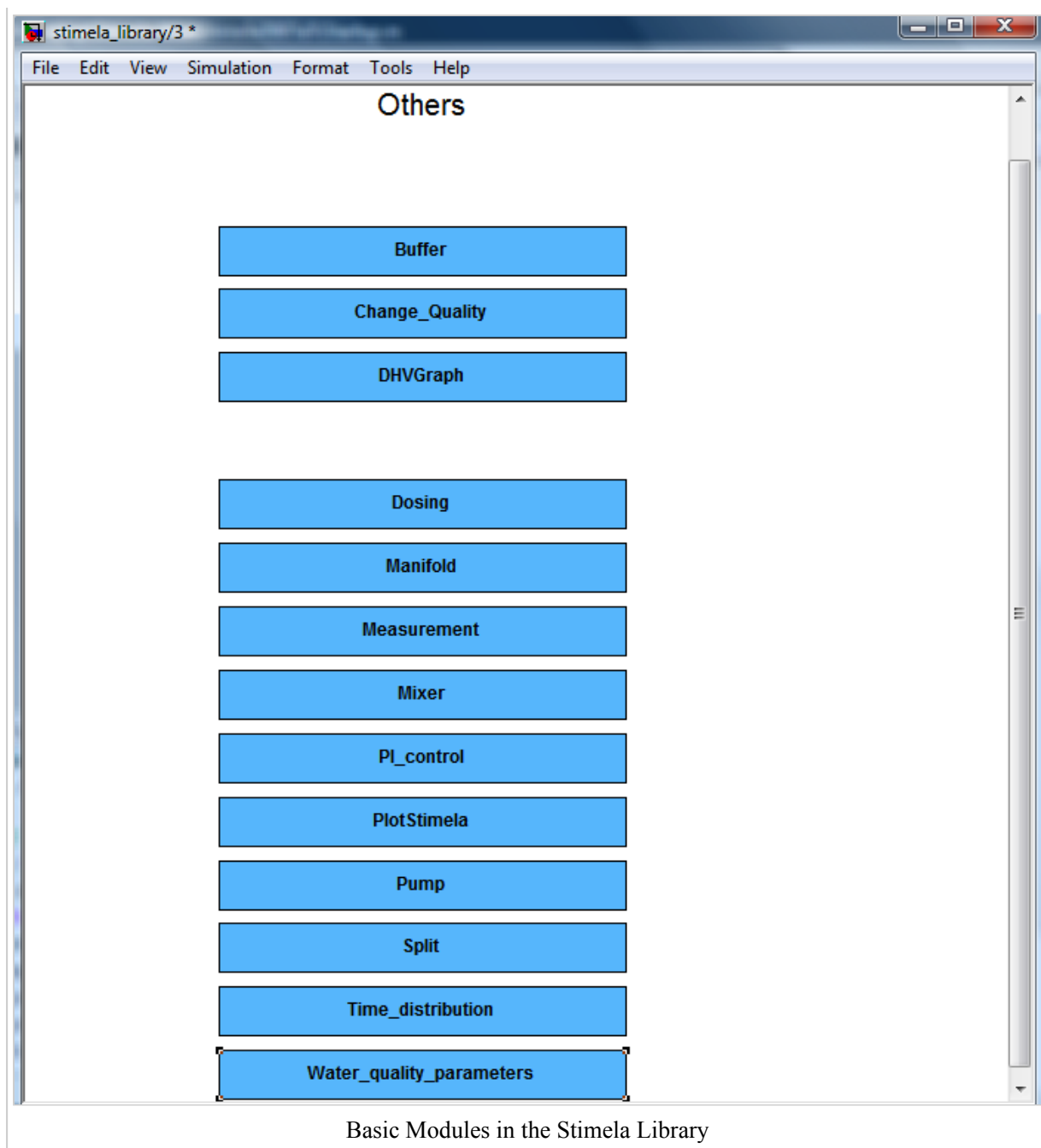
Adsorption_Activated_carbon	Aeration	Others	Oxidation_desinfection	Pellet_softening
GAC_filtration	Cascade_aerator	Buffer	Chloramination*	Caustic_soda_dosing
PAC_dosing	Plate_aerator	DHV_graph	Chlorine*	Lime_dosing
Regenerate_module	Tower_aerator	Dosing	Chlorine_dioxide*	
	Vacuum_degassifier_continuous	Manifold	Dechlorination*	
	Vacuum_degassifier_discontinuous	Measurements	Ozone	
		Mixer	Ozone_dosage	
		PI_control	UV_peroxide*	
		PlotStimela		
		Pump		
		Split		
		Time_distribution		
		Waterquality_params		

Overview all stimela models. Models marked with an asterisk have not yet been implemented.

In the next section, some of the models under the header "Others" will be discussed. The other models concern water treatment processes and are discussed in the section on Stimela Model Descriptions, which can be found on the main page of this Waterspot Wiki.

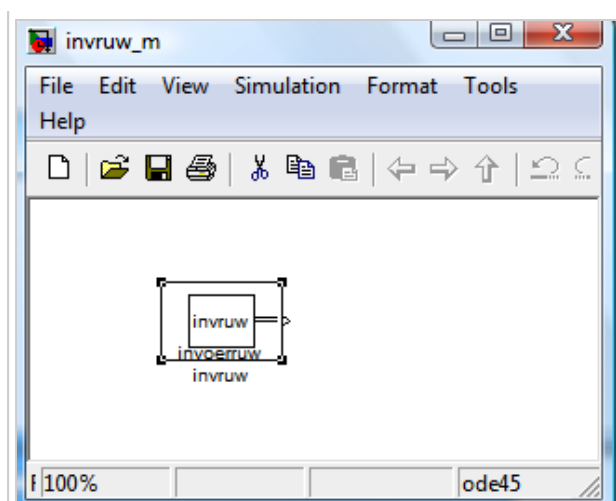
6.1 Basic modules

Some modules are used in a lot of (if not all) projects. These modules are shown in the next figure. We will now discuss these basic modules.



6.1.1 Water quality parameters

This basic module is included in any project, because it provides the input for the model. With the basic module Water quality parameters the different water quality parameters for the raw water can be filled out. The block for the Water quality parameters and its input screen are displayed below.



The water quality parameter block

Block Name : invruw_m/invruw

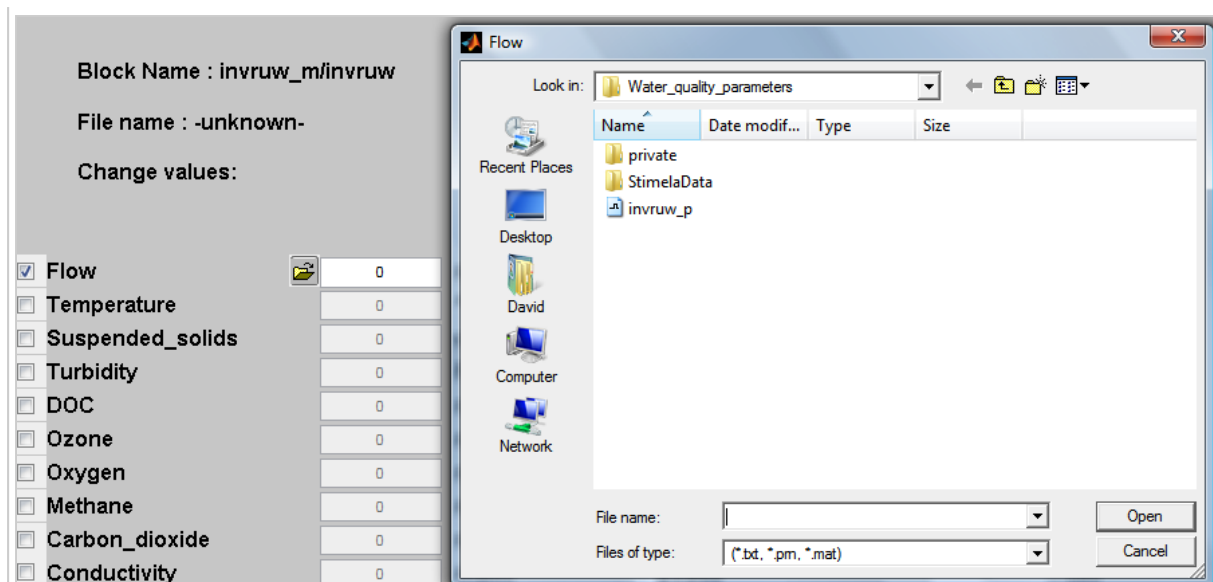
File name : -unknown-

Change values:

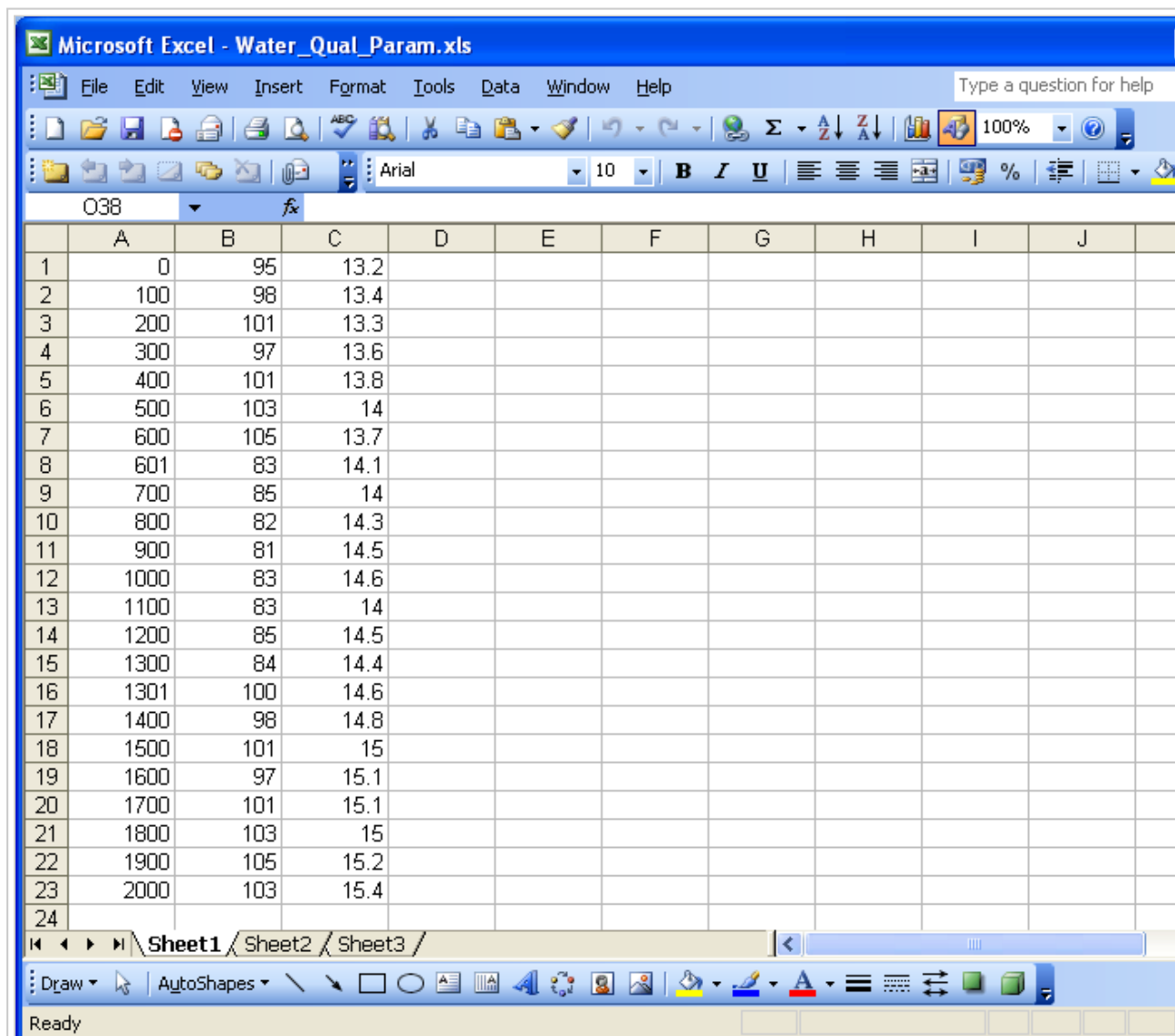
<input type="checkbox"/> Flow	<input type="text" value="0"/>	m ³ /h	<input type="checkbox"/> Ammonia
<input type="checkbox"/> Temperature	<input type="text" value="0"/>	°C	<input type="checkbox"/> Nitrite
<input type="checkbox"/> Suspended_solids	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Nitrate
<input type="checkbox"/> Turbidity	<input type="text" value="0"/>	FTE	<input type="checkbox"/> Phosphate
<input type="checkbox"/> DOC	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Bicarbonate
<input type="checkbox"/> Ozone	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> pH
<input type="checkbox"/> Oxygen	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Mnumber
<input type="checkbox"/> Methane	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Pnumber
<input type="checkbox"/> Carbon_dioxide	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Ionstrength
<input type="checkbox"/> Conductivity	<input type="text" value="0"/>	mS/m	<input type="checkbox"/> UV254
<input type="checkbox"/> Iron2	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Bromide
<input type="checkbox"/> Iron3	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Sulphate
<input type="checkbox"/> Calcium	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Virusses
<input type="checkbox"/> Magnesium	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Giardia
<input type="checkbox"/> Calcium_carbonate	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Cryptosporidium
<input type="checkbox"/> Nitrogen	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Trichlooretheen
<input type="checkbox"/> Hydrogen_sulfide	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Dichloorpropaan
<input type="checkbox"/> Atrazine	<input type="text" value="0"/>	mg/l	<input type="checkbox"/> Volatile_compound

The water quality parameters

In the input screen, checkboxes are placed in front of each water quality parameter. By checking the box, the parameter is being taken into account in the model and the value can be changed. Click on the folder icon to enter a series. A selection screen appears, where text files (*.txt), formatted text (space delimited) files (*.prn) and matlab files (*.mat) can be selected. An example of a series is shown in the figure below. The first column is the time in seconds, while the second and third column represent the flow. Which column is used depends on which column is selected when asked by Stimela. The series has been made in Excel, but can be saved as a text file by clicking save as and then "different file type" in Excel. An import aspect is that a point needs to be used as a decimal separator and not a comma.



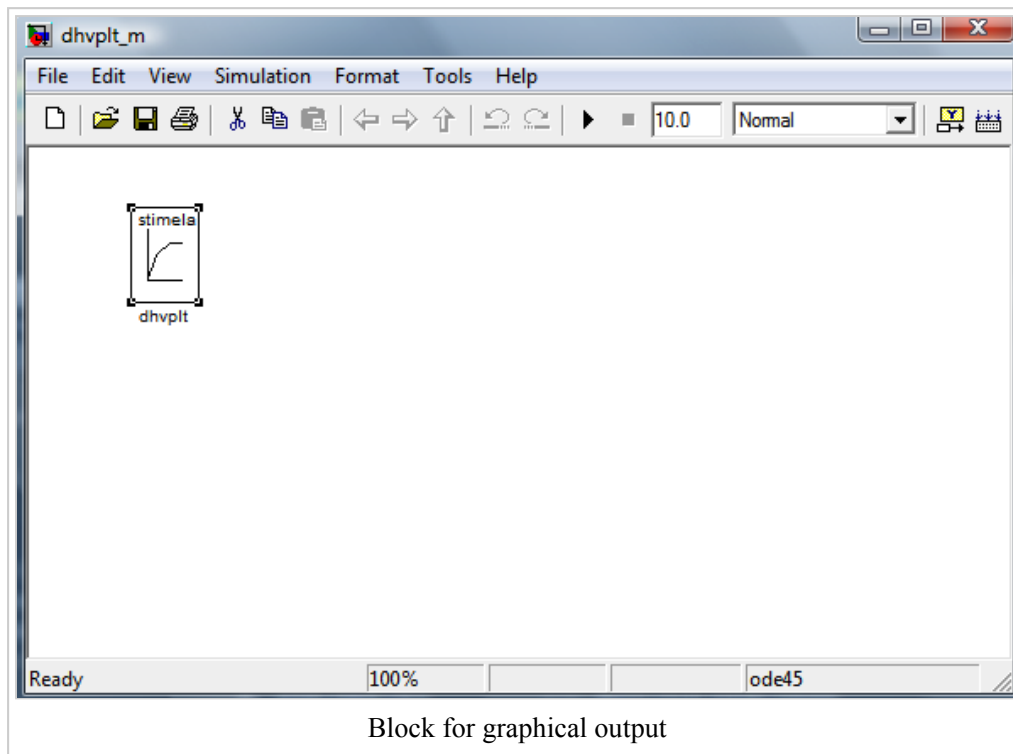
Importing a series from a file



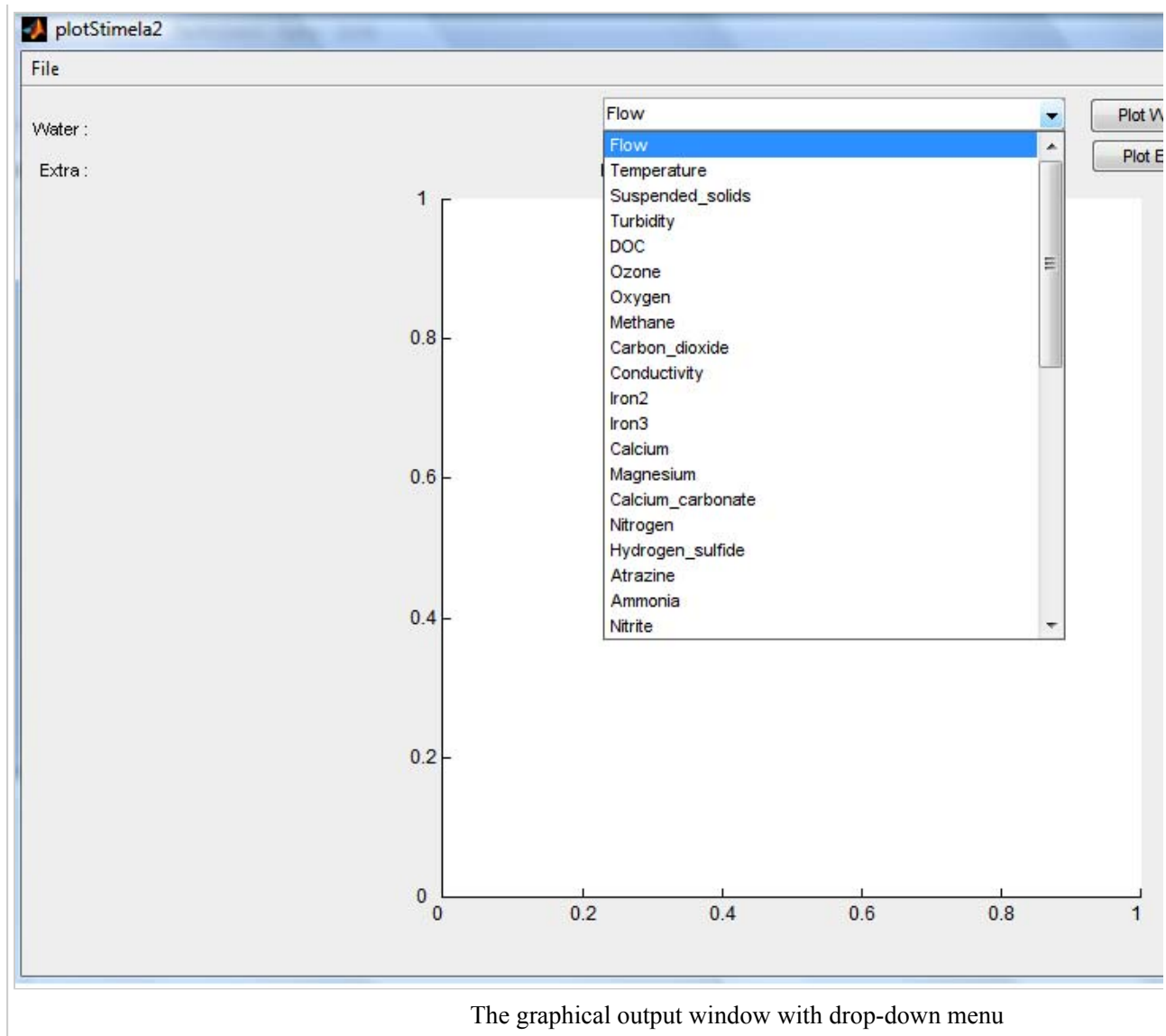
Example of a time series in Excel

6.1.2 DHV Graph

This module allows the user to generate graphical output of effluent concentrations over time on each connection between models.

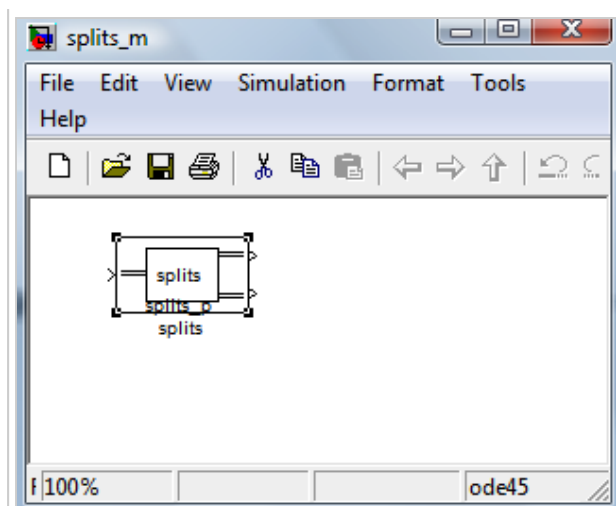


When double clicked the block will give the window shown in the next figure. In the drop-down menu, parameters of which the output needs to be displayed can be selected.

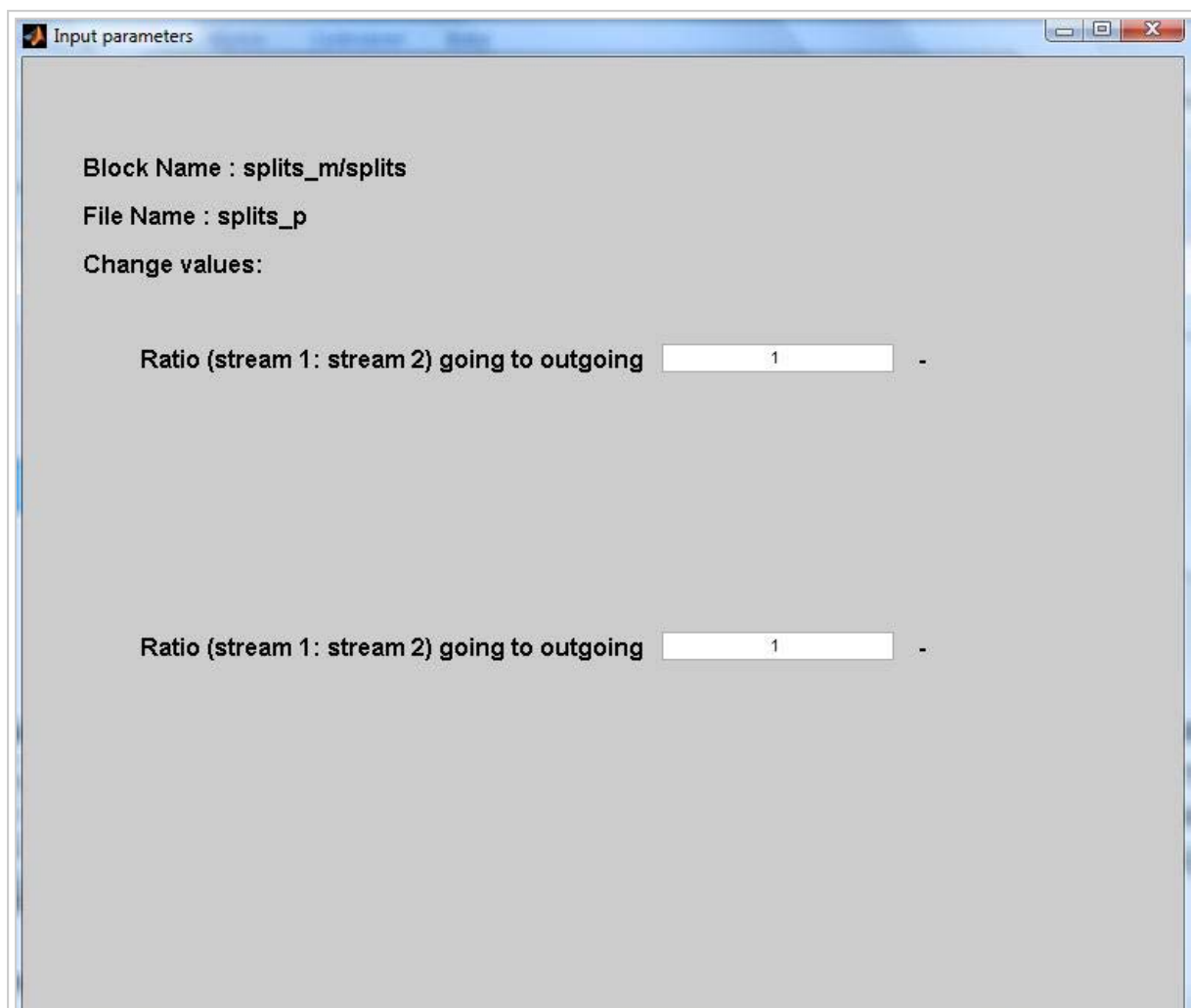


6.1.3 Split

This basic module allows the user to split a single flow into two flows according to a certain ration. If the incoming flow changes the two outgoing flows will change in the same ratio. In the next figures the block and the input screen for the Split module are shown.



The model block for the split module

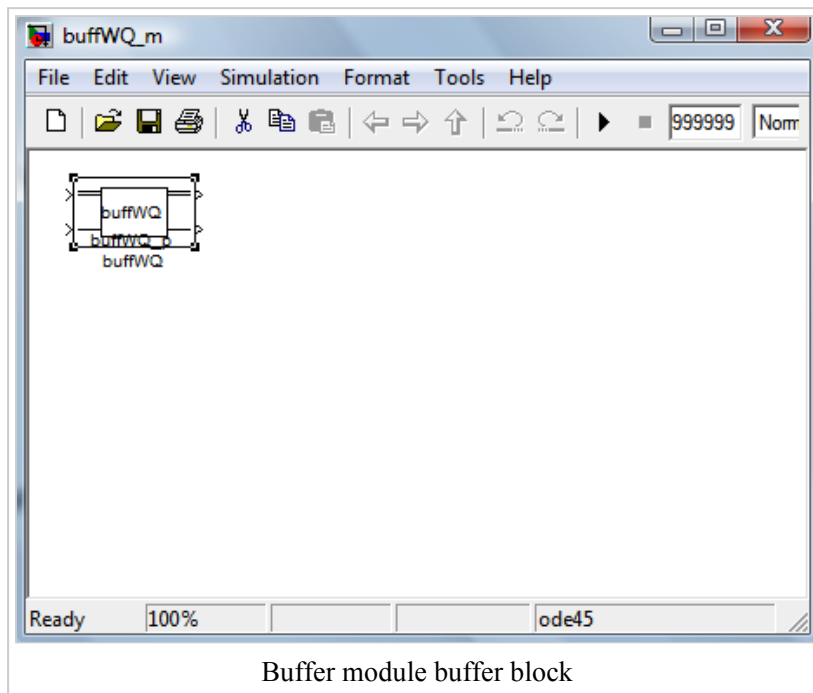


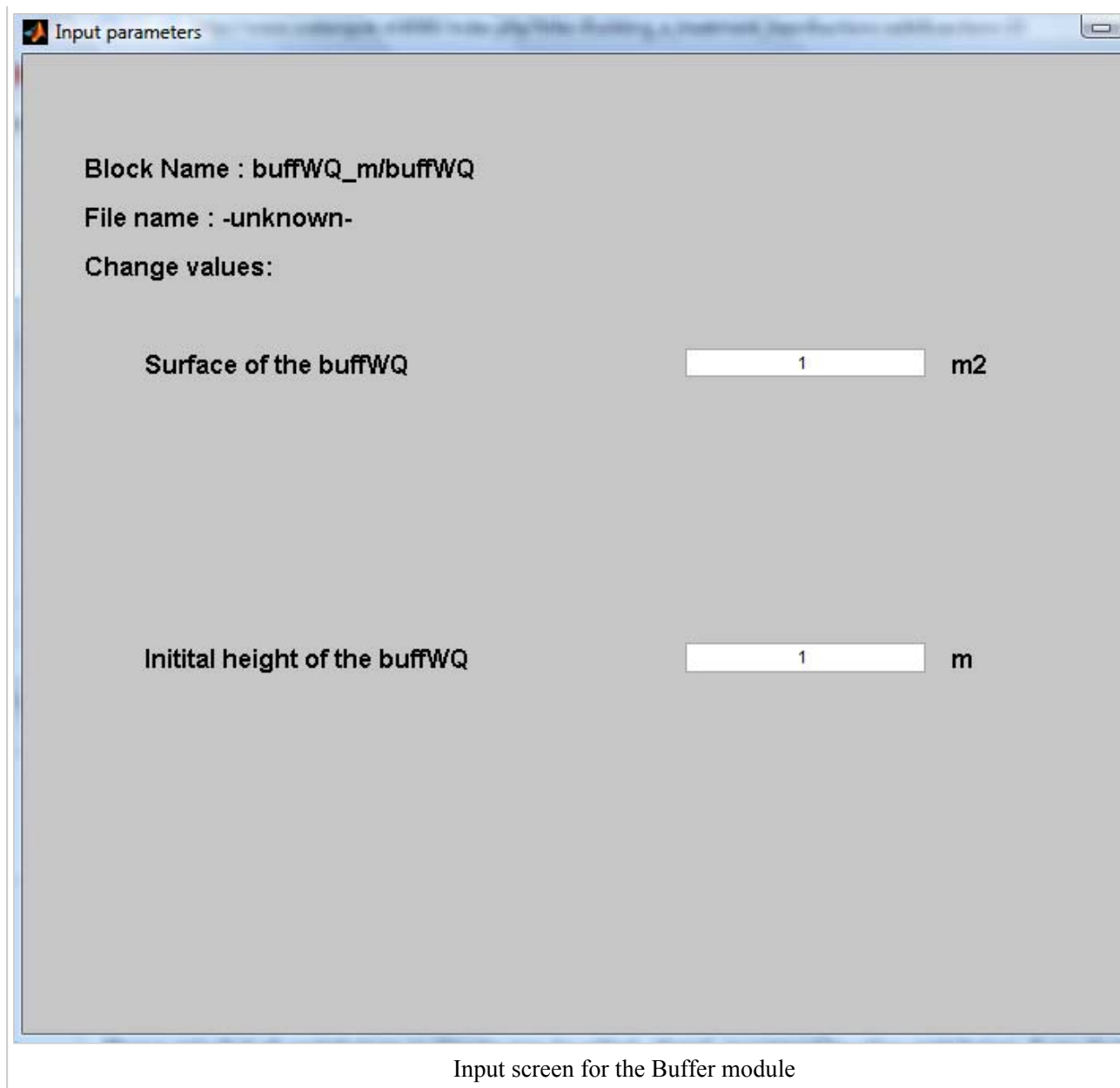
The input screen for the Split module

6.1.4 Buffer

The Buffer module puts a buffer reservoir in the treatment train with a certain depth and width,

thereby taking averages of concentrations over a certain period of time. Following figures show the model block and input screen.





Input parameters

Block Name : buffWQ_m/buffWQ

File name : -unknown-

Change values:

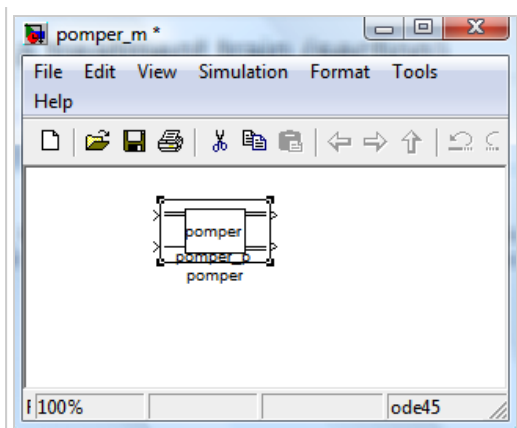
Surface of the buffWQ m2

Initial height of the buffWQ m

Input screen for the Buffer module

6.1.5 Pump

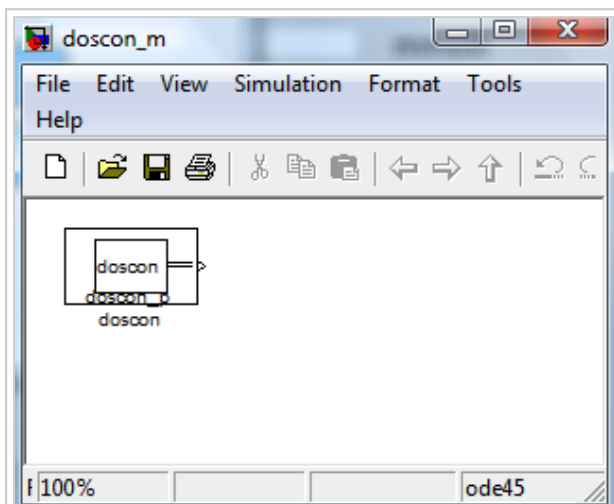
With the basic module Pump part of the flow of water can be diverted in a different direction, thereby rendering the user able to create bypasses. The diverted flow of water leaves the pump module at the bottom exit, while the remainder of the flow goes out the top exit. The pump model block is shown below.



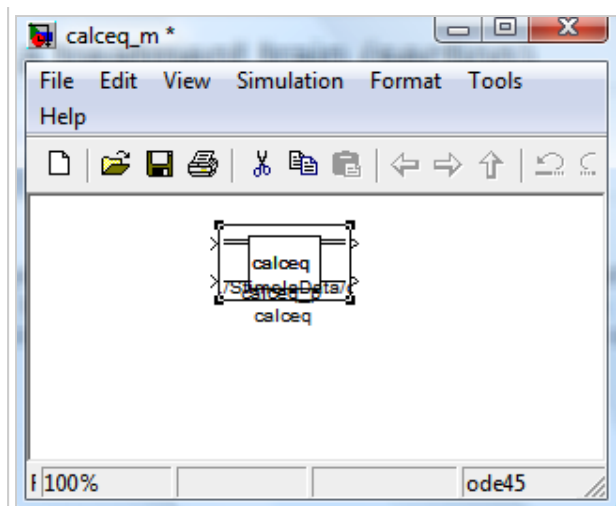
The model block for a Pump module

6.1.6 Dosing

The dosing modules enable the user to dose a certain amount of chemicals with the doscon module and mix it and calculate a new calcium carbonic acid equilibrium with the calceq module. For more information on pH calculation, please refer to the chapter on pH adjustment in the Stimela model descriptions section. The blocks and input screens for the doscon and calceq modules are shown below in the following figures.



Model block for a doscon module

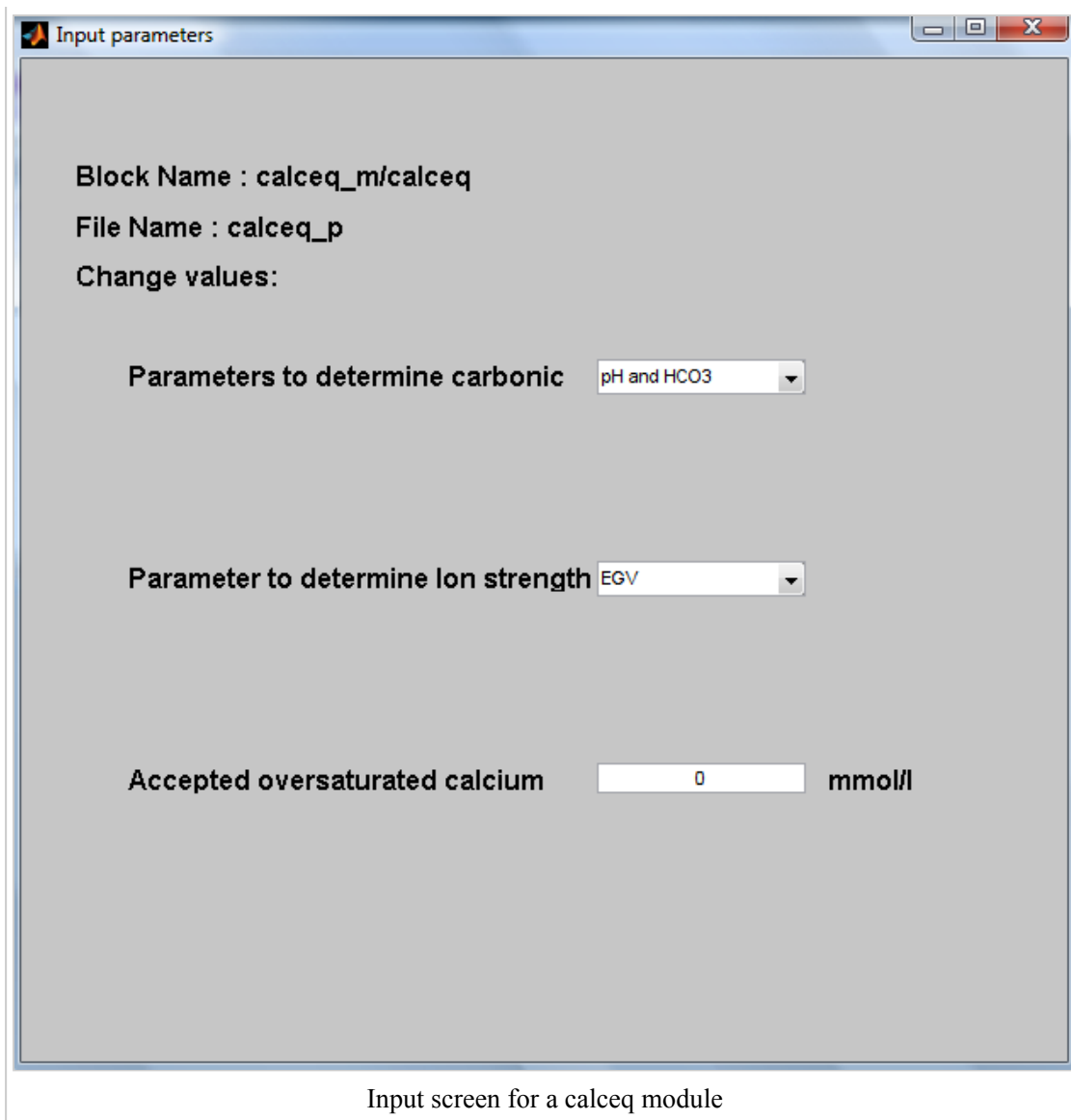


Model block for a calceq module

The 'Input parameters' dialog for the 'doscon_m/doscon' block shows the following settings:

Parameter	Value	Unit
HCl dosing in main flow	0	mmol/l
H2SO4 dosing in main flow	0	mmol/l
CO2 dosing in main flow	0	mmol/l
NaOH dosing in main flow	0	mmol/l
CaOH2 dosing in main flow	0	mmol/l
Na2CO3 dosing in main flow	0	mmol/l
CaCO3 dosing in main flow	0	mmol/l
FeCl3 dosing in main flow	0	mmol/l
Fe2SO43 dosing in main flow	0	mmol/l
Al2SO43 dosing in main flow	0	mmol/l

Input screen for a doscon module



Input parameters

Block Name : calceq_m/calceq

File Name : calceq_p

Change values:

Parameters to determine carbonic

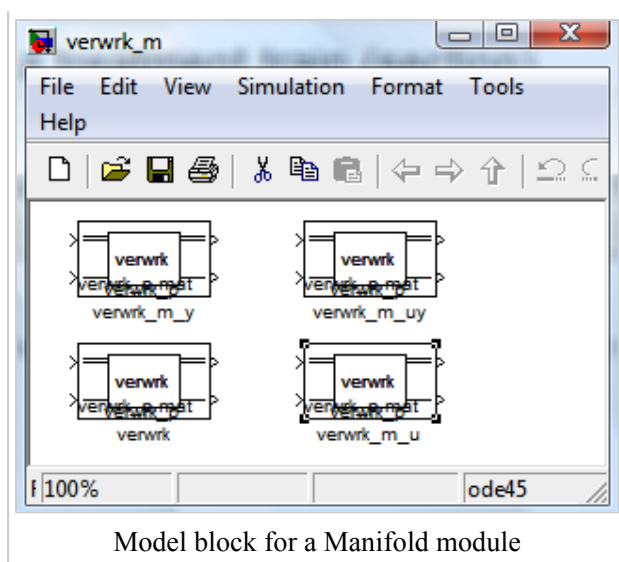
Parameter to determine Ion strength

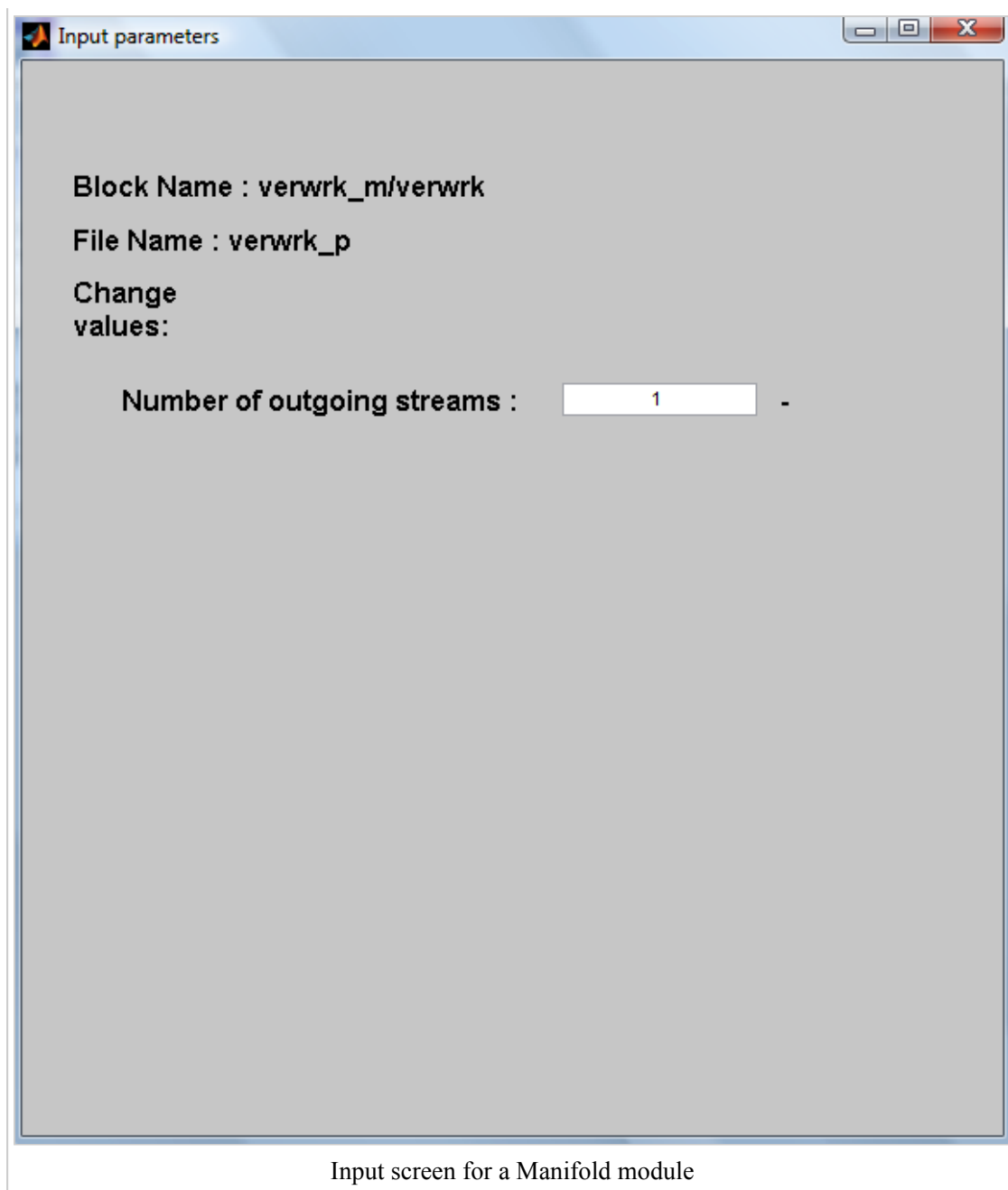
Accepted oversaturated calcium mmol/l

Input screen for a calceq module

6.1.7 Manifold

The Manifold module lets the user split the flow in a number of equally big flows. The model block and input screen are displayed below.





7 Simulink library

The ‘Simulink library’ contains a number of building blocks, Simulink blocks, which can be used while building the models. This library can be opened by double clicking the simulink library in the introduction screen of Stimela.

Depending on the version and package of Matlab[®] installed by the user, the library will be more or less extended. Figure 13 shows an example of a Simulink library. To learn more about the content of the Simulink library and the use of Simulink blocks, the manual of Simulink should be used.

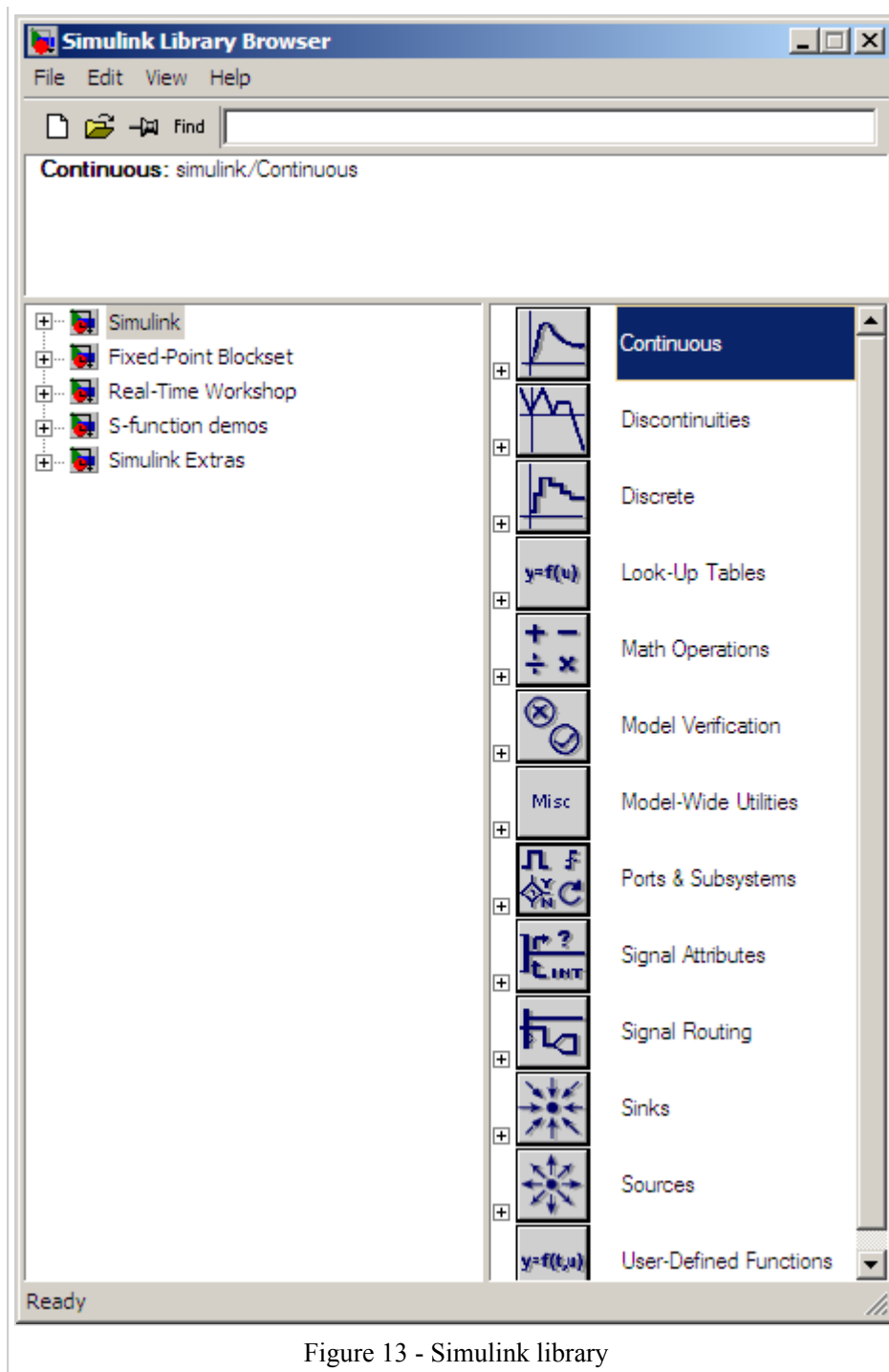
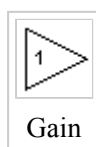
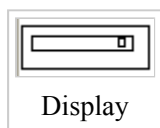
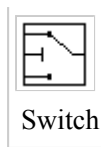


Figure 13 - Simulink library

Often used simulink blocks are:



(used to multiply a parameter or parameters with a fixed value)



8 Setting up a new project

In the introduction screen of Stimela (Chapter 2) the option ‘my Projects’ is available. This is the part where you can open an existing or set up a new project, the latter, if wanted, based on the template of an existing project. ‘My projects’ is used when a quick calculation is needed of a single or multiple treatment steps without being able to alter the equations of the models, solely changing the raw water influent parameters and the process parameters. By double clicking the ‘My projects’ block the menu depicted in Figure 14 opens.

By double clicking the green block a new project can be set up. The blue block indicates an existing project which can be reopened again by double clicking the project. A project can consist of a single model or several models linked together simulating a complete drinking water treatment plant.

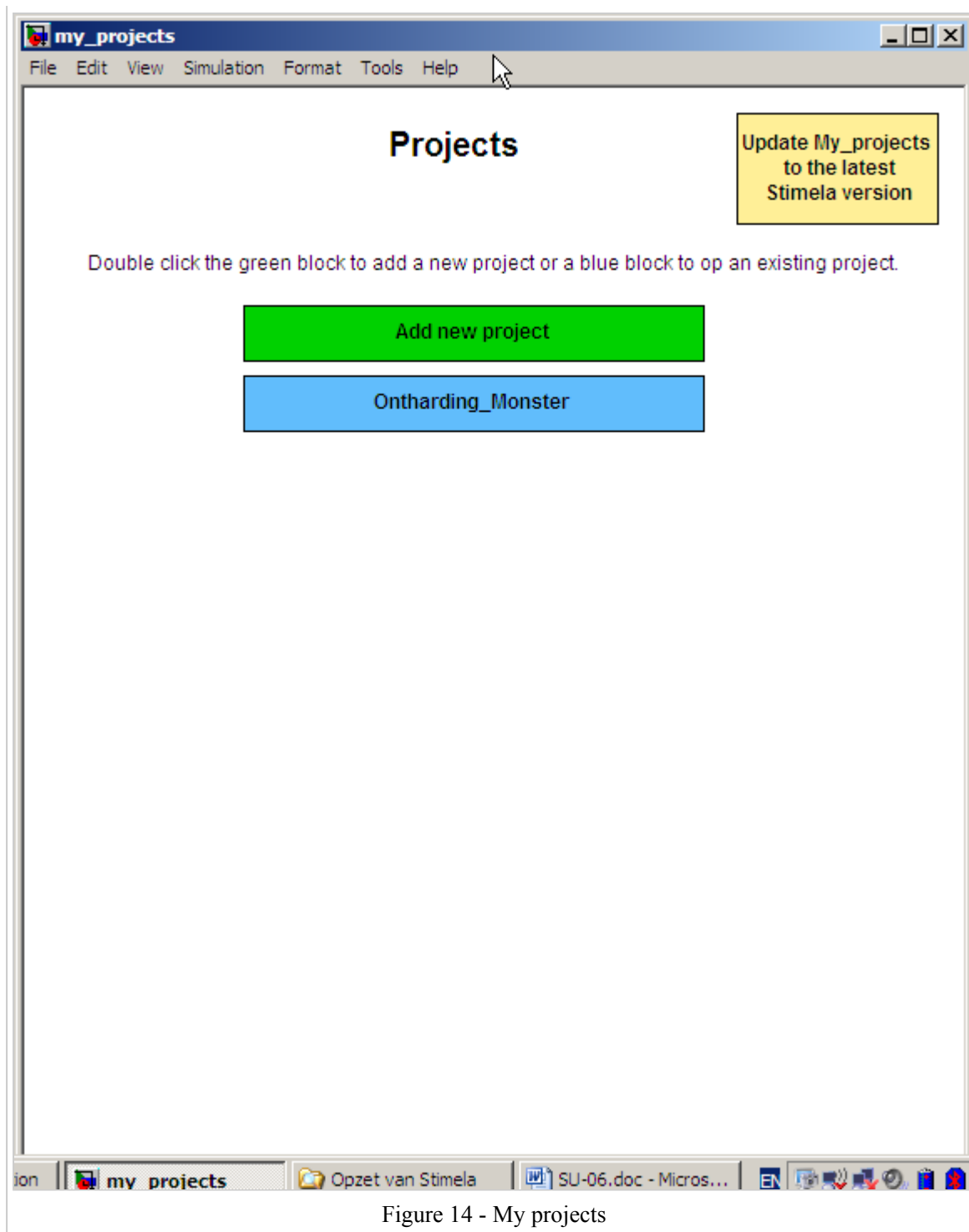


Figure 14 - My projects

To add a new project

By double clicking the green block “Add new project” a new project is made in the following way.
Choose project name:

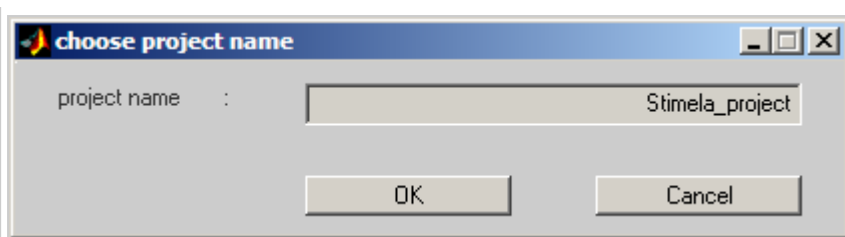


Figure 15 - Choose a name for a new project

After the project name is chosen and confirmed by clicking the 'OK'-button, a screen appears with all templates available in the Stimela library. In this screen the template of a standard project or an existing project can be chosen, see Figure 16.

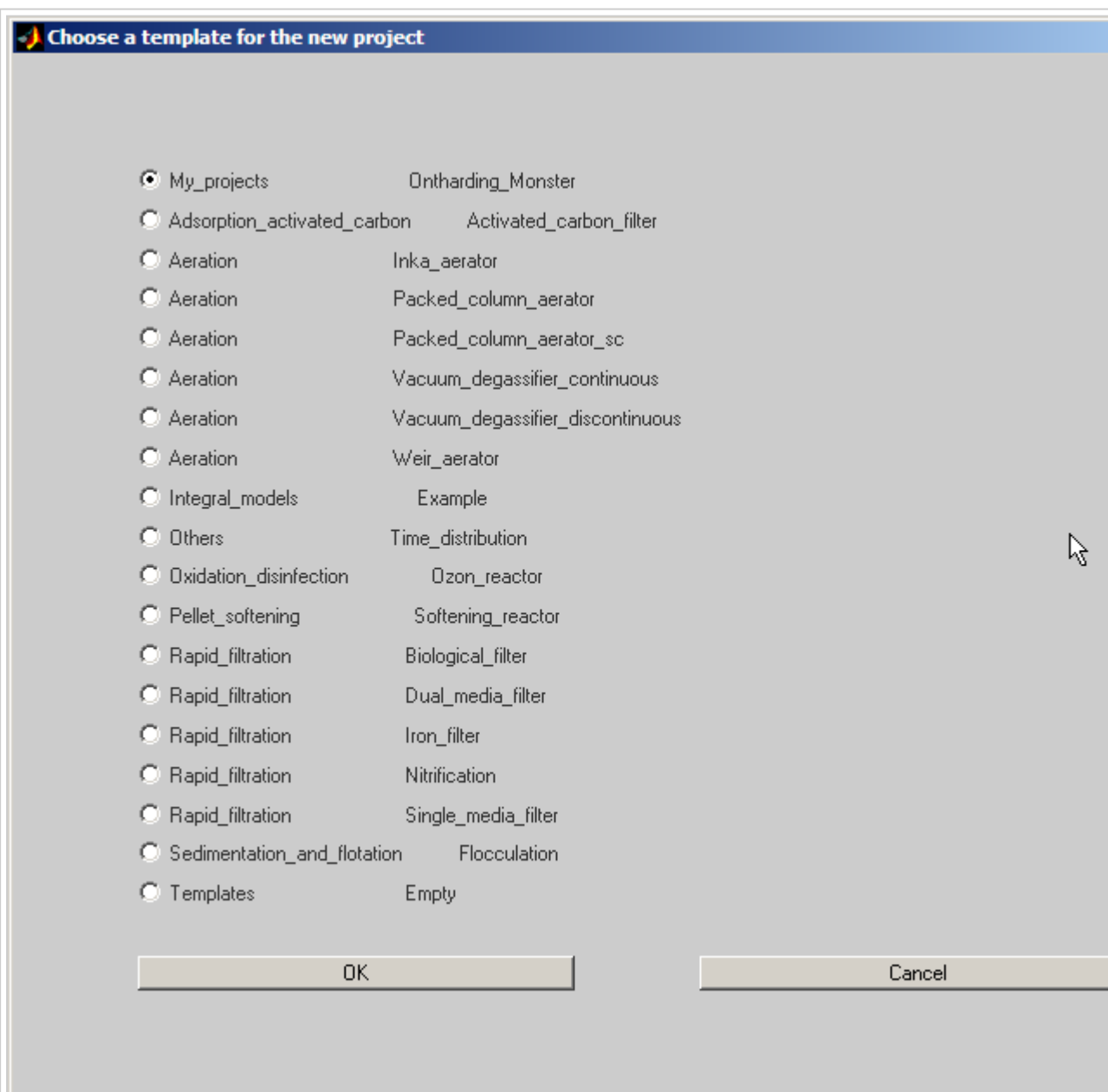


Figure 16 - Choose a template for a new project from the Stimela library of existing projects.

Now a project is compiled.

If a treatment train needs to be simulated, more treatment steps can be added in the following way:

- Create a new project for all single treatment steps of interest (for example the train aeration – RSF);
- After having created all single treatment steps (see Figure 17) a new project should be chosen, which eventually combines all single treatment steps into a treatment train.

Train: Aeration-RSFRSFAeration

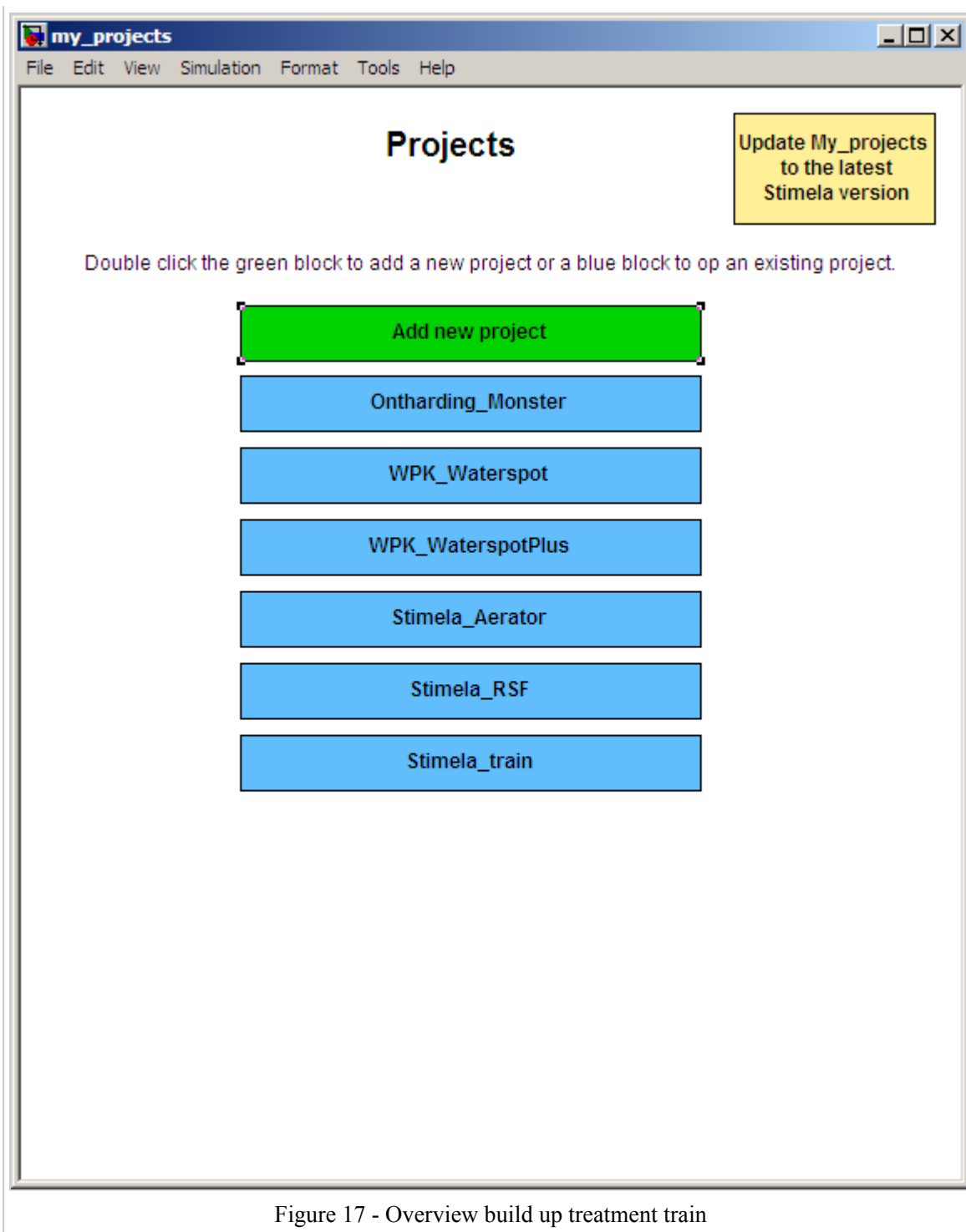


Figure 17 - Overview build up treatment train

To build the Stimela 'train' in a project, the first treatment step of this train is selected as template for the project, in this example the weir_aerator. To be able to add the rapid sand filtration template, open the constructed my project Stimela_RSf select all blocks except for the influent block and copy them into the project, see Figure 18.

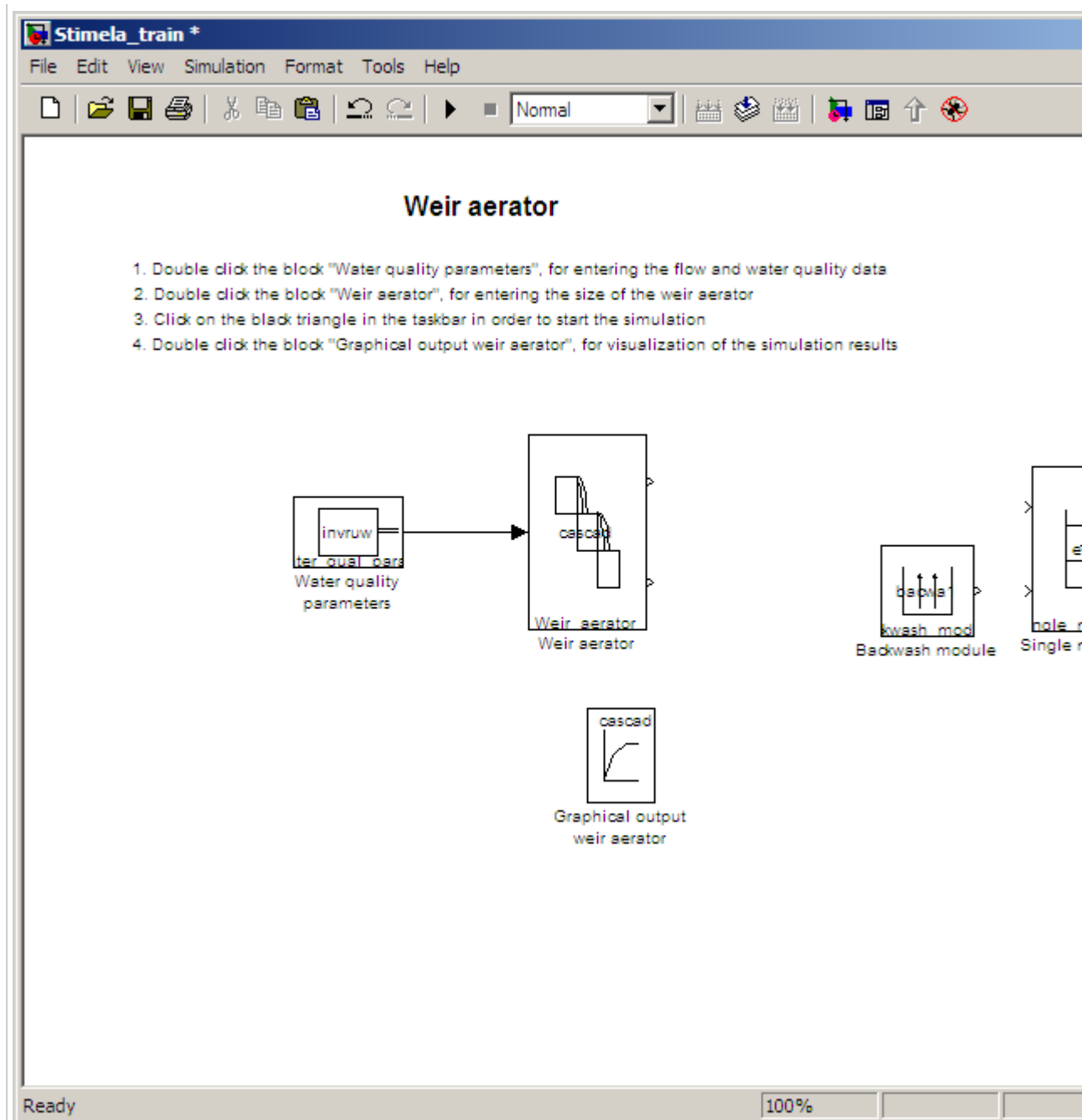


Figure 18 - Construction of treatment train

After the RSF model is copied into the project the following steps should be followed before the train is finished.

- Connect the effluent of the weir aerator to the influent of the RSF project (Figure 19);

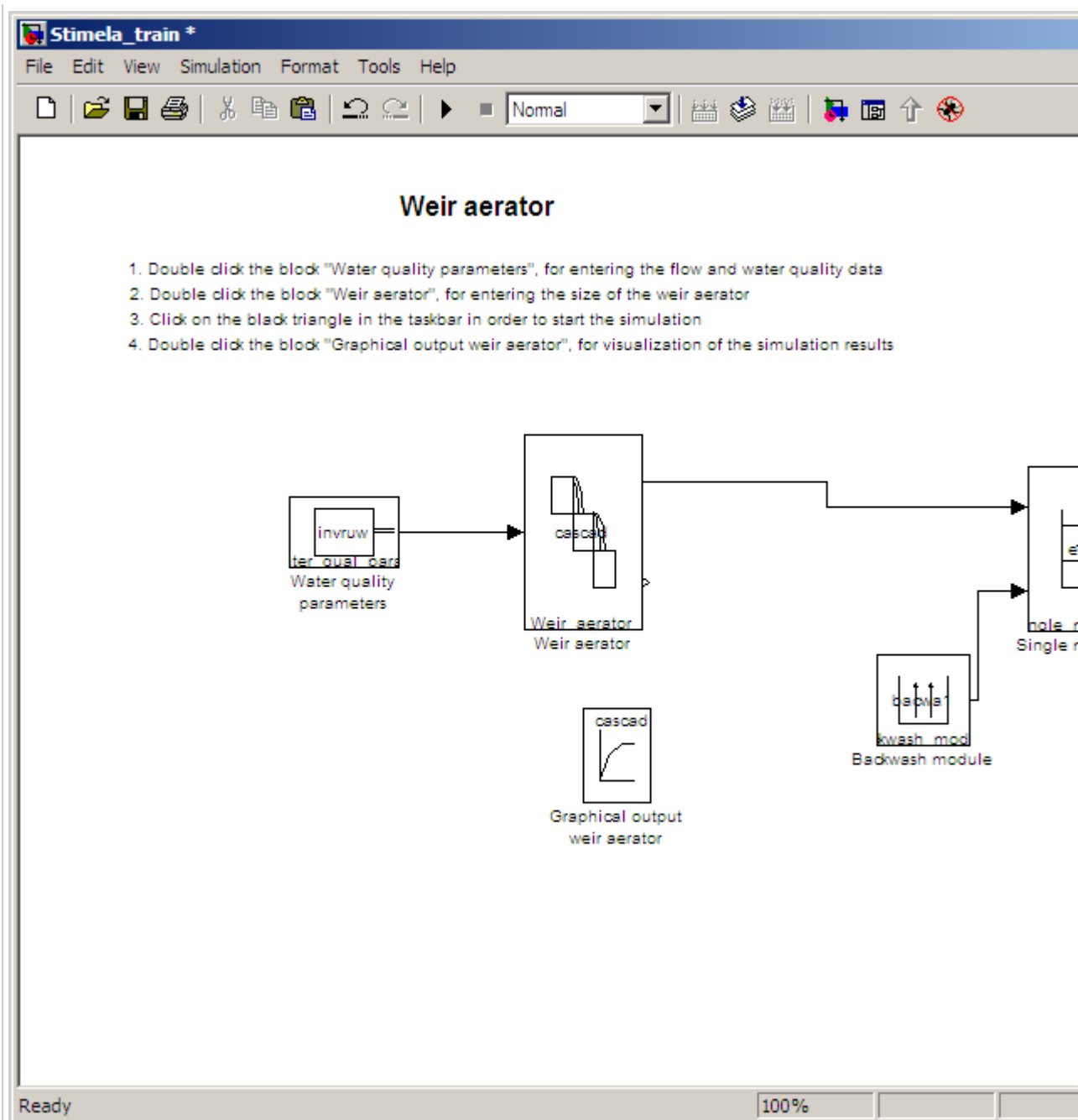
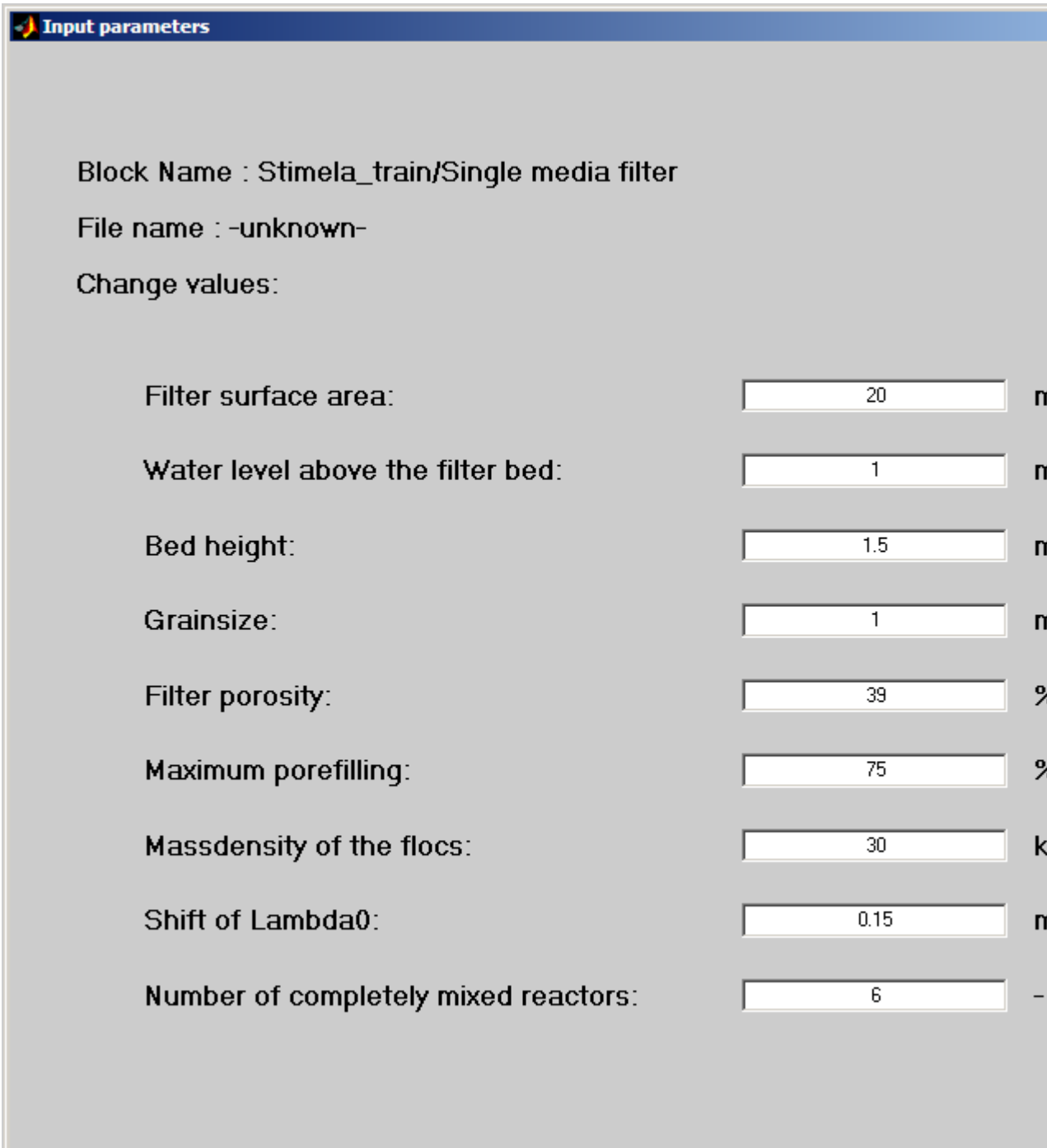


Figure 19 - Connect the different projects

- Fill out the values for the static parameters of each added model block. To do so open the form by double clicking the model block, see Figure 20. As mentioned in Chapter 4, the first time the static information form is opened, the file name is 'unknown'. After filling out the form, use the save as button to save the file containing the static information. When 'save as' is pushed the Stimeladata folder is opened, which is the right place to save the file. After saving you can close the form using the exit button.



Input parameters

Block Name : Stimela_train/Single media filter

File name : -unknown-

Change values:

Filter surface area:	<input type="text" value="20"/>	m
Water level above the filter bed:	<input type="text" value="1"/>	m
Bed height:	<input type="text" value="1.5"/>	m
Grainsize:	<input type="text" value="1"/>	m
Filter porosity:	<input type="text" value="39"/>	%
Maximum porefilling:	<input type="text" value="75"/>	%
Massdensity of the flocs:	<input type="text" value="30"/>	kg
Shift of Lambda0:	<input type="text" value="0.15"/>	m
Number of completely mixed reactors:	<input type="text" value="6"/>	-

Figure 20 - Fill out the values for the static parameters

- Fill out the influent quality and flow by double clicking on the block 'invruw' (see Chapter ???).

After these steps a treatment train is build.

Run a model or project

A simulation, calculation, can be started by pressing the 'play' button (▶). During the simulation the

play button will change into a 'pause' button (**II**). On the display at the bottom it is indicated that the simulation is running, how much time has collapsed (58018.848 seconds) and which solver is used, in this case the 'ode 15s'. Results can be viewed by double clicking the graphical output.

Before a simulation the simulation/configuration parameters can be adjusted, as shown in Figure 21.

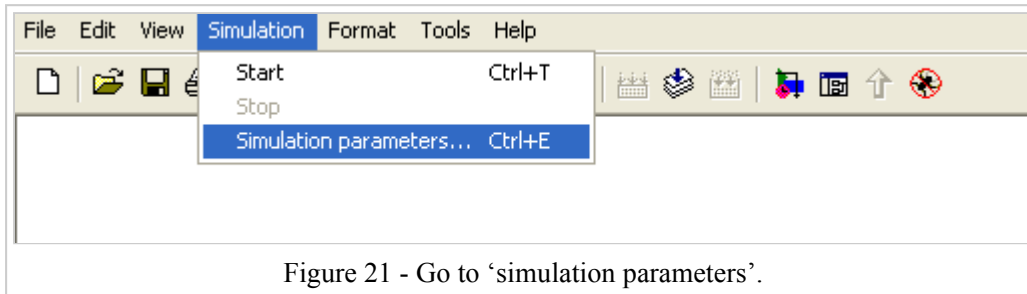


Figure 21 - Go to 'simulation parameters'.

The start and stop time of the simulation (in sec) can be filled out and the type of solver (integral solver). The mentioned fields are highlighted in red in Figure 22.

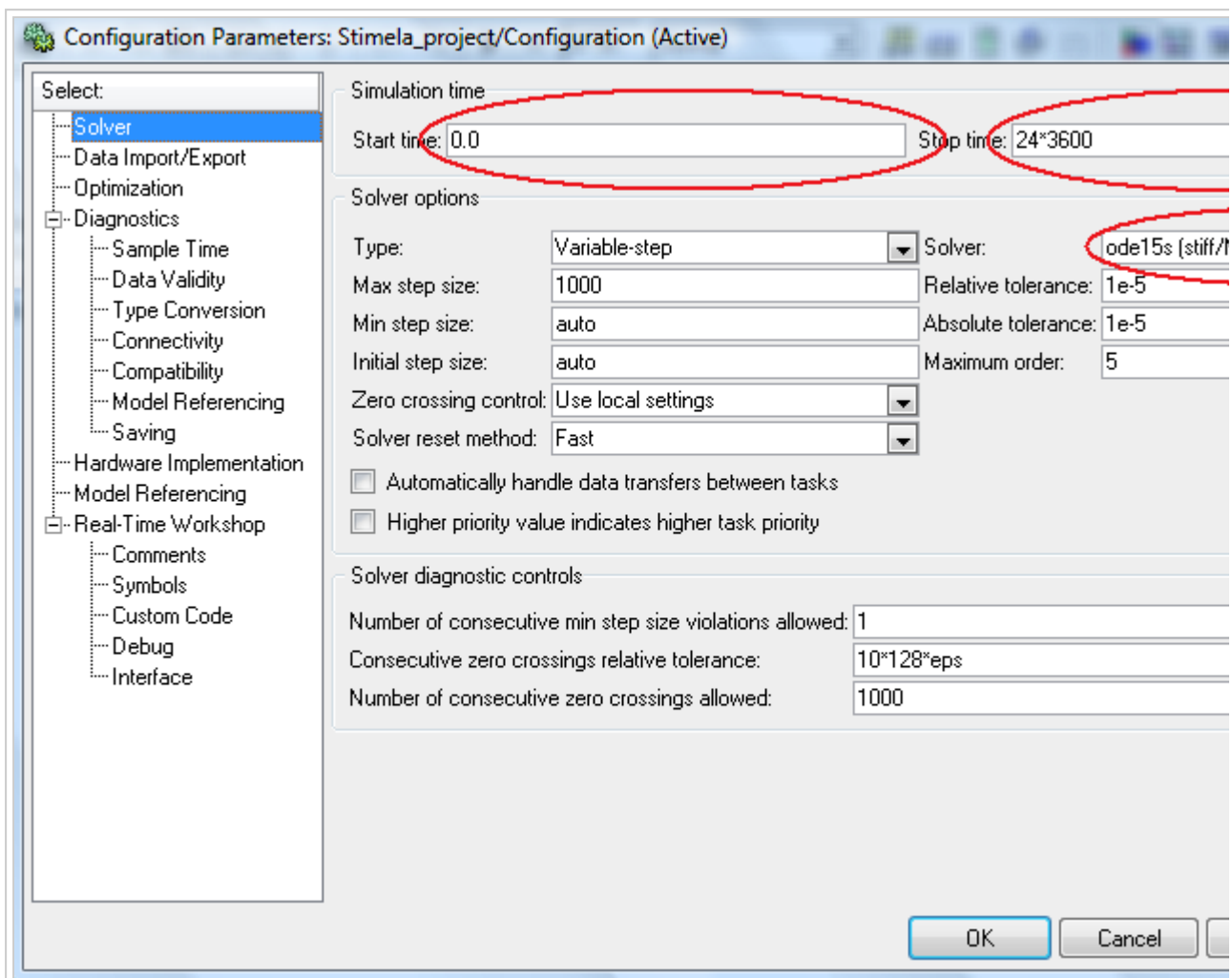


Figure 22 - Start and stop time and type of solver.

If an initial state is used and/or created, the relevant toggles should be switched on. In the example of Figure 23, the initial state 'xFinal' is used in the start of the simulation and a new initial state will be saved at the end, in this case overwriting the original initial state, as a consequence of the same name used.

The screenshot shows the 'Advanced' tab of the 'Workspace I/O' settings in Stimela. The interface is divided into three main sections: 'Load from workspace', 'Save to workspace', and 'Save options'.
- In the 'Load from workspace' section, the 'Initial state' checkbox is checked and set to 'xFinal'.
- In the 'Save to workspace' section, the 'Final state' checkbox is checked and set to 'xFinal'.
- In the 'Save options' section, the 'Limit data points to last' is set to 1000, 'Decimation' is 1, and 'Format' is set to 'Array'.
At the bottom, there are buttons for 'OK', 'Cancel', 'Help', and 'Apply'.

Figure 23 - Use and saving of an initial state in Stimela

Retrieved from "[http://www.waterspot.nl:8080/index.php/Building a treatment train](http://www.waterspot.nl:8080/index.php/Building_a_treatment_train)"

- This page was last modified on 16 December 2009, at 15:06.