



## **Cell Illustrator™: Reference Manual**

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Medical Science, The University of Tokyo

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# 1 Introduction

Cell Illustrator™ (CI) is a software tool that enables biologists to model, elucidate and simulate complex biological processes and systems. It allows researchers to model metabolic pathways, signal transduction cascades, gene regulatory pathways as well as dynamic interactions of various biological entities such as genomic DNA, mRNA and proteins. Cell Illustrator models are used to visualize biopathways, interpret experimental data and test hypotheses. In addition, it provides researchers with model diagrams of publication quality and simulation result charts.

Using a graphical user interface environment, researchers can create and simulate their own molecular pathway models. Some of the key features of Cell Illustrator are: (a) Pathway construction and visualization—construct models graphically by drag and drop Entities that represent bio-components in the biological pathways; (b) Pathways simulation—specify mathematical formulas for biochemical reactions in the pathway for simulation; The simulation can be run inside the workspace window in an interactive mode, or it can be sent to a remote server (Cell Illustrator Server) (c) Simulation replay – the simulation results can be logged and then visualized and analyzed in Cell Illustrator Player; (d) Simulation animation—Cell Illustrator’s simulation results can be edited into an animation script file and then be used as the input to Cell Animator—a module that produces high quality presentation of the studied mechanism’s dynamic behavior; (e) Model import - previously created models or sub-models can be imported from SBML, CellML files or from public or proprietary libraries and databases like KEGG.

Since the version 3.0, Cell Illustrator enables the users to view and analyze gene relationships networks. This functionality is available in the special Gene Network mode. Therefore the graphical user interface of CI offers the user two modes of working:

- (i) The Biopathway Modeling mode dedicated for simulation and modeling of complex biological processes and systems using Petri Net models – described in this manual
- (ii) The new Gene Network dedicated for analysis and exploration of gene relationship networks. This mode is described separately in the **CI Gene Net Reference Manual**.

The documentation for the Cell Illustrator software includes the manuals listed below:

**Cell Illustrator User Guide:** Introduction to Cell Illustrator system

**Cell Illustrator Reference Manual:** Detailed description of Cell Illustrator functions

**Cell Illustrator Player Reference Manual:** Detailed description of Cell Illustrator Player functions

**Cell Illustrator Server Installation Manual:** Installation instructions for Cell Illustrator Server product (for IT System Administrators)

**Cell Illustrator Gene Net Reference Manual:** Detailed description of Cell Illustrator functions (Gene Network mode)

**Cell Illustrator Gene Net User Guide:** Introduction to the Gene Network mode of Cell Illustrator system

This manual is a reference for the functional features of Cell Illustrator Online version 4.0 (CIO4.0) for the Biopathway modeling mode. It can be used to answer questions about specific system commands. For installation instructions and an introduction to modeling biological pathways with Cell Illustrator, please refer to the User Guide.

## 2 CI Online

Until version 3.0 Cell Illustrator was offered as desktop application. Since version 4.0 Cell Illustrator is available as Java Web Start application – *CI Online*. CI Online can be run directly from the website, without the need to install software on local computer.

CI Online is a client-server solution that enables the user to create, manipulate and simulate bio-pathway models locally within CI workspace and to store and organize them on the remote CI Online Server. Additionally CI Online gives the user convenient access to libraries and databases of bio-pathway models.

In CI Online, Cell Illustrator is the front-end, where the user prepares a pathway and simulates it. The Cell Illustrator client communicates with the CI Online Server over the internet (HTTP or HTTPS protocol). The CI Online Server is a place where the user logs-in to store and manage his pathways and to share them with other users.

## 3 Biopathway Modeling Mode

This manual describes only the functionality of the *Biopathway Modeling* mode. In this chapter it will be described:

- how to switch to the *Biopathway Modeling* mode
- what are the differences between the *Gene Network* and *Biopathway Modeling Modes*
- where to find the documentation for the *Gene Network* mode

### 3.1 Switching to the Biopathway Modeling Mode

The menu command View | Gene Net Mode switches between the biopathway modeling and gene network modes. If this menu item is checked then you are in the Gene Net mode, otherwise you are in the Biopathway modeling mode.

Any model that has been opened in the CI workspace (or imported) can be viewed in each of both CI modes: Biopathway Modeling and Gene Network mode. However there are the following limitations:

- Do not view large gene networks in the Biopathway Modeling mode

Displaying large networks with hundreds of edges in the biopathway modeling mode will cause performance problems. Therefore they should be displayed in the Gene Network mode only.

- A typical gene network cannot be simulated.

Originally a gene network does not contain any data useful for the simulation. After switching to the Biopathway Modeling mode you will see that all simulation parameters for a gene network have default values. Simulating such a net will not give any reasonable results. However such a net can be used as the starting point for creating a simulatable model.

- A biopathway model might not be a correct gene network model

This is the case if one process has more than one input or output entities, which is normal for Petri net models of biopathways, but forbidden for gene networks. In the case of such a conflict some connection between entities will be ignored. In the gene network view one process is represented by one edge connecting the input and output entity of this process. For each process with multiple input or output entities, the edge connects only one input and output entity of the process.

### 3.2 Differences between Gene Network and Biopathway Modeling Modes

The differences between the Biopathway modeling mode and the Gene network mode are listed in the table below.

	<b>Biopathway Modeling Mode</b>	<b>Gene Network Mode</b>
Model	<p>Includes 3 base elements: entity, process and connector.</p> <p>Models are created by the user within CI workspace.</p> <p>Biopathway models are smaller but more precisely defined than the Gene Network models.</p> <p>Biopathway models include quantitative simulation properties for studying the kinetics of biological processes.</p>	<p>Includes 2 basic elements: gene and edge.</p> <p>Gene networks are automatically generated by a special external software.</p> <p>Originally gene networks are large models without precise simulation data.</p>
Visualization	<p>More advanced graphics: images for each graph elements, polygon and curved edges for connectors, visualization and animation of simulation progress, etc.</p> <p>Visualization is slower but allows for displaying more details.</p>	<p>Simple graphics: default view styles for each gene and edge.</p> <p>Visualization is faster but includes less details. Thus it is more suitable for large networks.</p>
Editing	<p>Many commands enable building biopathway models from the scratch and defining the simulation properties (e.g. kinetic styles)</p>	<p>Extraction and Merging of subnetworks. Other edit commands are used in seldom cases.</p>
Simulation	<p>Simulation using Petri Net algorithm in interactive or remote mode.</p>	<p>no Simulation capabilities</p>
Analysis	<p>Analysis of simulation</p>	<p>Analysis of gene networks:</p>

	results: charts	Gene Mining, Pathway and Keyword Search, Expression Plot, tools for extraction of subnets
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### 3.3 Documentation for Gene Network Mode

Please refer to the **CI Gene Net User Guide** and **CI Gene Net Reference Manual** to learn more about the gene network mode and its capabilities.

## 4 Workspace - Main Window of CI

The Workspace is the main window of Cell Illustrator. The [Menu Bar](#) located at the top provides a set of commands for building and manipulating a model. Frequently used commands can be also executed by pushing a button on one of the [toolbars](#) on the sides of Workspace. Menu items and toolbar buttons corresponding to operations that cannot be performed at the moment are disabled (grayed out).

In the Workspace, multiple model files can be opened simultaneously for viewing and editing. A model file is displayed in a *canvas window*. The canvas window is the main view of the model and allows the model to be edited and a simulation run to be watched. You can open several canvas windows to view different parts of the model. However, only the canvas window active at the time of starting simulation remains open when the simulation runs.

In Cell Illustrator, the user can open several property *dialogs*. The contents of these dialogs reflect:

- user preferences (applicable to all models),
- properties of the model in the active canvas window, or
- properties of a selected model in the active canvas window.

The list of property dialogs follows:

<b>Dialog name</b>	<b>Purpose</b>
<a href="#">Element Lists</a>	Displays lists of model elements and values of their main properties.
<a href="#">Element Settings</a>	Allows the viewing and the setting of the properties of a selected element.
<a href="#">External References</a>	Allows for viewing/editing the list of external references for the selected entity
<a href="#">Navigator</a>	Shows the position of the canvas window relative to the whole model.
<a href="#">Preferences</a>	Allows the setting of application-wide usage options for CI16.
<a href="#">View Settings</a>	Allows the setting of application-wide view options.
<a href="#">Chart Settings</a>	Allows the selection of variables to be watched in a chart window when simulation is running.
<a href="#">Simulation Settings</a>	Displays simulation parameters.
<a href="#">Simulation History</a>	Displays the list of simulation logs
<a href="#">Edit Units</a>	Facilitates the definition of new units for the selected model
<a href="#">Graph Layout</a>	Facilitates an automated layout of model elements on the canvas

Finder	Searches for specified elements in the canvas.
Pathway Search	Searches for pathways in the selected network
Gene Mining	Searches for publications and links for the selected genes

Beside the property dialog boxes, Cell Illustrators offers dialog boxes that support building of pathways. These dialog boxes give the user the access to many predefined elements or pathway fragments and the ability to insert these fragments to the active canvas.

Edit Parts Dialog	Allows the addition of fragments from the repository of predefined models created by the user
Biological Elements	Allows the addition of model items from the set of predefined biological elements
Project Manager	Allows the addition of models from the set of pathways defined on the <i>CI Online</i> Server
CSMLDB Search	Allows the search through CSMLDB for molecules and/or reactions and the addition of model items found in the database

## 4.1 Menu Bar Commands

### 4.1.1 File | New

#### Description:

- Creates a new, empty model.
- The canvas name is “New Canvas *number*”, where the number is the number of currently opened models + 1 (this means “New Canvas 1” if there are no canvases at the time the operation is executed)
- CTRL+N is the keystroke shortcut for this command.

#### Constraints:

- No simulation is running

## 4.1.2 File | Open

### Description:

- Opens a model from an Cell Illustrator model file. The native CI file format is the XML format called CSML – Cell System Markup Language - [www.csml.org](http://www.csml.org)
- The CSML files can be written in various versions: CSML 3.0, which normally should have .csml extension or the older CSML 1.9 files which normally have the .gon extension. This command opens all versions of CSML files.
- It is not possible to open the same file twice. If the user attempts to open a file that is already opened, then the canvas window of that file is activated and displayed in the foreground.
- Since a CI Log (.cil extension) stores the model in the same format as in the original project file, you can open a log file with Cell Illustrator as well and edit the model. However, saving the edited model into the original log file will erase the time series and any other simulation history information. Therefore, you should use the Save As command of Cell Illustrator if you would like to recover the model from a log file for further editing.
- CTRL+O is the keystroke shortcut for this command.

### Constraints:

- You can not execute this command if a simulation is running.

## 4.1.3 File | Open Recent Files

### Description:

- Displays a list of recently opened files. Click on an item in the list to open the corresponding file.
- Up to 5 recently opened files are in the list.
- The list does not contain duplicates.
- It is not possible to open the same file twice. If the user attempts to open a file that is already opened, then the canvas window of that file is activated and displayed in the foreground.

### Constraints:

- You can not execute this command if a simulation is running.

## 4.1.4 File | Close File

### Description:

- Closes the active model file without exiting the program.

- If a file has been modified, you are prompted to save the changes before closing the file.
- CTRL+W is the keystroke shortcut for this command.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- You cannot execute this command if a simulation is running.

#### 4.1.5 File | Close All Files

**Description:**

- Closes all model files without exiting the program.
- If a file has been modified, you are prompted to save the changes before closing the file.
- You are always prompted for a file name if you want save a canvas created with the File | New command.
- CTRL+Shift+W is the keystroke shortcut for this command.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- You cannot execute this command if a simulation is running.

#### 4.1.6 File | Save

**Description:**

- Saves the active canvas in a file under the current filename.
- By default the model is saved in the CSML 3.0 file, however you may also save the model to the older CSML 1.9 file format. For this, select the CSML 1.9 in the File Type combo box of the File Save dialog.
- Regardless of the selected CSML format, the saved file can be opened in CI workspace again using the File | Open command.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- You cannot execute this command if a simulation is running.

#### 4.1.7 File | Save as

**Description:**

- Saves the active file under a new filename selected by the user.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- You cannot execute this command if a simulation is running.
- By default the model is saved in the CSML 3.0 file, however you may also save the model to the older CSML 1.9 file format. For this, select the CSML 1.9 in the File Type combo box of the File Save dialog.
- Regardless of the selected CSML format, the saved file can be opened in CI workspace again using the File | Open command.

**4.1.8 File | Insert**

- ➔ Model
- ➔ As Group
- ➔ As Object

**Description:**

- Inserts the elements from a Cell Illustrator model file into the active canvas.
- *Insert Model* inserts the elements of the external file as they are.
- *Insert Group* inserts the contents of the external file as one group.
- *Insert Object* inserts the contents of the external file as one hierarchical object.
- All inserted elements are in the selected state after the operation completes.
- All previously selected elements become deselected.
- The inserted item (a model, a group or an object) is placed in the center of the visible area of the canvas.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- No simulation is running.

**4.1.9 File | Import | CSO Model****Description:**

- Imports a pathway model from a Cell System Ontology (CSO) file. Converts the CSO file to a CI model and opens it in a new canvas.
- The imported CSO models should conform to the specification of CSO at [www.csml.org](http://www.csml.org)
- After importing the CSO file, it is stored in the CI model and can be saved to a CSML file using the **File | Save as** command or exported to CSO using the **File | Export | CSO Model**.
- CSO supports most of CSML features and allows for more flexible and extensible handling of biological data using Semantic Web OWL and RDF languages.

**Constraints:**

- No simulation is running.

#### 4.1.10 File | Import | BioPAX Model

##### Description:

- Imports a pathway model from a Biological Pathway Exchange (BioPAX) ontology file. Converts the BioPAX file to a CI model and opens it in a new canvas.
- The imported BioPAX models should conform to the specification of BioPAX level 2 at [www.biopax.org](http://www.biopax.org)
- After importing the BioPAX file, it is stored in the CI model and can be saved to a CSML file using the [File | Save as](#) command or exported to CSO using the [File | Export | CSO Model](#) command

##### Constraints:

- No simulation is running.

#### 4.1.11 File | Import | BioPACS

##### Description:

- Imports a metabolic pathway map from the KEGG Web site.
- The command opens the [KEGG-BioPACS](#) dialog box where you can select the map file and import options.
- Cell Illustrator connects to BioPACS web system that converts the map file to the XML file GON format used by Cell Illustrator.
- You have an option to open the imported map in a new canvas window.

##### Constraints:

- At least one canvas window must be opened in the workspace.
- No simulation is running.

#### 4.1.12 File | Import | SBML

##### Description:

- Imports the SBML file. Converts the SBML file to a CI model and opens it in a new canvas.
- The imported SBML models should conform to the specification of SBML, i.e., SBML version 2.1
- After importing the SBML file, it is stored in the CI model and can be saved to a CSML file using the [File | Save as](#) command.

- SBML models differ from the CI ones. E.g. SBML uses differential equations for representing relationships between entities, while CI use the Petri Net model. Therefore the conversion process has the following limitations:
  - o Not all SBML models can be imported to CI
  - o the simulation results might differ, for a SBML model imported to CI.
- It is recommended to run a simulation after a successful model import to verify whether the results of the converted model are identical to the simulation results of the original SBML model. Before running the simulation, the user should check and set the proper *Simulation Time* and *Sampling Interval* in the [Simulation Settings](#) dialog box.

**Constraints:**

- No simulation is running.

#### 4.1.13 File | Import | CellML

**Description:**

- Imports the CellML file. Converts the CellML file to a CI model and opens it in a new canvas.
- The imported CellML models should conform to the specification of CellML, i.e., CellML version 1.1
- After importing the CellML file, it is stored in the CI model and can be saved to a CSML file using the [File | Save as](#) command.
- CellML models differ from the CI ones. E.g. CellML uses differential equations for representing relationships between entities, while CI use the Petri Net model. Therefore the conversion process has the following limitations:
  - o Not all CellML models can be imported to CI
  - o the simulation results might differ, for a CellML model imported to CI.
- It is recommended to run a simulation after a successful model import to verify whether the results of the converted model are identical to the simulation results of the original CellML model. Before running the simulation, the user should check and set the proper *Simulation Time* and *Sampling Interval* in the [Simulation Settings](#) dialog box.

**Constraints:**

- No simulation is running.

#### 4.1.14 File | Export | CSO Model

**Description:**

- Exports a pathway model from the active canvas to a Cell System Ontology (CSO) file.
- The exported CSO models conform to the specification of CSO at [www.csml.org](http://www.csml.org)

- After exporting the CSO file, it can be imported to the CI workspace using the [File | Import | CSO](#) command
- CSO supports most of CSML features and allows for more flexible and extensible handling of biological data using Semantic Web OWL and RDF languages.

**Constraints:**

- No simulation is running.

**4.1.15 File | Export**

- ➔ Entity List
- ➔ Connector List
- ➔ Process List

**Description:**

- The commands export, respectively, the list of entities, connectors and processes to a file in the CSV format.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- You cannot execute this command if a simulation is running.

**4.1.16 File | Export | Simulation Log**

**Description:**

- For the model in the active canvas, the command exports the log of the most recent simulation to a file in the CSV format.
- The log contains a time series of values for variables selected in the [Element Lists](#) dialog box.
- The log is reinitialized when the simulation is restarted, i.e., when any of the simulation play commands are executed after the *Stop and Initialize* command. (*Stop and Initialize* command by itself does not reset the log. Also, executing play command to resume a paused simulation does not reset the log.)
- The *Max Log Steps in Memory* option in [Preferences](#) specifies the maximum number of time points stored in the in-memory log buffer.

**Constraints:**

- The command is disabled if none of entities is selected for logging (*Save Log* property is set to *off* for each entity) or there is no log to save
- An exported CSV file will contain time series that remains in the in-memory log buffer of Cell Illustrator at the time the export command is executed. In

case of a large log, the buffer may contain only a part of the log; The time series data is being saved to a hard disk while the simulation is running. You can set the size of the in-memory log buffer in the Preferences dialog in Cell Illustrator. To export the whole log, open the respective CI Log (CIL) file in the CI Player from the Simulation History dialog and execute the Export Simulation Log command in the CI Player.

#### **4.1.17 File | Export | Engine Source Code**

- ➔ Java
- ➔ C
- ➔ C++
- ➔ Fortran
- ➔ Perl
- ➔ Python

#### **Description:**

- For the model in the active canvas, the command generates and exports the source code of that model in the selected language
- The source code can be afterwards compiled and executed, resulting in a program which performs simulation of the model
- Compilation of java program requires additionally a library named Engine.jar, this library also provides a way of executing compiled engine, by starting the java program from EngineRunner class
- For all other languages except java, additional files are needed. These files will be saved in the directory where the main engine file exists (if they aren't there yet)
- If the canvas has been edited since the last save operation, the File Save prompt will be displayed before the simulation starts

#### **Constraints:**

- At least one canvas is opened in the workspace

#### **4.1.18 File | Look&Feel**

- ➔ Metal
- ➔ CDE/Motif
- ➔ Windows

**Description:**

- With these commands, you can set the look and feel of Cell Illustrator to a GUI selected style.
- The selected GUI style is preserved upon restart of the program

**4.1.19 File | Print Area****Description:**

- With this command, you can print a portion of the canvas or save it to an image file in the PostScript, PNG, or JPEG format.
- The command opens the [Print Area Setup](#) dialog where you specify a canvas area to be printed.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- You cannot execute this command if a simulation is running.

**4.1.20 File | Print****Description:**

- With this command, you can print the whole model diagram and simulation charts or save them in an image file in PostScript, PNG, or JPEG format.
- The command opens the [Print](#) dialog where you select the scope and destination of the print function.

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.21 File | Exit****Description:**

- Exits the application.
- If any of the opened files has been modified after the last save operation, you will be prompted to save the changes before closing the file.

**4.1.22 Edit | Undo****Description:**

- Reverses the most recent edit action.
- Execute this command several times to undo results of subsequent edit commands.
- Starting (playing) simulation empties the Undo/Redo list. It is not possible to undo/redo any edit operation after a simulation starts.
- CTRL+Z is the keystroke shortcut for this command.

**Constraints:**

- There is an action to undo.
- No simulation is running.

#### 4.1.23 Edit | Redo

**Description:**

- Reverses the action of the last Undo command.
- Effects of subsequent Undo commands are reversed by executing the corresponding sequence of Redo commands
- Starting (playing) the simulation empties the Undo/Redo list. It is not possible to undo/redo any edit operation after a simulation starts.
- Shift+CTRL+Z is the keystroke shortcut for this command.

**Constraints:**

- There is an action to redo.
- No simulation is running.

#### 4.1.24 Edit | Cut

**Description:**

- Removes the selection from the active canvas and places it in the clipboard.
- CTRL+X is the keystroke shortcut for this command.

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

#### 4.1.25 Edit | Copy

**Description:**

- Copies the selected elements into the system clipboard
- CTRL+C is the keystroke shortcut for this command.

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

**4.1.26 Edit | Paste****Description:**

- Inserts the contents of the clipboard into the active canvas
- CTRL+V is the keystroke shortcut for this command.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- The clipboard must contain elements copied with the Copy or Cut operation.
- No simulation is running.

**4.1.27 Edit | Delete****Description:**

- Deletes the selected elements from the canvas.
- Del is the keystroke shortcut for this command.

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

**4.1.28 Edit | Duplicate****Description:**

- Duplicates the currently selected elements in the canvas.
- CTRL+M is the keystroke shortcut for this command.

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

**4.1.29 Edit | Extract**

**Description:**

- Extracts the selection and displays in a new canvas.
- This command has the same result as the sequence of commands: Edit | Copy, File | New and Edit | Paste.

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

**4.1.30 Edit | Find****Description:**

- Opens the [Finder](#) dialog where you can specify the text to search for in the canvas
- CTRL+F is the keystroke shortcut for this command.

**Constraints:**

- The command is disabled if the active canvas is empty.

**4.1.31 Edit | Select All****Description:**

- Selects all objects in the active canvas.
- CTRL+A is the keystroke shortcut for this command.

**Constraints:**

- The command is disabled if the active canvas is empty.

**4.1.32 Edit | Select None****Description:**

- Deselects all elements in the active canvas
- Shift+CTRL+A is the keystroke shortcut for this command.

**Constraints:**

- The command is disabled if the active canvas is empty.

### 4.1.33 Edit | Select Inverse

**Description:**

- Inverts the selection in the active canvas.
- CTRL+I is the keystroke shortcut for this command.

**Constraints:**

- The command is disabled if the active canvas is empty.

### 4.1.34 Edit | Align Selected Elements to Grid

**Description:**

- Aligns selected elements to the grid.
- When you insert or move entities they are aligned to the grid automatically. However, changing a grid size ([View | Grid Size](#)) may disturb the alignment. Also, a process inserted into a canvas by joining two entities with a connector is sometimes not aligned to a grid. In such a situation, the elements can be aligned using this command.
- See also the related commands: [View | Show Grid](#), [View | Grid Size](#)
- CTRL+Shift+G is the keystroke shortcut for this command.

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

### 4.1.35 Edit | Align all elements to Grid

**Description:**

- Aligns all elements to the grid
- When you insert or move entities they are aligned to the grid automatically. However, changing a grid size ([View | Grid Size](#)) may disturb the alignment. Also, a process inserted into a canvas by joining two entities with a connector is sometimes not aligned to a grid. In such a situation, the elements can be aligned using this command.
- See also the related commands: [View | Show Grid](#), [View | Grid Size](#)

**Constraints:**

- At least one element exists in the active canvas.
- No simulation is running.

#### 4.1.36 Edit | Align to

- Top
- Bottom
- Left
- Right
- Vertical
- Horizontal

##### **Description:**

- Aligns all the selected elements in one line to, respectively, the top-, bottom-, left- and rightmost element in the selection.
- *Align Vertical* and *Horizontal* position the selected elements along the vertical or horizontal line respectively, in the middle of the selection area.
- *Align to Top* and *Align to Bottom* command the placing of all selected elements in one horizontal line. *Align to Left* and *Align to Right* command the placing of all selected elements in one vertical line.

##### **Constraints:**

- At least two elements must be selected.
- No simulation is running.

#### 4.1.37 Edit | Insert Entity

- Continuous
- Discrete
- Generic

##### **Description:**

- Inserts an entity into the active canvas.
- The new entity is positioned in the center of the visible area of the canvas.

##### **Constraints:**

- at least one canvas is opened in the workspace
- No simulation is running.

#### 4.1.38 Edit | Insert Process

- Continuous
- Discrete
- Generic

##### **Description:**

- Insert a process into the active canvas
- The new process is positioned in the center of the visible area of the canvas.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- No simulation is running.

#### 4.1.39 Edit | Insert Image

**Description:**

- Inserts an image in a JPEG, GIF, or PNG file onto the active canvas. SVG (Scalable Vector Graphics) images can also be inserted.
- In the File Open dialog you can select the file name and type (Image File or SVG Image File) of the image to be inserted. The option “Save Internally” specifies whether the image should be saved internally - inside the model CSML file, or externally – as a reference to an external graphics file.
- The new image is positioned in the center of the visible area of the canvas.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- No simulation is running.

#### 4.1.40 Edit | Insert Text

**Description:**

- Inserts an empty text box into the active canvas.
- Double-click the text box and enter text from the keyboard.
- The new text box is positioned in the center of the visible area of the canvas.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- No simulation is running.

#### 4.1.41 Edit | Insert Frame

**Description:**

- Inserts a rectangular frame into the active canvas
- The new frame is positioned in the center of the visible area of the canvas.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- No simulation is running.

**4.1.42 Element | Entity Type**

- ➔ Continuous
- ➔ Discrete
- ➔ Generic

**Description:**

- Sets the type of the selected entities.
- Note that not all type combinations of connected processes, entities and connectors are valid. Observe the connection rules specified in the User Guide.

**Constraints:**

- At least one entity or process must be selected.
- No simulation is running.

**4.1.43 Element | Connector Type**

- ➔ Process
- ➔ Inhibitory
- ➔ Association

**Description:**

- Note that not all type combinations of connected processes, entities and connectors are valid. Observe the connection rules specified in the User Guide.

**Constraints:**

- At least one connector must be selected
- No simulation is running.

**4.1.44 Element | Reverse Direction****Description:**

- Reverses the connector direction.

**Constraints:**

- At least one connector must be selected.
- No simulation is running.

**4.1.45 Element | Transform****→ Rotate**

- 90
- 180
- 270

**Description:**

- Rotates the selected figures (entities, processes, text boxes, frames, etc.) by the specified angle. The rotation center is the center of the rectangular boundary for all the selected items.
- Connectors are not rotated. The position of a connector is always adjusted to the position of its start and end elements (entities, processes).

**Constraints:**

- At least one figure must be selected in the active canvas.
- No simulation is running.

**→ Size****Description:**

- Sets the size of the selected figures (process rectangles, connector circles, text boxes, frames, etc).
- Connector arrows are not resized.

**Constraints:**

- At least one figure must be selected in the active canvas.
- No simulation is running.

**→ Round Corners****Description:**

- For frames and hierarchical objects selected in the canvas, the command rounds the corners of their rectangular shapes.

**Constraints:**

- At least one figure must be selected in the active canvas.
- No simulation is running.

#### 4.1.46 Element | Arrange

- ➔ Bring to Front
- ➔ Bring Forward
- ➔ Send Backward
- ➔ Send to Back

##### **Description:**

- With this set of commands, you can set the depth of overlapping figures in the canvas. Depth defines the way in which overlapping figures are displayed. A figure with a lower depth value is displayed over a figure with a higher depth value.
- The depth value of each figure can be viewed and edited in [Element Settings](#) dialog box.
- *Bring Forward* increases the depth value of the selected figures by one.
- *Send Backward* decreases the depth value of the selected figures by one.
- *Bring to Front* shows the selected figure at the front.
- *Send to Back* hides the selected figure behind the other figures.

##### **Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

#### 4.1.47 Element | Group

##### **Description:**

- Assembles two or more selected elements into a single group element.
- A group can be moved or edited as one element.

##### **Constraints:**

- At least two elements must be selected in the active canvas.
- No simulation is running.

#### 4.1.48 Element | Ungroup

##### **Description:**

- Disassembles a selected group into individual elements.

##### **Constraints:**

- At least one group element must be selected in the active canvas
- No simulation is running.

#### 4.1.49 Element | Fill Color

**Description:**

- Fills the inside of selected figures with the specified color.

**Constraints:**

- At least one figure must be selected in the active canvas.
- No simulation is running.

#### 4.1.50 Element | Line Color

**Description:**

- Sets the line color of a selected figure to a color from the list.

**Constraints:**

- At least one figure must be selected in the active canvas.
- No simulation is running.

#### 4.1.51 Element | Line Style

- Straight
- Curve

**Description:**

- Sets the line style of the selected connectors. The user may choose between straight and curved lines.

**Constraints:**

- At least one connector must be selected in the active canvas.
- No simulation is running.

#### 4.1.52 Element | Show Support Path

**Description:**

- Switches on and off the display of the support path for the selected connectors. The support path is useful when drawing curved lines. It is a broken-line that surrounds the curved line.

**Constraints:**

- At least one connector must be selected in the active canvas.
- No simulation is running.

#### 4.1.53 Element | Stroke

**Description:**

- Sets the stroke (line pattern) of selected figures to a pattern from the list of available patterns.

**Constraints:**

- At least one figure must be selected in the active canvas.
- No simulation is running.

#### 4.1.54 Element | Replace Figure

- ➔ Association Connector
- ➔ Association Connector Arrow
- ➔ Continuous Entity
- ➔ Continuous Process
- ➔ Cross

**Description:**

- For one or more elements in the canvas, the command replaces their figures with the figure from the list.
- This operation changes the look of an element only; It has no impact on simulation results

**Constraints:**

- At least one figure must be selected in the active canvas.
- Not all figures can be replaced with different ones, e.g., a text box cannot be replaced with an ellipse, arrow, triangle or rectangle.
- No simulation is running.

#### 4.1.55 Element | Replace Arrow Start

- ➔ Association Connector Arrow
- ➔ Ellipse Arrow

- Image Arrow
- Inhibitory Connector Arrow
- Inhibitory Connector Arrow (bio)
- Process Connector Arrow
- Rectangle Arrow
- Triangle Arrow
- None

**Description:**

- With this command, you can replace the head of selected connector arrows with the arrow type from the list.

**Constraints:**

- At least one connector must be selected in the canvas.
- No simulation is running.

**4.1.56 Element | Replace Arrow End**

- Association Connector Arrow
- Ellipse Arrow
- Image Arrow
- Inhibitory Connector Arrow
- Inhibitory Connector Arrow (bio)
- Process Connector Arrow
- Rectangle Arrow
- Triangle Arrow
- None

**Description:**

- With this command, you can replace the tail of selected connector arrows with the figure from the list.

**Constraints:**

- At least one connector must be selected in the canvas.
- No simulation is running.

**4.1.57 Element | Remove Anchor**

**Description:**

- Transforms broken line connectors selected in the canvas into straight lines by removing an anchor.
- If a connector line is broken in several places (by several anchors), only the last anchor is removed.

**Constraints:**

- At least one broken line connector is selected.
- No simulation is running.

**4.1.58 Element | Remove All Anchors****Description:**

- Transforms broken-line connectors selected in the canvas into straight lines by removing all anchor points.
- If a line is broken in several places (with several anchors), all anchor points will be removed.

**Constraints:**

- At least one broken-line connector line must be selected.
- No simulation is running.

**4.1.59 Element | Edit Image****Description:**

- Opens the editor for the selected image.
- SVG files are edited by the GLIPS Graffiti SVG editor, which is an integral part of CI package.
- Other files, JPEG, PNG, and GIFF are edited by the default graphics editor that is associated with the PNG extension of your Windows or Mac OS. On Linux platform the default graphics editor is gimp.
- Standard CI images, e.g. process, entity or connector images cannot be edited. Only images inserted into the canvas from user files can be edited. To insert an image use the commands: Element | Replace Figure | Image or Edit | Insert Image.

**Constraints:**

- Exactly one editable image must be selected.
- Editable images are images saved in external or internal image files: JPEG, PNG, GIFF or SVG files.
- No simulation is running.

**4.1.60 Element | Reload Image****Description:**

- Reloads and redraws the image at the highest possible quality.

- The quality of scalable images (SVG) can lose quality during resize or replace operation.

**Constraints:**

- This command can be applied to SVG images only.
- No simulation is running.

#### 4.1.61 Element | References

**Description:**

- Displays the list of references available for this element.
- Choose an item from the pop up menu to open the URL in a Web Browser window.
- References define links from the selected element to external resources specified as URLs. Reference may define a link from the selected element to a database element, such as an entry in a database or a term in a controlled vocabulary
- References can be associated to all elements: entities, processes, connectors.
- You can view/edit the list of references by choosing [Element | References | Add/Edit URL](#)

**Constraints:**

- Exactly one element is selected in the active canvas.

#### 4.1.62 Element | References | Add/Edit URL

**Description:**

- Enables adding new references to the reference list of the selected element.
- This command opens the [External References Dialog Box](#) where you can define a reference. You can view the list of references associated with an element in the [Element Settings Dialog Box](#) in the *Biological* tab
- URL References can be associated to all elements: entities, processes, connectors.

**Constraints:**

- Exactly one element is selected in the active canvas.

#### 4.1.63 Element | URL Templates

**Description:**

- Displays the list of URL templates available for this element.
- Choose a link from the list to open the URL in a Web Browser window.

- The URL templates are associated to all elements: entities, processes, connectors. You can view/edit the list of predefined URL templates in the *Hyperlink Templates* section in the [Preferences Dialog](#)

**Constraints:**

- Exactly one element is selected in the active canvas.

#### 4.1.64 Element | Text

- Fill Color
- Line Color
- Stroke

**Description:**

- The Fill Color command sets the text background color for all selected items: elements, text boxes, etc.
- The Line Color command sets the text field border color.
- The Stroke command sets the text field border pattern.

**Constraints:**

- At least one item must be selected in the active canvas.
- No simulation is running.

#### 4.1.65 Element | Font

- Name
- Size
- Style
- Color

**Description:**

- Sets the text font style in all selected items: elements, text boxes, etc.

**Constraints:**

- At least one item must be selected in the active canvas.
- No simulation is running.

#### 4.1.66 Element | Show Element

- On
- Off

**Description:**

- Shows or hides the graphical representation of all selected elements including the child figures, e.g. shows/hides an element and all its labels: name, variable, value.

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

**4.1.67 Element | Show Name**

- On
- Off

**Description:**

- Shows or hides, respectively, names of all selected elements.

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

**4.1.68 Element | Show Variable**

- On
- Off

**Description:**

- Shows or hides, respectively, the variable name for all selected elements

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

**4.1.69 Element | Show Value**

- On

→ Off

**Description:**

- Shows or hides the value labels of selected elements

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

#### 4.1.70 Element | Show Firing Style

→ On

→ Off

**Description:**

- Shows or hides the firing style of the selected elements. The firing style is the property of process elements.

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

#### 4.1.71 Element | Create Chart

**Description:**

- Creates a new chart for the entities that are selected in the canvas window.
- If a chart that contains selected entities already exists, no new chart is created; the existing chart is opened.

**Constraints:**

- If more than eight entities are selected, a warning message appears.
- At least one entity must be selected in the canvas to execute this command.
- No simulation is running.

#### 4.1.72 Simulation | Play

**Description:**

- If the model in the active canvas is in the “initialized” or “paused” state, the command starts the simulation.
- The accuracy and length of simulation are controlled by the *Sampling interval* and the *Simulation time* which are properties of the model. You can set these parameters in the [Simulation Settings](#) dialog.
- For a new canvas, the *Sampling Interval* and the *Simulation Time* are initialized on the base of user preference settings. See [Preferences](#) for more details.

- The speed of simulation is roughly 1pt per 1 sec.
- The *Current speed* setting in the Simulation Settings dialog is not relevant for simulations started with the Play command.
- Other simulation options, e.g., *Enhanced firing*, are used according to the settings in the user preferences. (The Enhanced firing should be always *on* in CI3.0. The option remains for backward compatibility with the previous versions of Cell Illustrator and will be removed in future releases.)
- Process firing and changes of entity values are shown in the canvas during the simulation.
- The status of a simulation run is displayed at the bottom of the CI main window.
- If there are any charts defined for the model, one or more [Chart Windows](#) are opened when the command is executed. The charts are periodically updated as the simulation runs. You can define new charts in the [Chart Settings](#) dialog.
- Only the active canvas is available in the workspace. All other canvas windows are temporally closed in order to avoid inconsistent states.
- The simulation stops when: (1) the user has executed the [Simulation | Stop and Initialize](#) command, or (2) the user has executed the [Simulation | Pause](#) command, or (3) the simulation time has reached the value specified (in pt units) by the *Simulation time* setting in the Simulation Settings dialog.
- Only one simulation at a time can be executed.
- If the canvas has been edited since the last save operation, the *Save Modified File* prompt will be displayed before the simulation starts

#### **Constraints:**

- At least one canvas is opened in the workspace
- The model in the active canvas is not in the “simulation end” state

#### **4.1.73 Simulation | Step Play**

##### **Description:**

- The command executes one simulation step for the model in the active canvas.
- One step corresponds to 1 *Sampling interval* in Petri net time units.
- The *Sampling interval* is a property of the active canvas and it is displayed in the [Simulation Settings](#) dialog.
- For a new canvas, the *Sampling interval* is initialized on the base of the user preference settings. See [Preferences](#) for more details.
- The *Current speed* setting and the *Simulation time* displayed in the Simulation Settings dialog do not matter for this command.
- Other simulation options, e.g., *Enhanced firing*, are used according to the settings in the category *Simulation| Extra Options* in the user preferences.
- Process firing and changes of entity values are shown in the canvas during the simulation according to *Simulation | Animation Options* in the user preferences. No tokens are displayed, however, i.e., the *Token image* setting is ignored.
- If there are any charts defined for the model, one or more [Chart Window](#) is opened when the command is executed.

- The simulation status is displayed at the bottom of the CI main window.

**Constraints:**

- At least one canvas is opened in the workspace

#### 4.1.74 Simulation | Pause

**Description:**

- Pauses a running simulation.
- The simulation can be resumed with the [Simulation | Play](#) and other play commands.
- Also, the simulation can be continued in the step mode with [Simulation | Step Play](#) or [Simulation | Step Play with Animation](#)

**Constraints:**

- The command is disabled if no simulation is running.

#### 4.1.75 Simulation | Stop and Initialize

**Description:**

- If there is a running simulation, it is stopped.
- Variables associated with entities are reset to their initial values.

**Constraints:**

- The command is enabled if a simulation for the model in the active canvas has been paused or completed.

#### 4.1.76 Simulation | Fast Play

**Description:**

- Starts the simulation in fast mode for the model in the active canvas. The command behaves like [Simulation | Play](#) with the following exceptions
- The speed of simulation corresponds to the *Simulation Speed* setting in the [Simulation Settings](#) dialog. However, it is limited by the hardware on which the program runs.
- The *Simulation Speed* range displayed in the Simulation Settings dialog is defined by the *Max speed* setting in the category *Simulation | Extra Options* of the user preference settings. See [Preferences](#) for more details.

#### 4.1.77 Simulation | Max Speed Play

##### Description:

- Starts the simulation in the fastest mode. The command behaves like [Simulation | Fast Play](#) with the following exceptions:
- The speed of the simulation is the highest possible speed given by the hardware limits. The canvas is not updated until the simulation is finished. The simulation animation settings in the *Simulation | Extra Options* in the user [Preferences](#) are ignored.

#### 4.1.78 Simulation | Play with Animation

##### Description:

- Starts the simulation in animation mode for the model in the active canvas. The command behaves like [Simulation | Play](#) with the following exceptions
- For discrete processes, a moving token is displayed when a process fires, according to the setting of *Token image* option *Simulation | Animation Options* in the user [Preferences](#),
- For a discrete entity, tokens remaining at the entity are shown graphically if there are less than 5 of them. Otherwise, the numerical value is displayed.

#### 4.1.79 Simulation | Step Play with Animation

##### Description:

- For the net in the active canvas, the command executes one simulation step with animation. The command behaves like the [Simulation | Step Play](#) with the following exceptions:
- For discrete processes, a moving token is displayed when a process fires, according to the setting of *Token image* option *Simulation | Animation Options* in the user [Preferences](#),
- For a discrete entity, tokens remaining at the entity are shown graphically if there are less than 5 of them. Otherwise, the numerical value is displayed.

#### 4.1.80 Simulation | Send to Server

##### Description:

- Submits the model in the active canvas for simulation at a remote Cell Illustrator Server selected from the pop up list and opens the [Submitted Simulations](#) dialog box.
- One or more entities and/or processes must be selected for logging in the active model. This can be done in the [Element Lists](#) dialog box. Otherwise, the simulation will finish immediately with the error: “Nothing has been selected for logging. Simulation has been aborted”
- After submitting the simulation to a remote server, you may continue to work in CI workspace or even close the CI workspace. CI will reconnect to the submitted simulation the next time you start CI. If the simulation is finished then the output files will be downloaded.
- After the simulation is finished successfully or interrupted, the simulation results are automatically returned in the simulation log file. The simulation log is copied into the output directory of the submitted input file and added to the simulation history. It can be analyzed in CI Player as any other log file.
- A remote simulation may also finish with an error. See the table below for the most common remote simulation problems:

<b>Problem</b>	<b>Reason</b>	<b>Fix</b>
The “Authorization Error” dialog is displayed	The user name or password is invalid	Ask the Cell Illustrator Server administrator for the correct authorization data and enter the user name and password again.
One of the following messages is displayed: “Axis engine could not find the target service” or “(404) ...”	There are connection problems with the server, e.g., the URL is invalid or the server is disconnected from the network	Check the engine URL. Check the connection to the server.

**Constraints:**

- At least one server must be registered in the CI workspace. The list of servers can be viewed and managed in the [Setup Servers](#) dialog box.

**4.1.81 Simulation | Show Submitted Simulations**

**Description:**

- Opens the [Submitted Simulations](#) dialog box, with progress and status information about the submitted simulations.

**4.1.82 Simulation | Setup Servers**

**Description:**

- Opens the [Setup Servers](#), with detailed information about the registered *CI Servers*.
- This command also facilitates management of the server list, e.g. the addition of new servers, or the editing or removal of existing ones.

**4.1.83 Simulation | Run SECG Simulation****Description:**

- Starts the SECG simulation.
- Simulation Engine Code Generator (SECG) is a simulation engine that enables you to simulate the selected model in a special way. SECG performs the simulation in the following steps:
  - o Generate the Java source code that represents the Petri Net model of the selected canvas
  - o Compile the source code using Java Compiler (javac)
  - o Execute the compiled program
  - o Starts the SECG simulation.
  - o Save simulation log
- Thanks to this approach large models can be simulated much faster than using the default simulation engine included in CI.
- The simulation (running) is done in a separate process (not in CI program)
- The model for the simulation and parameters, such as sampling interval, chart setup, update of log, are obtained from the csml file
- The products of the simulation can be set using [Simulation | Setup SECG](#) command
- Result of a SECG simulation can be CSV log, charts or a CI log file (CIL), which can be viewed by CI Player

**Constraints:**

- At least one canvas is opened in the workspace
- The java compiler should be available and path to it should be setup correctly

**4.1.84 Simulation | Run Reference Simulation****Description:**

- This task is analogical to the [Simulation | Run SECG Simulation](#)
- At the start of the simulation a CSV data file must be selected, the file can contain time series of values (format similar to Cell Illustrator CSV simulation log)
- If the simulation results are show as charts, then the charts will contain reference plot obtained from the CSV data file (if values for the entity with given name is present in that file)

**Constraints:**

- Similar to [Simulation | Run SECG Simulation](#)
- The file must be chosen and it must be a proper CSV file

#### 4.1.85 Simulation | Run Parameterized Simulation

##### Description:

- Starts the SECG simulation in the bulk mode
- Allows specifying some entities as parameters (their start value will change in different simulations)
- For each parameter a value range is specified (the smallest/starting and the biggest possible value of the entity is selected, as well as description how the values should differ from each other). The parameters are set in the [SECG Passing Parameters](#) dialog
- Runs simulation for each combination of parameter values
- Runs the simulations in an external process
- For a long simulations allows canceling it
- The view of the simulation results is controllable by the [Parameterized Simulation Results](#)

##### Constraints:

- Similar to [Simulation | Run SECG Simulation](#)
- At least one parameter must be selected

#### 4.1.86 Simulation | Setup SECG

##### Description:

- Opens the [SECG Configuration](#) dialog, which contains settings related to running SECG simulations and exporting source code of the simulation

##### Constraints:

- At least one canvas is opened in the workspace

#### 4.1.87 View | Gene Net Mode

##### Description:

- Switches between the *Biopathway Modeling* and *Gene Network* modes
- If this menu item is checked then you are in the *Gene Net* mode
- A network build in the *Biopathway Modeling* mode might not be a correct *Gene Network*. This is the case if one process has more than one input or output entities, which is normal for Petri net models of biopathways, but forbidden for gene networks. In the case of such a conflict, a warning is displayed when switching from the biopathway modeling to the gene networks view saying the model is not a correct gene network and some connection between entities will be ignored. In the gene network view one process is represented by one edge connecting the input and output entity of this process.

For each process with multiple input or output entities, the edge connects only one input and output entity of the process.

#### 4.1.88 View | Show User Units

##### Description:

- Switches between the standard unit and user unit modes
- The units for each entity are defined in [Element Settings Dialog Box](#)
- If this menu item is unchecked then you are in the standard (absolute) unit mode. In this mode the values of all entities are expressed in the standard (absolute) unit. This view allows for better understanding of the mathematical Petri net model and its processes, since the simulation is done in this absolute units.
- If this menu item is checked then you are in the user unit mode. In this mode the entity value is expressed in the selected unit along with and displayed along with unit name in the lower-right corner. This view allows for better understanding of the physical model, since the entity values are given in user specified units.

**Note:** The simulation engine supports non-standard units, however it performs the calculation in standard units. The value of each entity expressed in standard units is the absolute value that is used by in the Petri Net model. This has the following consequences:

- Process speed should be always defined in standard units
- Entities representing two different physical properties, e.g. mass and volume can be connected by a process or used in one mathematical formula (script). The process or formula will operates on the absolute entity values expressed in standard units of each physical property.
- Non-standard units are converted to standard ones during initialization of the entity value, e.g. during the file open operation.

#### 4.1.89 View | Zoom In

##### Description:

- The command brings a virtual camera closer to the model in the active canvas
- If necessary, the command will enlarge the canvas by increasing its width and/or height.
- [View | Actual Size](#) reverts the canvas to its original scale and size.

##### Constraints:

- At least one canvas window must be opened in the workspace.

#### 4.1.90 View | Zoom Out

**Description:**

- The command brings a virtual camera farther from the model in the active canvas window.
- [View | Actual Size](#) reverts the canvas to its original scale

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.91 View | Fit in Canvas****Description:**

- If one or more elements are selected, the command moves the virtual camera to display the selected elements in the canvas window.
- Otherwise, the virtual camera is moved to fit the display of all elements in the active window.
- If necessary, the command will enlarge the canvas by increasing its width and/or height.
- [View | Actual Size](#) reverts the canvas to its original scale and size

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.92 View | Actual Size****Description:**

- The command moves the virtual camera so that the canvas is displayed with its actual size.
- If necessary, the command will shrink the canvas by decreasing its width and/or height.

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.93 View | View inside****Description:**

- Displays the internal structure (model) of the selected hierarchical object in a new canvas window.
- The model of the hierarchical object cannot be edited; the edit options are disabled for this canvas window.

- The canvas window name for the opened object is the name of the object.

**Constraints:**

- Exactly one hierarchical object must be selected in the active canvas.

#### **4.1.94 View | Show All Charts**

**Description:**

- Opens all [Chart Windows](#) defined for the active canvas

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### **4.1.95 View | Hide All Charts**

**Description:**

- Closes all [Chart Windows](#) defined for the active canvas

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### **4.1.96 View | Show Grid**

**Description:**

- Toggles the grid display on and off for all canvas windows.
- The setting is preserved in the user preference settings and applies also when the application is started next time. See [Preferences](#) for more details.

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### **4.1.97 View | Antialiasing**

**Description:**

- Toggles antialiasing on and off for all canvas windows.
- With the antialiasing in the *on* state, model diagrams look better but it takes more time to draw them.
- The setting is preserved in the user preference settings and applies also when the application is started next time. See [Preferences](#) for more details.
- During simulation, antialiasing is temporarily forced to the off state.

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### 4.1.98 View | Grid Size

**Description:**

- Sets the grid size for all canvas windows
- The setting is preserved in the Canvas section of user preference settings and applies also when the application is started next time. See [Preferences](#) for more details.

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### 4.1.99 View | Background Color

**Description:**

- Sets the background color for the active canvas window

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### 4.1.100 Analyze | Add to Subnet

**Description:**

- Adds the selected elements (entities, processes and connectors) to the *subnet*.
- If an connector is added, both the source and target vertex are additionally added to the subnet
- If an entity or process is added, all connectors that connect this element with other subnet elements are additionally added
- The color scheme of the canvas is changed if the *subnet* is not empty: *Subnet* elements (entities, processes and connectors) are marked in red, while all other elements are displayed in gray. If the subnet is empty the network elements are displayed in their normal colors.

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

**4.1.101 Analyze | Remove from Subnet****Description:**

- Removes the selected elements (entities, processes and connectors) from the *subnet*
- The color scheme of the canvas is changed if the *subnet* is not empty: *Subnet* elements (entities, processes and connectors) are marked in red, while all other elements are displayed in gray. If the subnet is empty the network elements are displayed in their normal colors.

**Constraints:**

- At least one element must be selected in the active canvas.
- No simulation is running.

**4.1.102 Analyze | Clear Subnet****Description:**

- Removes all elements (entities, processes and connectors) from the *subnet*.
- After this operation the *subnet* is empty.
- The color scheme of the canvas is changed if the *subnet* is not empty: *Subnet* elements (entities, processes and connectors) are marked in red, while all other elements are displayed in gray. If the subnet is empty the network elements are displayed in their normal colors.

**Constraints:**

- At least one subnet element is selected.
- No simulation is running.

**4.1.103 Analyze | Extract Subnet****Description:**

- Copies the subnet elements (entities, processes and connectors) from the active canvas and creates a new canvas with the *subnet* elements only.

**Constraints:**

- At least one element must be in the subnet.
- No simulation is running.

**4.1.104 Analyze | Pathway Search****Description:**

- Opens the [Pathway Search Dialog Box](#) where you can search for subnetworks around the selected entity.

**Constraints:**

- At least one canvas window must be opened in the workspace.
- No simulation is running.

**4.1.105 Analyze | Compare**

**Description:**

- Compares (merges) two networks from the canvases in the workspace.
- Exactly two canvases must be opened in the workspace
- The merging operation compares the two networks and finds the common part of the networks (intersection), the differences between the networks and the sum of the two networks (union). The networks are compared by searching for identical entities, processes and connectors, the definition of entity process and connectors identity is described below.
- The selected network (*Network 1*) is treated in a unique way during networks merging: The processes, entities and connectors in the intersection network and also common processes, entities and connectors in the union network inherit their properties from corresponding processes, entities and connectors from the selected network.
- The comparison results are displayed in four new canvases arranged side by side for simultaneous display:
  - the Differences between *Network 1* and *Network 2*
  - the Differences between *Network 2* and *Network 1*
  - the Union of *Network 1* and *Network 2*
  - the Intersection of *Network 1* and *Network 2*
- All connectors in *Network 1* are marked by one color denoted by the *difference1* color (default is red) and all connectors in *Network 2* are marked by another color denoted by the *difference2* color (default is green). The same colors are used for the corresponding connectors in the resulting networks. The connectors that are common in *Network1* and *Network2* are colored by the *intersection* color (default value is magenta).
- The default values for the predefined colors *difference1*, *difference2* and *intersection* can be defined in the [Preferences Dialog Box](#) (section Compare).
- The connector colors resulting from the merging operation are persistent, i.e., you can save the output networks and view the connector colors after you open these files.
- The difference between the *Networks 1* and *2*, contains those connectors of the *Network 1*, which are not in the *Network 2*. Please note that the difference operation gives priority to connectors, rather than to their source and target vertexes. The difference between *Network 1* and *Network 2* excludes the common (intersecting) connectors from the original *Network 1* first. Then, all source and target vertexes are added for these connectors that are left. This means that a common (intersecting) entity or process might be in the difference network, but a common connector must not be included in the difference network.

**Identity Definitions:**

- Equality between two entities: two entities are equal if their corresponding values of Name is equal.
- Equality between two processes: two processes are equal if their corresponding values of Name is equal.
- Equality between two connectors: two connectors are equal if their corresponding source and target are equal according to the above definition of the relation of equality between the objects.

**Constraints:**

- Exactly two canvases must be opened in the workspace.

**4.1.106 Analyze | Gene Mining****Description:**

Opens the [Gene Mining Dialog Box](#)

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.107 Dialog | Hide All Dialogs****Description:**

- Closes all property dialogs

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.108 Dialog | Restore All Dialogs Display****Description:**

- Restores initial positions of all dialogs.

**4.1.109 Dialog | Element Lists****Description:**

- Toggles on and off the display of the [Element Lists](#) dialog
- The contents of the dialog correspond to the active canvas window.
- The dialog gets the focus in case it gets opened.

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### **4.1.110 Dialog | Element Settings**

##### **Description:**

- Toggles on and off the display of the [Element Settings](#) dialog
- The contents of the dialog correspond to the current selection in the active canvas window
- The dialog gets the focus in case it gets opened

##### **Constraints:**

- At least one canvas window must be opened in the workspace.

#### **4.1.111 Dialog | Navigator**

##### **Description:**

- Toggles on and off the display of the [Navigator](#) dialog
- The contents of the dialog correspond to the active canvas window
- The dialog gets the focus in case it gets opened

##### **Constraints:**

- At least one canvas window must be opened in the workspace.

#### **4.1.112 Dialog | Simulation Settings**

##### **Description:**

- Toggles on and off the display of the [Simulation Settings](#) dialog
- The contents of the dialog correspond to the active canvas window
- The dialog gets the focus in case it gets opened

##### **Constraints:**

- At least one canvas window must be opened in the workspace.

#### **4.1.113 Dialog | Chart Settings**

##### **Description:**

- Toggles on and off the display of the [Chart Settings](#) dialog

- The contents of the dialog correspond to the active canvas window
- The dialog gets the focus in case it gets opened

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### **4.1.114 Dialog | Preferences**

**Description:**

- Toggles on and off the display of the [Preferences](#) dialog
- The dialog gets the focus in case it gets opened

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### **4.1.115 Dialog | View Settings**

**Description:**

- Toggles on and off the display of the [View Settings](#) dialog
- The contents of the dialog correspond to the active canvas window
- The dialog gets the focus in case it gets opened

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### **4.1.116 Dialog | Finder**

**Description:**

- Toggles on and off the display of the [Finder](#) dialog
- The newly opened dialog displays the results of the last search
- The dialog gets the focus in case it gets opened

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### **4.1.117 Dialog | Simulation History**

**Description:**

- Toggles on and off the display of the [Simulation History](#) dialog
- The opened dialog gets the focus

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.118 Dialog | Graph Layout****Description:**

- Toggles on and off the display of the [Graph Layout](#) dialog
- The opened dialog gets the focus

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.119 Dialog | Edit Units****Description:**

- Toggles on and off the display of the [Edit Units](#) dialog
- The opened dialog gets the focus

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.120 Dialog | Biological Elements****Description:**

- Toggles on and off the display of the [Biological Elements](#) dialog
- The dialog gets the focus in case it gets opened

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.121 Dialog | CSMLDB Search****Description:**

- Toggles on and off the display of the [CSMLDB Search Dialog](#)
- The dialog gets the focus in case it gets opened

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.122 Dialog | Project Manager****Description:**

- Toggles on and off the display of the [Project Manager Dialog](#)
- The dialog gets the focus in case it gets opened

**4.1.123 Window | Cascade Canvases****Description:**

- The command cascades canvas windows.

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.124 Window | Tile Canvases****Description:**

- The command tiles canvas windows.

**Constraints:**

- At least one canvas window must be opened in the workspace.

**4.1.125 Window | Minimize All Canvases****Description:**

- The command minimizes all canvas windows

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### 4.1.126 Window | Maximize All Canvases

**Description:**

- The command maximizes all canvas windows.

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### 4.1.127 Window | Duplicate Canvases

**Description:**

- The command duplicates an active canvas window by creating a new view for the same model file
- The name of the new window is the name of the original window with “+”
- All duplicate canvases represent the same model. Thus, any modification of the model in one canvas is immediately updated in all the duplicate canvases.
- [File | Close File](#) closes all the duplicate canvases that correspond to the active canvas

**Constraints:**

- At least one canvas window must be opened in the workspace.

#### 4.1.128 Help | Cell Illustrator Help

**Description:**

- Opens the HTML help system for Cell Illustrator.

#### 4.1.129 Help | User Guide

**Description:**

- Opens the Cell Illustrator User Guide.

**Constraints:**

- The User Guide is a PDF document. Adobe Acrobat Reader or another software capable of reading PDF documents needs to be installed and configured on your machine.

#### 4.1.130Help | Cell Illustrator Online

**Description:**

- Opens the home page for CI Online project <https://cionline.hgc.jp/> in the default browser.
- This project research project at the University of Tokyo drives the development of Cell Illustrator.

**Constraints:**

- The Internet connection must be available.

#### 4.1.131Help | CSML Online

**Description:**

- Opens the [www.csml.org](http://www.csml.org) web site in the default browser.
- CSML (Cell System Modeling Language) is the XML file format and OWL ontology that is used in Cell Illustrator to store and exchange models.

**Constraints:**

- The Internet connection must be available.

#### 4.1.132Help | Cell Illustrator User Forum

**Description:**

- Opens the user forum in the default browser.

**Constraints:**

- The Internet connection must be available.

#### 4.1.133Help | GNI Website

**Description:**

- Opens the home page of GNI Ltd.

**Constraints:**

- The Internet connection must be available.

#### 4.1.134 Help | About Cell Illustrator

**Description:**

- Displays the dialog [About Cell Illustrator](#) with the version and license information

## 4.2 CI Toolbars

### 4.2.1 Edit Toolbar

This toolbar is located at the top of the main window and contains a set of buttons for the most frequent edit operations.

Icon	Button Name	Description
	Edit Parts	Opens the <a href="#">Edit Parts</a> drop-down menu with commands to use a repository of reusable model parts
	Biological Elements	Toggles <a href="#">Biological Elements</a> dialog box
	CSMLDB Search	Toggles <a href="#">CSMLDB Search Dialog</a>
	Project Manager	Toggles <a href="#">Project Manager Dialog</a>
	Selection Mode	In this mode, you can select elements on the canvas with the arrow cursor.
	Create Continuous Entity	Push this button and click on the active canvas to insert a continuous entity. Each subsequent click adds a new entity.
	Create Continuous Process	Push this button and click on the active canvas to insert a continuous process. Each subsequent click adds a new process.
	Create Discrete Entity	Push this button and click on the active canvas to insert a discrete entity.
	Create Discrete Process	Push this button and click on the active canvas to insert a discrete process.
	Create Generic Entity	Push this button and click on the active canvas to insert a generic entity.
	Create Generic Process	Push this button and click on the active canvas to insert a generic process.
	Create Process Connector	Push this button and draw a line between two elements on the active canvas to insert a process connector.

	Create Inhibitory Connector	Push this button and draw a line between two elements on the active canvas to insert an inhibitory connector
	Create Association Connector	Push this button and draw a line between two elements on the active canvas to insert an association connector
	Create Frame	Push this button and drag the mouse cursor on the active canvas to insert a frame
	Create Note	Push this button and drag the mouse cursor on the active canvas to insert a text note.
	Manual Move	Switches Cell Illustrator to the mode, where you can change the visible area of the active canvas by dragging the canvas with the mouse.
	Zoom In	In this mode, click on the active canvas to zoom in.
	Zoom Out	In this mode, click on the active canvas to zoom out.
	Reset Zoom	See <a href="#">View   Actual Size</a>
	Fit in Canvas	See <a href="#">View   Fit in Canvas</a>
	Group	See <a href="#">Element   Group</a>
	Ungroup	See <a href="#">Element   Ungroup</a>
	Insert Image	See <a href="#">Edit   Insert Image</a>
	Set Color	Click on the popup list of colors to apply the color to selected elements on the canvas.
	Select Color Tool	With this button, you can select the Fill Color, Line Color or the Text Color as the current setting for the Set Color command
	Set View Mode	With this button, you can set global view mode. See <a href="#">View Settings   Global Setting</a>
	Set Stroke	The command applies a stroke from a drop-down list to selected elements on the

		canvas.
	Toggle the Antialiasing Status	See <a href="#">View   Antialiasing</a>
	Toggle the Grid Visible Status	See <a href="#">View   Show Grid</a>
	Go To BioPACS	See <a href="#">File   Import   BioPACS</a>

#### 4.2.2 File Toolbar

This toolbar is located at the left side of the main window, above the Undo/Redo and Simulation toolbars. It consists of a set of buttons for file management operations.

Icon	Toggle Button	Name	Full Description
	No	Create New Canvas	See <a href="#">File   New</a>
	No	Open Canvas File	See <a href="#">File   Open</a>
	No	Close Canvas	See <a href="#">File   Close File</a>
	No	Save Active Canvas	See <a href="#">File   Save</a>
	No	Save Canvas To Selected File	See <a href="#">File   Save as</a>
	No	Close All Canvases	See <a href="#">File   Close All Files</a>

#### 4.2.3 Undo/Redo Toolbar

This toolbar is located at the left side of the main window, below the File Toolbar and above the Simulation Toolbar. It contains buttons for Undo/Redo and Align commands.

Icon	Name	Description
	Undo	See <a href="#">Edit   Undo</a>
	Redo	See <a href="#">Edit   Redo</a>

	Align Top	See <a href="#">Edit   Align to</a>
	Align Bottom	See <a href="#">Edit   Align to</a>
	Align Left	See <a href="#">Edit   Align to</a>
	Align Right	See <a href="#">Edit   Align to</a>
	Align Vertical	See <a href="#">Edit   Align to</a>
	Align Horizontal	See <a href="#">Edit   Align to</a>

#### 4.2.4 Simulation Toolbar

This toolbar is located on the left side of the main window below the File Toolbar and Undo/Redo Toolbar. It contains buttons for starting and stopping simulation.

Icon	Name	Description
	Play Simulation	See <a href="#">Simulation   Play</a>
	Step Play simulation	See <a href="#">Simulation   Step Play</a>
	Pause Simulation	See <a href="#">Simulation   Pause</a>
	Stop Simulation and Initialize	See <a href="#">Simulation   Stop and Initialize</a>
	Fast Play Simulation	See <a href="#">Simulation   Fast Play</a>
	Max Speed Play Simulation	See <a href="#">Simulation   Max Speed Play</a>
	Play with Animation	See <a href="#">Simulation   Play with Animation</a>
	Step Play Simulation with Animation	See <a href="#">Simulation   Step Play with Animation</a>
	Export Simulation Log	See <a href="#">File   Export   Simulation Log</a>

#### 4.2.5 Dialog Toolbar

This toolbar is located on the right side of the main window and contains buttons that open and close property dialog windows.

Icon	Name	Description
	Toggle Element Lists Visible Status.	See <a href="#">Dialog   Element Lists</a>
	Toggle Element Settings Visible Status	See <a href="#">Dialog   Element Settings</a>
	Toggle External References Visible Status	See <a href="#">Element   References</a>
	Toggle Navigator Visible Status	See <a href="#">Dialog   Navigator</a>
	Toggle Preferences Visible Status	See <a href="#">Dialog   Preferences</a>
	Toggle View Settings Visible Status	See <a href="#">Dialog   View Settings</a>
	Toggle Chart Settings Visible Status	See <a href="#">Dialog   Chart Settings</a>
	Toggle Simulation Settings Visible Status	See <a href="#">Dialog   Simulation Settings</a>
	Toggle Simulation History Visible Status	See <a href="#">Dialog   Simulation History</a>
	Toggle Edit Units Visible Status	See <a href="#">Dialog   Edit Units</a>
	Toggle Graph Layout Visible Status	See <a href="#">Dialog   Graph Layout</a>
	Toggle Finder Visible Status	See <a href="#">Dialog   Finder</a>
	Toggle Pathway Search Visible Status	See <a href="#">Analyze   Pathway Search</a>
	Toggle Gene Mining Visible Status	See <a href="#">Analyze   Pathway Search</a>
	Hide all dialog windows	See <a href="#">Dialog   Hide All Dialogs</a>

## 5 Drawing Canvas

The canvas window is the place where you build a model. In addition to commands available in the Menu Bar and the toolbars, you can right click (CTRL click on a Macintosh) on the canvas or on a selected element in the canvas to access a popup menu customized to your selection.

During simulation, the canvas window is updated with entity value changes. In some simulation modes, processes that fire are marked with color and animated tokens move between entities.

You can customize the background color and other properties of your canvas windows by editing the Canvas section of the application global settings in the [Preferences](#) dialog. Simulation visualization options are defined in the Animation Options section.

### 5.1 Canvas Popup Menus

Selection	Popup Menu
Canvas	Find
	-----
	Undo
	Redo
	-----
	Select All
	-----
	Paste
	-----
	Insert Entity
	Insert Process
	Insert Image
	-----
	Import
	-----
Background Color	
-----	
Duplicate Canvas	

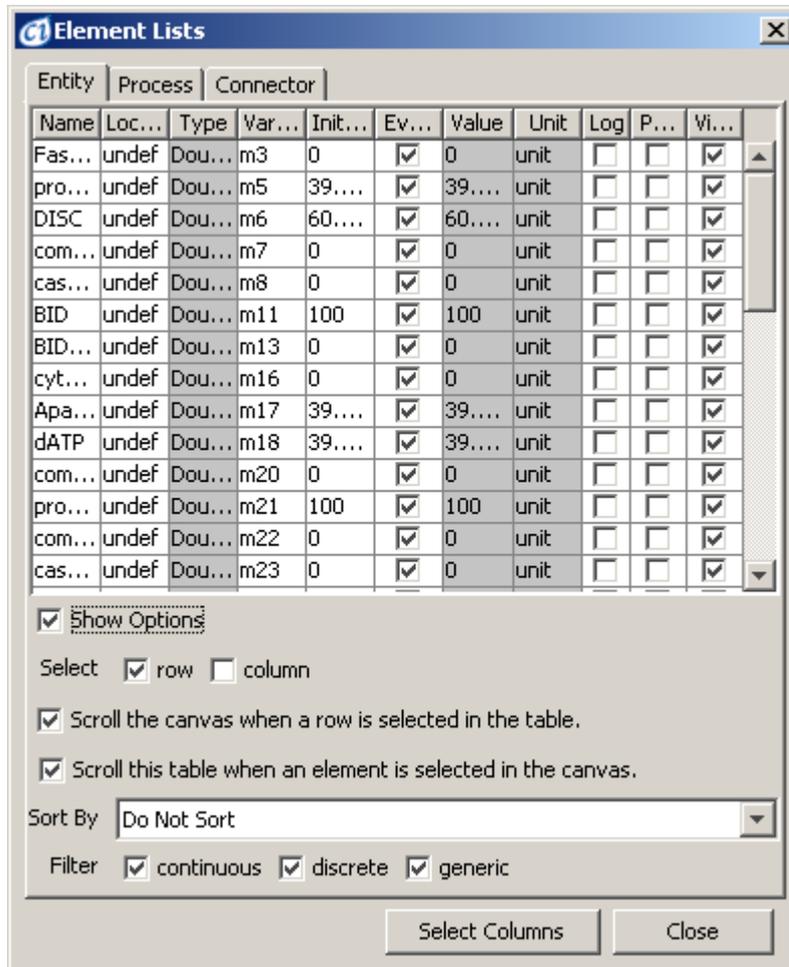
<b>Entity</b>	Add to Subnet
	Remove from Subnet
	-----
	Cut
	Copy
	Delete
	Duplicate
	-----
	Arrange
	Edit Image
	Reload Image
	-----
	Type
	-----
	Transform
	-----
	Fill Color
	Line Color
	Stroke
	-----
	Replace Figure
	-----
	Create Chart
	-----
	References
URL Templates	

<b>Process</b>	Add to Subnet
	Remove from Subnet
	-----
	Cut
	Copy
	Delete
	Duplicate
	-----
	Arrange
	-----
	Type
	Edit Image
	Reload Image
	-----
	Transform
	-----
	Fill Color
	Line Color
	Stroke
	-----
	Replace Figure
	-----
	References
URL Templates	
<b>Connector</b>	Cut
	Delete
	-----
	Arrange
	-----
	Connector Type
	Reverse Direction
	-----
	Remove Anchor
	Remove All Anchors
	-----
	Fill Color
	Line Color
	Stroke
	-----
	Replace Arrow Start
	Replace Arrow End
-----	
References	

<b>Object</b>	Cut
	Copy
	Delete
	Duplicate
	-----
	Arrange
	-----
	View inside
	-----
	Transform
	-----
	Fill Color
	Line Color
	Stroke
	-----
	Replace Figure
-----	
References	

## 6 Element Lists

For the model in the active canvas, the Element Lists modeless dialog displays lists of entities, processes and connectors together with values of their major properties.



The *Element Lists* dialog box consists of the tabbed tables *Entity*, *Process*, *Connector* and the *Options* controls.

The following operations can be done for each of the table:

- Select an element on the canvas by clicking on a row
- Sorts all rows according to the specified column by clicking on the column header,
- Edit a given property by clicking or double clicking a cell
- Define the same value of all elements in a column by selecting the Select column option and editing one cell of the column to be set.

### 6.1.1 Entity Table

Each row in the table corresponds to an entity in the active canvas. The following properties are listed in the table:

- Name – entity name
- CSO Class – Cell System Ontology Class, e.g. cell
- Location - biological location of the entity, e.g. cytoplasm
- Type – the value type of the entity, *integer* or *long* represent a discrete entity, *double* – a continuous entity, *string* or *boolean* – a generic entity
- Variable – name of variable associated with the entity
- Initial Value – initial value or script for simulation
- Eval Once – tells whether the Initial Value script is evaluated only once at the simulation start up, or many times at each simulation step.
- Value – current value calculated during simulation
- Max Value – maximum value of the entity during simulation
- Min Value – minimum value of the entity during simulation
- Log – if the box is checked the entity is included in a simulation log. The logged values can be viewed and analyzed in CI Player – see [Simulation History](#) or exported to a CSV file.
- Global – by default, for normal entities this flag is false. If the flag is true, the entity is global. Global entities are used to represent cell biological compartments, containers for normal entities, such as cell components. The global entities cannot be connected to any process using connectors.
- Public – tells whether to make this element public, i.e., visible in higher level models. Public entities are “connection points” of hierarchical objects.
- Visible – toggles element visibility on the canvas.
- Show Name – toggles visibility of name label on the canvas
- Show Variable - toggles visibility of variable label on the canvas
- Show Value - toggles visibility of variable label on the canvas

### 6.1.2 Process Table

Each row in the table corresponds to a process in the active canvas. The following process properties are listed in the table:

- Name – process name
- CSO Class – Cell System Ontology Class, e.g. biological process
- Location - biological location of the process
- Process – biological process
- Type – discrete, continuous or generic
- Firing Style – determines the firing style of the process. For “And” style, the process fires if all input connectors fulfill the firing

condition. The “Or” firing style can be used if the process has two or more input connectors of type *Inhibitor* or *Association*. For the “Or” firing style, at least one *Inhibitor* or *Association* connector must fulfill the firing condition in order for the process to be enabled.

Additionally, all input *Process* connectors must be enabled.

- Kinetic Script – a value or script that defines how to calculate the value change in each simulation step. The meaning of the Kinetic Script depends on the process type. The *Speed property is displayed* for a continuous process, for a discrete process – the *Add property* , and for a generic process – the *Update script*.
- Kinetic Value – current value of the *Kinetic Script* calculated during simulation
- Delay Script – definition of the delay parameter
- Delay Value – current value of the process delay calculated during simulation
- Activity – If the activity is set to *false* a process does not fire. The activity can be defined by mathematical formula.
- Priority - priority of the process used during simulation. A process with higher priority will fire before a process with lower priority
- Log – if the box is checked the process state is included in a simulation log. The logged values can be viewed and analyzed in CI Player – see [Simulation History](#) or exported to a CSV file.
- Visible – toggles element visibility
- Show Name – toggles visibility of name label on the canvas
- Show Speed/Delay - toggles visibility of speed/delay label on the canvas
- Show Firing Style - toggles visibility of firing style label on the canvas

### 6.1.3 Connector Table

Each row in the table corresponds to a connector in the active canvas. The following connector properties are listed in the table:

- Name – connector name
- CSO Class – Cell System Ontology Class
- Type – process, inhibitory or association
- Kinetic Script – a value or script that defines how to calculate the value change in each simulation step. The meaning of the Kinetic Script depends on the type of the connected process. The *Connector Speed* property is displayed for a continuous process, for a discrete process – the *Connector Add* property , and for a generic process – the *Connector Update* script.
- Kinetic Value – current value of the *Kinetic Script* parameter calculated during simulation
- Firing Style – the firing style of the connector.
- Firing Script – the script or value that defines the firing condition.

- Firing Value – current value of the Threshold parameter or Firing Rule script calculated during simulation
- From – the input node (entity or process) of the connector
- To – the output node (entity or process) of the connector
- Visible – toggles element visibility
- Show Name – toggles visibility of name label on the canvas
- Show Firing Operation - toggles visibility of firing operation label on the canvas
- Show Firing Style - toggles visibility of firing style label on the canvas

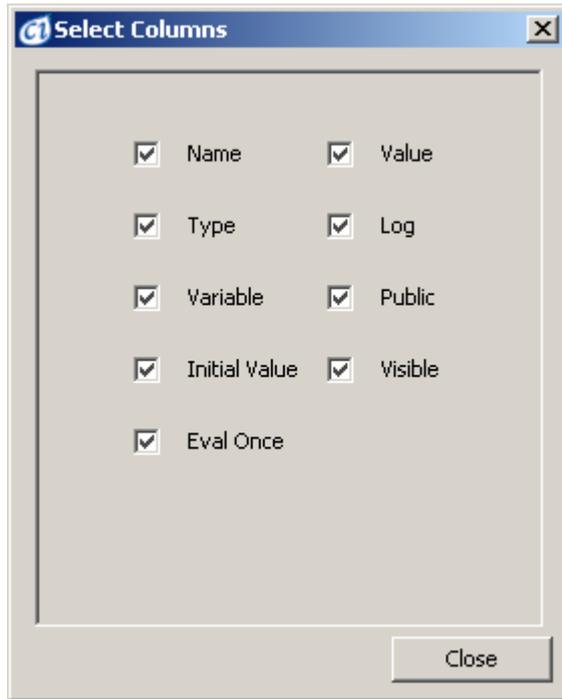
#### 6.1.4 Options

The bottom part of the Element Lists contains several options that control the *Entity, Process or Connector Table* display. The **Show Options** checkbox toggles the visibility of these auxiliary options:

- *Select Row/Column* – highlight rows or columns in the table. You can change the property value for all rows in the table at once.
- *Scroll this table when an element is selected in the canvas* and *Scroll the canvas when a row is selected in this table* – define interactions between selections in the canvas and in the Element List dialog
- *Filter* checkboxes – specify filtering criteria for the table rows. The table can be filtered by element type. Allowed types are:
  - continuous, discrete or generic for entities and processes
  - process, inhibitory or association for connectors

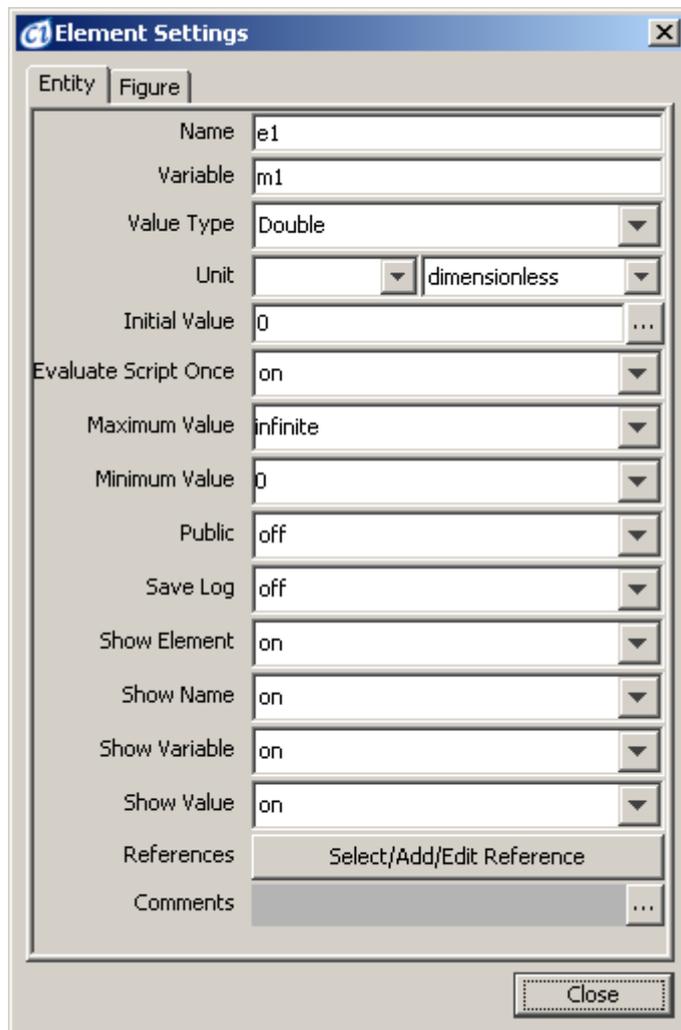
#### 6.1.5 Columns

The *Columns...* button opens the *Select Columns* dialog box, which allows for selecting the columns to be displayed.



The *Select Columns* dialog box consist of the list of columns that can be displayed in the Element List window. Each column is represented by its name and the checkbox which defines the column visibility (checked means visible, unchecked hidden). The list of columns that can be displayed depend on the tab that is currently active in the *Element List* window, e.g. another columns can be displayed in the various tables available in Element Lists dialog box: Entity, Process, Connector.

## 7 Element Settings



The Element Settings is a modeless dialog that allows the viewing and setting of properties of a selected element:

- If a single entity, connector or process is selected, the dialog displays its properties. Otherwise the dialog shows global properties of the model in the active canvas.
- Change of selection or switching between canvas windows results in an update of the dialog.
- Changing a setting in the dialog has an immediate effect in the model.
- The display properties associated with an element are preserved in the model file and override global view settings.

The Element Settings dialog allows the setting of mathematical formulas as element properties to define dependencies between elements during the simulation.

The mathematical formulas can be set for specific entity, process or connector properties with the help of the [Script Editor](#) dialog box. The Script Editor dialog can be opened by pressing the button “...” left of the element property edit box.

## 7.1 Model and Canvas Property Sheet.

This tab displays a number of properties describing the model in the active canvas and the canvas window itself. These properties cannot be edited.

## 7.2 Entity Property Sheets

For a selected entity, its properties are presented in the Entity Sheet and the Figure Sheet.

### 7.2.1 Entity Sheet

Property Name	Description
Name	Name of the entity
CSO Class	Cell System Ontology (CSO) Class, e.g. protein, DNA, RNA, can be selected from the drop-down list. The button “...” allows for the definition of the CSO Class with the help of the <a href="#">CSO Class Tree</a> dialog box.
Type	Continuous or Discrete, or Generic
Variable	Name of variable associated with the entity
Value Type	The <i>Double</i> type is associated with continuous entities, <i>Long</i> and <i>Integer</i> with discrete entities, the other value types: <i>Boolean</i> and <i>String</i> with generic entities.
Physical Property	Defines the physical property for the entity value such as <i>mass</i> or <i>length</i> . The physical property can be selected from the drop-down list.
Unit	Defines the unit for the entity value such as <i>mol</i> or <i>kilogram</i> . The unit can be selected from the drop-down list. The list of available units depends on the selected physical property.
Initial Value	The value of the entity at the simulation startup. The property can be a fixed value or a script. If it is a script, it can be evaluated only at simulation startup (normal case), or at each simulation step (special case) - see <i>Evaluate Script Once</i> . The button “...” allows for the definition of the mathematical formula within the <a href="#">Script Editor</a> dialog box.
Evaluate Script Once	This property is ignored if the <i>Initial Value</i> is a fixed

	value. Otherwise, if the <i>Initial Value</i> is a script, there are 2 possibilities: <ul style="list-style-type: none"> <li>- If the property is <i>on</i>, the <i>Value</i> property is initialized with value set by the script at the beginning of simulation.</li> <li>- If the property is <i>off</i>, the <i>Value</i> property is set by evaluating the script at each simulation step.</li> </ul>
Maximum Value	The maximum value that can be assigned to the variable associated with the entity. It can be 1, <i>infinite</i> or any other value entered by the user. This entry is enabled only for scalar value types: <i>Integer</i> , <i>Long</i> or <i>Double</i> .
Minimum Value	The minimum value that can be assigned to the variable associated with the entity. It can be 0 or <i>-infinite</i> or any other value entered by the user. This entry is enabled only for scalar value types: <i>Integer</i> , <i>Long</i> or <i>Double</i> .
Public	The <i>on</i> value denotes that the associated variable can be referenced in models in which the entity is encapsulated in a hierarchical object element.
Save Log	If the property has the <i>on</i> value, the value of the associated variable will be logged during simulation.
Show Element	Turns the display of the whole element on and off. This setting is preserved in the model file and overrides global view settings.
Show Name	Turns on and off display of the whole element.
Show Variable	Turns on and off display of the name of the variable associated with the entity.
Show Value	Turns on and off display of the name of the variable associated with the entity.
References	List of URL sites related to the entity
Comments	Comment field

### 7.2.2 Figure Sheet

Property Name	Description
Name	Name of the entity
Figure	Type of figure representing the entity
Depth	Depth defines the way in which overlapping figures are displayed. A figure with a lower depth value is displayed over a figure with a higher depth value.
Size	Size of the figure in pixels. The figure width and height are <i>given</i> as two integer values separated by the space character.
Fill Color	Color of the figure
Line Color	Color of the border line
Stroke	Type of the border line

In CI3.0, *Biological Property Sheet* has been added to the *Element Setting* dialog. It is a special panel that allows for viewing and editing biological properties of single element (entity and process) or the whole model.

### 7.2.3 Biological Sheet

The screenshot shows a window titled 'Element Settings' with three tabs: 'Entity', 'Figure', and 'Biological'. The 'Biological' tab is active. It contains several input fields for biological identifiers: Name (e1), Location (undef), Pubmed ID (12345), GO ID (0005741), UnitProt ID, EntrezGene ID (1234), MIM ID, UCSC ID, Ensembl ID, KeggGene ID, RefSeq ID, and Compound ID. A 'Close' button is located at the bottom right of the dialog.

Property Name	Description
Name	Name of the entity
Location	Biological Location of the element can be selected from the list of available choices. The button “...” allows for the definition of the biological location with the help of the <a href="#">CSO Class Tree</a> dialog box
Pubmed ID	The IDs of publication associated with the element.
GO ID	The IDs of GO’s associated with the element.
Other IDs: UniProt, EntrezGene MIM UCSC, Ensembl, KEGG, RefSeq, Compound	References to external databases

You may specify several IDs separated with semicolon in the *Pubmed ID*, *GO ID*, *UniProt ID*, *etc* fields. Each ID is added to the external references list together with the automatically generated URL. The external reference generated for this ID can be opened in the Web Browser or edited using the [Element | References](#) command.

### 7.3 Process Property Sheets

For a selected process, its properties are presented in the Process Sheet and the Figure Sheet.

#### 7.3.1 Process Sheet

Property Name	Description
Name	Name of the process
CSO Class	Cell System Ontology Class, e.g. biological process, can be selected from the drop-down list. The button “...” allows for the definition of the CSO Class with the help of the <a href="#">CSO Class Tree</a> dialog box
Type	Continuous, Discrete or Generic. The process type determines the <i>Calc Style</i> . A continuous process has always the <i>Speed</i> calculation style, discrete – the <i>Add</i> calculation style and a generic one – the <i>Update</i> style. Continuous processes will always have the <i>Delay</i> property set to zero, while discrete and generic processes have a user defined delay. (The default value is 1.)
Firing Style	Determines how the enabled/disabled state of the process is calculated. The following styles can be selected from the drop-down list: <ul style="list-style-type: none"> <li>- <i>and</i> : All connected input connectors must fulfill their conditions to enable the process .</li> <li>- <i>or</i> : At least one <i>Inhibitor</i> or <i>Association</i> input connector must fulfill its condition to enable the process. Additionally, all <i>Process</i> input connectors must fulfill their conditions.</li> </ul>
Activity	If the property is set to <i>false</i> , the process does not fire. . The button “...” allows for the definition of the mathematical formula within the <a href="#">Script Editor</a> .
Calc Style	Determines how the variables in the connected entities are modified when the process fires. The following operations (calculation styles) can be specified: <ul style="list-style-type: none"> <li>- <i>speed</i> – the process defines the speed of production or consumption of the entities</li> <li>- <i>add</i> – the process calculates the concrete values that should be added (subtracted) to the entities</li> <li>- <i>update</i> – the process calculates a concrete value, that will replace the entity value.</li> </ul> <p>The <i>Update</i> calculation style should be used when the process is connected to generic entities with String or Boolean values.</p> <p>Note: The <i>Update</i> and <i>Add</i> calculation styles are time</p>

	<p>independent. Thus it is recommended that they be used in conjunction with a <i>Delay</i> value. This will assure that the process fires at a constant time interval and makes the simulation results independent of the sampling interval.</p>
Kinetic Style	<p>The following values can be selected from the drop down list:</p> <ul style="list-style-type: none"> <li>- <i>custom</i></li> <li>- <i>connector custom</i></li> <li>- <i>mass</i></li> <li>- <i>stochastic mass</i></li> <li>- <i>connector rate</i></li> </ul> <p>Each kinetic style requires different parameters. These parameters can be specified at the bottom of the <i>Process Sheet</i> in the edit box fields:</p> <ul style="list-style-type: none"> <li>- <i>coefficient1, coefficient2,</i></li> <li>- <i>variance,</i></li> <li>- <i>rate,</i></li> <li>- <i>connector stoichiometry,</i></li> <li>- <i>speed/add/update</i></li> <li>- <i>connector speed/add/update.</i></li> </ul> <p>Only the parameter fields that are meaningful for the selected kinetic style are displayed. See <a href="#">Kinetic Styles_Kinetic_Styles_2</a> for more detailed description.</p> <p>Note: The parameters <i>Speed, Add and Update</i> depend on the process type. A continuous process utilizes the <i>Speed</i> property, a discrete process – the <i>Add</i> property and a generic process – the <i>Update</i> property.</p>
Delay	<p>For discrete and generic processes, if the delay time <math>T &gt; 0</math>, then the process fires just after the delay time <math>T</math> if it is still active. Otherwise, it can lose its chance to fire. If the delay time <math>T = 0</math>, the process fires immediately when it is possible. For continuous processes, there is no delay; The process fires immediately when the enabling conditions become true and its Activity property is set to <i>true</i>.</p>
Priority	<p>Sets the priority of the process during simulation. If two processes P1 and P2 with equal priority fire at the time <math>t</math>, the order of firing P1 and P2 is random. But if the priority of P1 is larger than P2, then P1 always fires before P2.</p>
Show Element	Turns on and off display of the whole element
Show Name	Turns on and off display of the element name.
Show Speed/Delay	Turns on and off display of the process speed.
Show Firing Style	Turns on and off display of the firing style
References	List of URL sites related to the entity.
Comments	Comment field

Speed / Add / Update	Field appears when <i>custom</i> kinetic style is chosen. Field contains script describing process behavior. See <a href="#">Kinetic Styles_Kinetic_Styles_1</a> for more details.
Connector Speed / add / Update	Fields appear when connector <i>custom</i> kinetic style is chosen. Each field contains script describing connector behavior. Number of fields depends on number of input and output connectors. See <a href="#">Kinetic Styles_Kinetic_Styles_1</a> for more details.
Coefficient1	This field appears if the mass or stochastic mass kinetic style is chosen. It contains a constant used in mass and stochastic mass equations. See <a href="#">Kinetic Styles_Kinetic_Styles_1</a> for more details.
Coefficient2	This field appears if the mass or stochastic mass kinetic style is chosen. It contains a constant used in mass and stochastic mass equations. See <a href="#">Kinetic Styles_Kinetic_Styles_1</a> for more details.
Standard Deviation	This field appears if the stochastic mass kinetic style is selected. The field contains the value of standard deviation. See <a href="#">Kinetic Styles_Kinetic_Styles_1</a> for more details.
Connector Stoichiometry	These fields appear if the mass, stochastic mass or connector rate kinetic styles are selected. The number of fields depends on the number of input and output connectors. See <a href="#">Kinetic Styles_Kinetic_Styles_1</a> for more details.
Rate	This field appears if the connector rate kinetic style is selected. The field contains a script defining the process behavior. See <a href="#">Kinetic Styles_Kinetic_Styles_1</a> for more details.

### 7.3.1.1 Calculation Style

This section gives more details on the calculation style concept. The table below describes the impact of a firing process on the connected entities for different process types and calculation styles.

Process type (Calc Style)	Process behavior
------------------------------	------------------

Continuous (speed calc style)	<p>When the process fires, the value of each input/output entity is decreased/increased by change value (delta). The formula for the change value (delta) depends on the kinetic style – see the table below.</p> <p>For the kinetic style <i>Custom</i> the absolute value of delta is the same for all input/output entities. For all other kinetic styles, the value of delta depends on connector specific parameters (e.g. <i>Connector Stoichiometry</i> or <i>Connector Custom</i>). Thus, the delta value may be different for different input/output entities.</p>
Discrete (add calc style)	<p>When the process fires, the value of each input/output entity is decreased/increased by change value (delta). The formula for the change value (delta) depends on the kinetic style – see the table below.</p> <p>For the kinetic style <i>custom</i> the absolute value of delta is the same for all input/output entities. For all other kinetic styles, the value of delta depends on connector specific parameters (e.g. <i>connector stoichiometry</i> or <i>connector add</i>). Thus, the delta value may be different for different input/output entities.</p>
Generic (update calc style)	<p>When the process fires, the value of each input/output entity is set to the update value. The script for the update value is specified in the <i>connector update</i> field. The update value may be different for different input/output entities.</p>

### 7.3.1.2 Kinetic Styles

This section gives more details on the kinetic style concept. The table below specifies the mathematical formula that is used to calculate the entity value change (delta) for all the various kinetic styles. Also, the parameters used for each kinetic style are listed in the table

Kinetic style	Process type	Formula for the change value delta
<b>Custom</b> parameter: speed / add	continuous (speed calc style)	$\text{delta} = \text{speed} * \text{sampling interval}$
	discrete (add calc style)	$\text{delta} = \text{add}$

<b>connector custom</b>  parameters: speed / add / update for each connector	continuous (speed calc style)	$\text{delta} = \text{connector\_speed} * \text{sampling\_interval}$
	discrete (add calc style)	$\text{delta} = \text{connector\_add}$
<b>Mass</b>  parameters: coefficient1, coefficient2, stoichiometry for each connector	continuous (speed calc style)	$\text{delta} = \text{m\_product} * \text{coefficient1} * \text{coefficient2}^{[\text{number\_of\_input\_entities}] * \text{stoichiometry}} * \text{sampling\_interval}$  where $\text{m\_product}$ is the product of all input entity values. For the input entity variables ( $\text{m1}, \text{m2}, \dots, \text{mN}$ ) $\text{m\_product} = \text{m1} * \text{m2} * \dots * \text{mN}$
	discrete (add calc style)	$\text{delta} = \text{m\_product} * \text{coefficient1} * \text{coefficient2}^{[\text{number\_of\_input\_entities}] * \text{stoichiometry}}$  where $\text{m\_product}$ is the product of all input entity values. For the input entity variables ( $\text{m1}, \text{m2}, \dots, \text{mN}$ ) $\text{m\_product} = \text{m1} * \text{m2} * \dots * \text{mN}$

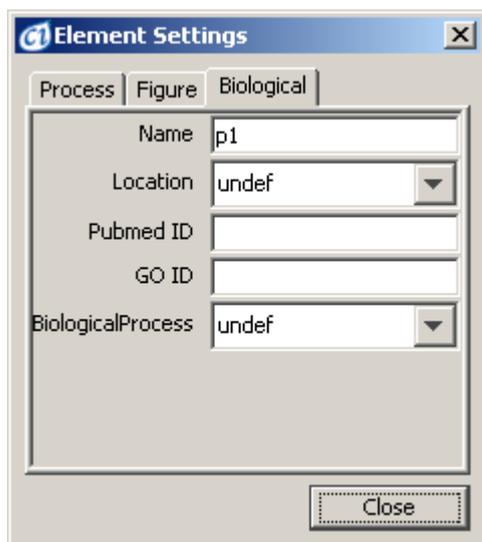
<b>stochastic mass</b>  parameters: coefficient1, coefficient2, standard deviation and stoichiometry for each connector	continuous (speed calc style)	delta is randomly generated using the Gaussian distribution with the calculated <code>delta_mean</code> and specified standard deviation.  <code>delta_mean</code> is calculated using the formula for the mass kinetic style:  <code>delta_mean = delta_mass (coefficient1, coefficient2, stoichiometry)</code>
	discrete (add calc style)	delta is randomly generated using the Gaussian distribution with the calculated <code>delta_mean</code> and specified standard deviation  <code>delta_mean</code> is calculated using the formula for the mass kinetic style:  <code>delta_mean = delta_mass (coefficient1, coefficient2, stoichiometry)</code>
<b>connector rate</b>  parameters: rate and stoichiometry for each connector	continuous (speed calc style)	<code>delta = rate * stoichiometry * sampling_interval</code>
	discrete (add calc style)	<code>delta = rate * stoichiometry</code>

### 7.3.2 Figure Sheet

Property Name	Description
Name	Name of the process
Figure	Type of figure representing the process
Depth	Depth defines the way in which overlapping figures are

	displayed. A figure with a lower depth value is displayed over a figure with a higher depth value.
Size	Size of the figure in pixels. The figure width and height are <i>given</i> as two integer values separated by the space character.
Fill Color	Color of the figure
Line Color	Color of the border line
Stroke	Type of the border line

### 7.3.3 Biological Sheet



Property Name	Description
Name	Name of the entity
Location	Biological Location of the element can be selected from the list of available choices. The button “...” allows for the definition of the Location with the help of the <a href="#">CSO Class Tree</a> dialog box
Pubmed ID	The IDs of publication associated with the element.
GO ID	The IDs of GO’s associated with the element.
Biological Process	Biological Process associated with the selected process can be selected from the list of predefined choices. Changing this property automatically changes the image of the process on the canvas. The button “...” allows for the definition of the Biological Process with the help of the <a href="#">CSO Class Tree</a> dialog box

You may specify several IDs separated with semicolon in the *Pubmed ID* and *GO ID* fields. Each ID is added to the external references list together with the automatically generated URL. The external reference generated for this ID can be opened in the Web Browser or edited using the [Element | References](#) command. Setting the biological process property using the combo box automatically changes the image of the process on the canvas.

## 7.4 Connector Property Sheets

For a selected connector, its properties are presented in the Connector Sheet and the Figure Sheet.

### 7.4.1 Connector Sheet

Property Name	Description
Name	Name of the connector
CSO Class	Cell System Ontology Class can be selected from the drop-down list. The button “...” allows for the definition of the CSO Class with the help of the <a href="#">CSO Class Tree</a> dialog box
Type	Process, Inhibitor or Association
Firing Style	Specifies the way, and how to calculate the firing activity of the connector. The Firing Style can take one of the following values: <ul style="list-style-type: none"> <li>- threshold</li> <li>- rule</li> <li>- none</li> </ul>
Firing Threshold	The Threshold option is enabled only in case the connector is an input connector and the type of source entity is discrete or continuous. The Threshold can be a real value or a script that returns real value. The Threshold is used to control the connected discrete or continuous process; If the current value of source entity is larger than the threshold specified by the connector, the connector is enabled. If all input connectors of a process are enabled and the Activity property of the process is <i>true</i> , the process is enabled. The button “...” opens the <a href="#">Script Editor</a> that allows the writing of a script.
Firing Rule	The Firing Rule is used to control the enabled/disabled state of a linked generic process; If the Firing Rule is set to <i>true</i> , the connector is enabled. As with discrete and continuous processes, a generic process is enabled if all of its input connectors are enabled and the Activity property of the process is set to <i>true</i> . The Firing Rule option can be a Boolean value or a script that returns a Boolean value.
Show Element	Turns on and off display of the whole element
Show Name	Turns on and off display of the element name.
Show Firing Operation	Turns on and off display of the firing operation
Show Firing Style	Turns on and off display of the firing style
References	List of URL sites related to the entity
Comments	Comment field

## 7.4.2 Figure Sheet

Property Name	Description
Name	Name of the connector
Depth	Depth defines the way in which overlapping figures are displayed. A figure with a lower depth value is displayed over a figure with a higher depth value.
Line Color	Color of the connector line
Stroke	Type of the connector line
Head	Type of the connector head
Head Size	Size of the connector head
Head Fill Color	Color of the connector head
Tail	Type of the connector tail
Tail Size	Size of the connector tail
Tail Fill Color	Color of the connector tail

## 7.5 Object Property Sheets

For a selected object, its properties are presented in the Object Sheet and the Figure Sheet.

### 7.5.1 Object Sheet

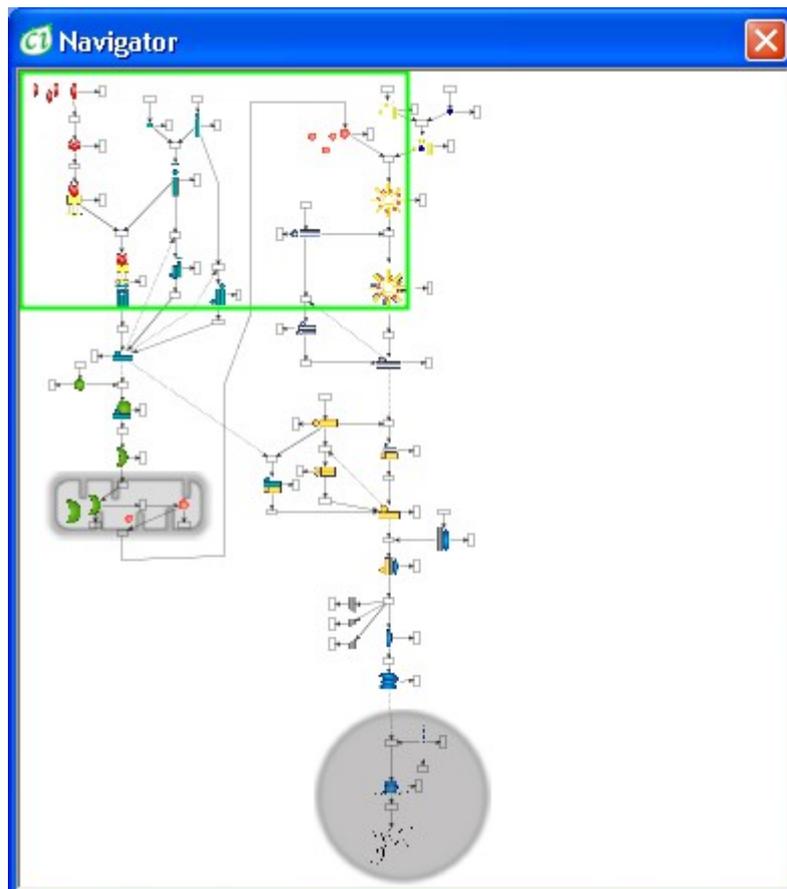
Property Name	Description
Name	Name of the object
File	File that contains the model represented by the object
File Modified Time	Time when the file was last modified.
File Loaded Time	Time when the file was loaded into CI.
File Edited Time	Time when the model was last edited in CI.
Total Count	Total number of elements encapsulated in the object
Entity Count	Number of entities that are encapsulated in the object.
Process Count	Number of processes that are encapsulated in the object.
Connector Count	Number of connectors that are encapsulated in the object.
Object Count	Number of objects that are encapsulated in the object.
Variable	Name of variable that is associated with the object
References	List of URL sites related to the entity
Comments	Comment field

### 7.5.2 Figure Sheet

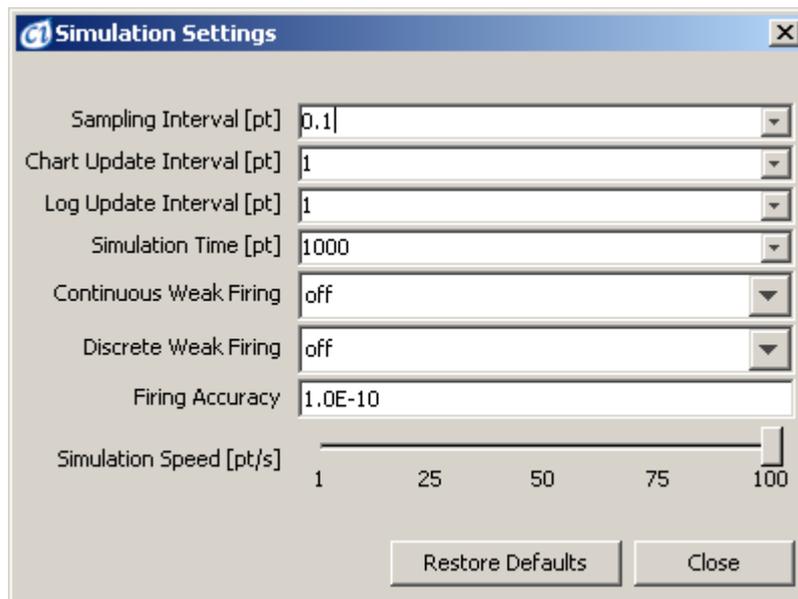
Property Name	Description
Name	Name of the object
Figure	Type of figure representing the object
Depth	Depth defines the way in which overlapping figures are displayed. A figure with a lower depth value is displayed over a figure with a higher depth value.
Size	Size of the figure in pixels. The figure width and height are <i>given</i> as two integer values separated by the space character.
Fill Color	Color of the figure
Line Color	Color of the border line
Stroke	Type of the border line
Round Corner	The property is enabled when the selected figure is the "hierarchical element", i.e. default figure. The property sets the round ratio of corners of the rectangular shape representing the object

## 8 Navigator

For a large model, the Navigator dialog provides a convenient way to locate and display in the canvas window a desired part of the model. The Navigator displays a small view of the entire model, with a green rectangle marking the portion of the model currently shown in the active canvas. You can drag this rectangle around in order to navigate the model in the canvas window.



## 9 Simulation Settings



The *Simulation Settings* dialog allows the setting of parameters that control the simulation execution for the model in the active canvas:

- *Sampling Interval* is the basic simulation input parameter that controls the simulation accuracy and performance. The smaller the *Sampling Interval*, the higher the accuracy.
- *Simulation Time* tells how long the simulation should last. The ratio  $\text{Simulation Time} / \text{Sampling Interval}$  defines the number of steps to be executed in the simulation.
- *Chart Update Time* defines how often the [Chart Windows](#) should be updated. This parameter has no impact on simulation results
- *Log Update Time* defines how often the internal simulation log should be updated. This internal simulation log can be saved by [Simulation | Save Simulation Log](#). This parameter has no impact on simulation results. The *Log Update Time* is ignored if the simulation is played in step mode.
- All the times are specified in Petri net time units (pt).
- For a new model, all the settings are initialized on the base of user preferences – see the *Simulation Extra Options* in [Preferences](#) dialog box. The current settings are preserved in the model file.
- For the *Fast Play* and *Max Speed Play* menu commands, the *Current Speed* option specifies how many times the simulation speed should increase over the speed in the regular Play mode. In reality, the maximum speed is limited by the hardware on which Cell Illustrator runs. For simulations started with the *Play* command, *Current Speed* has no effect. In this mode, 1pt should be executed by the program in 1 second. The *Current Speed* setting is application-wide and it is not preserved in the model file. The range of Current Speed is controlled by the *Max Speed* parameter in the Simulation settings in [Preferences](#).

- *Continuous Weak Firing* enables/disables the weak firing option for continuous processes. By default, if this option off, a process cannot fire if there are not enough tokens in a connected input entity, i.e. if the calculated delta value is greater than the available entity value . Such behavior is in agreement with the Petri Net model, but is sometimes difficult to understand for normal biological reactions. If this option is on and weak firing is enabled, the process can fire even if the connected entity value is smaller than the delta calculated for the current step. In such a case the weak firing scale is calculated using the formula:

- $scale = availableDeltaValue / calculatedDeltaValue$

After this the delta value for all input and output entities connected to the “weak firing” process are multiplied by the scale. The scale value is less than 1.

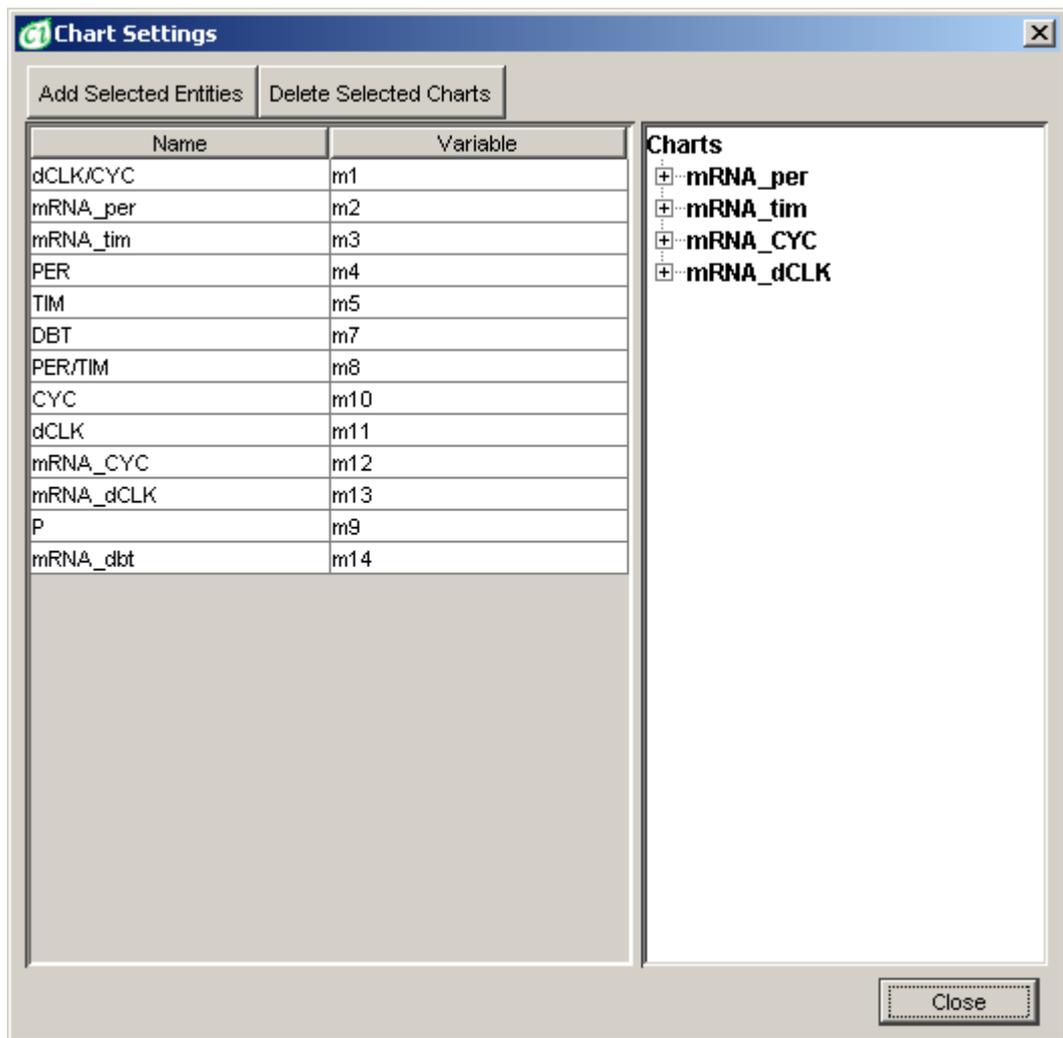
- *Discrete Weak Firing*. Enables/disables the weak firing option for discrete processes. By default this options is off.
- *Firing Accuracy*. The minimum change value for which a process fires. If the calculated delta value is less than the *firing accuracy*, the delta value is threaten as zero and the process does not fire. This option is useful for the case of entity value converging to a given value in an asymptotic way.

The *Restore Defaults* button re-initializes the Simulation Settings with the values from the user preference settings. You need to set simulation parameters prior to starting simulation. All controls are disabled when a simulation is running.

## 10 Chart Settings

The Chart Settings dialog allows the visualizing of the simulation results with concentration or amount versus time graphs. You can:

- create a new chart,
- edit/customize an existing chart, and
- remove an existing chart.



The *Entity List* at the left side of the dialog displays all entities in the active canvas. It supports multiple selections – several entities can be selected at once. The displayed entity properties - Name and Variable - can be edited in the *Entity List*. Selecting an element on the CI canvas points the element in the element list of the *Entity List* and vice-versa choosing an element in the *Entity List* selects the corresponding entity on the canvas.

The *Chart Tree* displays all defined charts and their properties on two levels. The main level of the tree is the list of charts labeled by the chart names. The leaves of the tree are entities that are included in the parent chart. One chart can include up to eight entities. Also, one entity can be included in one or more charts.

You can change the name of a chart by clicking on its label. The entity names cannot be edited in the *Charts Tree*. The *Charts Tree* supports multiple selections including all possible combinations of chart and entity nodes - several charts and entities can be selected at once.

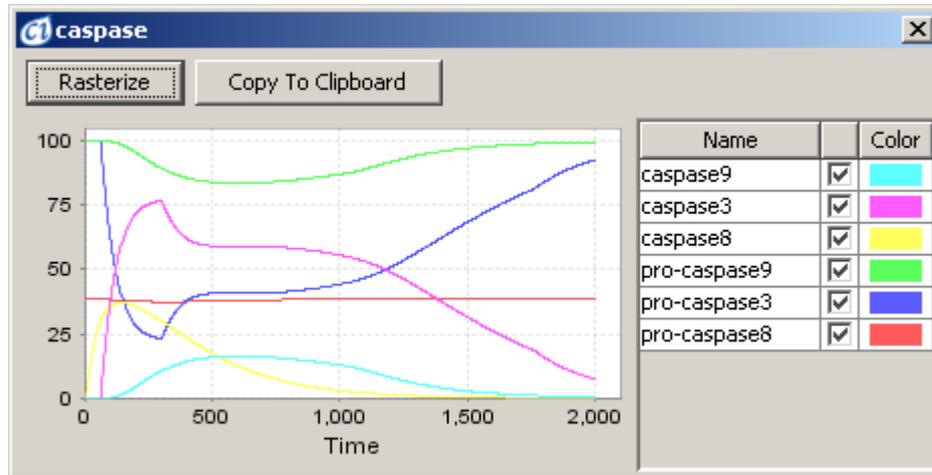
The *Add Selected Entities* button adds the entities selected in the *Entities List* to the chart selected in the *Charts tree* control. The entities appear as child-nodes of the chart node.

If no chart is selected, a new chart is created and the selected entities are added to it. The name of the new chart is the name of the first selected entity. If more than one chart is selected, the entities are added only to the first one.

*Remove Selected Entities* **deletes** selected items (charts and entities) in the *Chart Tree*. The set of simulation charts defined for the model is modified accordingly.

## 11 Chart Window

A *Chart Window* presents how entity values change over time in the course of simulation and the time dependence of one or more entity variables in a chart.



After simulation is started the *Chart Windows* appear. Each *Chart Window* contains the list of the plots defined in the [Chart Settings](#) Dialog. The *Chart Window* enables you to:

- display plots with time series of entity values,
- choose which of the plots are displayed or hidden,
- set properties of the *Chart Window* and the Plots (colors, fonts etc.),
- save *Chart Window* as PNG files,
- zoom in, zoom out and auto range axes.
- rasterize (freeze) a specified chart for later analysis or comparison.
- copy the time series to system clipboard in a tab-separated format. You can export the chart to another application, e.g., Microsoft Word or Excel, in this way.

The *Chart Window* consist of the *Chart Panel* with the time series plots, the *Entity List Panel*, the *Rasterize* and the *Copy To Clipboard* buttons.

### 11.1.1 Chart Panel

The *chart panel* presents how entity values change over time in the course of simulation and the time dependence of one or more entity variables in a chart.

Chart Panel update interval depends on the mode of simulation:

- in the *Step* mode: for each step the *Chart Window* is updated,
- in the *Play* mode: one update per 1 second,
- in the *Fast Play* and *Max Speed* mode: each time the time series increased by 10% in comparison to the last updated time and at the end of simulation.

You can see the value of the data point once you move the mouse cursor over it. You can zoom into a chart area by dragging the mouse over this area from upper

left to the bottom right corner. To reset the original size drag the mouse in the opposite direction from the bottom right to the upper left corner.

Right-click on the chart control opens the popup menu:

- *Properties* - set chart visualization properties.
- *Save As* – save the chart in PNG file.
- *Zoom In/ Zoom Out* – specify the range for x and y axis. Only the data points that fit that range will be displayed
- *Auto Range* – Automatically adjusts the range of X and Y axis.

### 11.1.2 Entity List Panel

The entity panel contains the list of entities displayed in the chart. It consist of 3 columns: *Entity Name*, *Plot Visibility*, *Plot Color*. In this panel you can:

- Show or hide the plot associated with a given entity by clicking on the *Visibility* cell of a given entity.
- Customize colors of data series in the chart by clicking on the *Color* cell of a given entity.

### 11.1.3 Rasterize Button

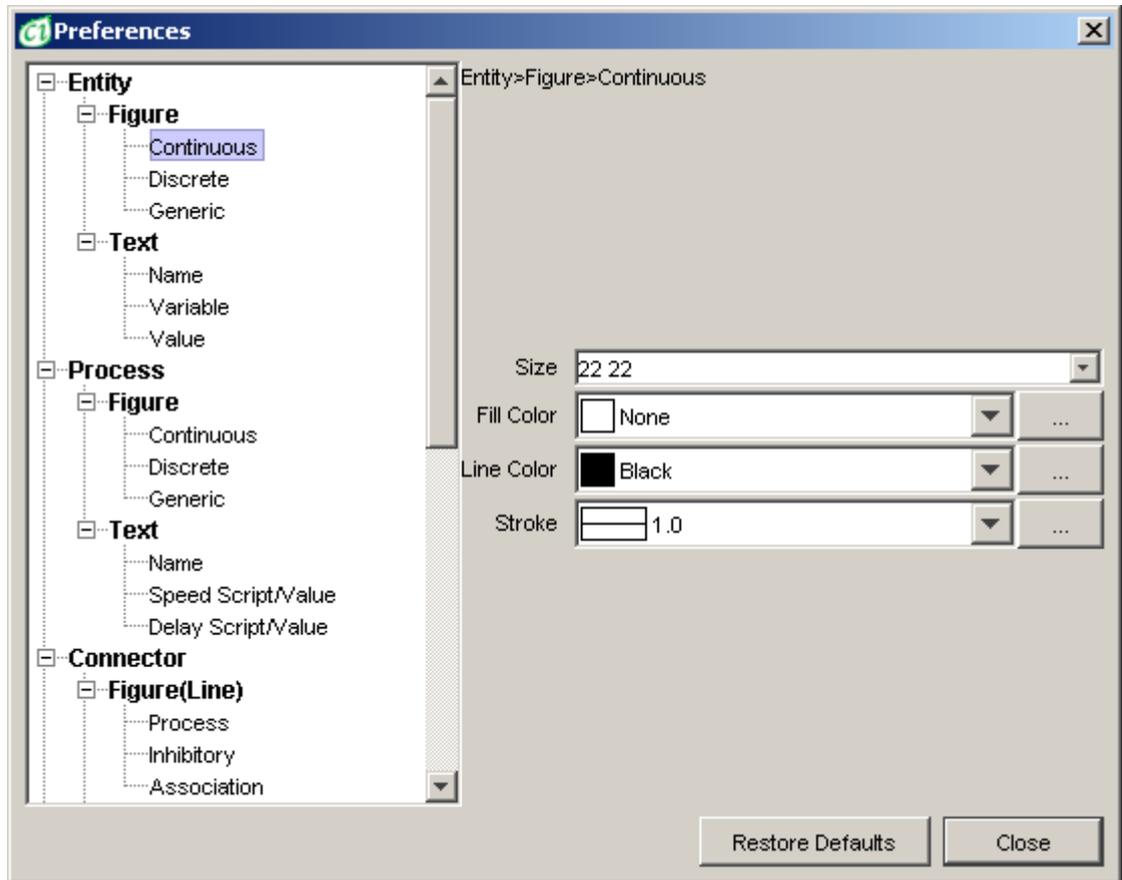
The *Rasterize* button creates a window that is a snapshot of the chart. The snapshot has the gray background color and it is not updated during simulation. If you close it, the chart is destroyed. In contrast, if the original chart is closed, it just becomes hidden and reappears at the simulation start

Right-click on the chart control to open a popup menu:

- *Grid On* - Turns on and off the background grid.
- *Tool Tip On* – If the option is enabled, you can see the value of the data point once you move the mouse cursor over it.
- *Area Zoom* – Turns on and off the zoom in feature. You can drag the mouse over an area in the chart to zoom into it.
- *Colors* - Opens a dialog where you can customize colors of data series in the chart.
- *Copy to Clipboard* - Copies the chart to the system clipboard. You can export the chart to another application, e.g., Microsoft Word, in this way.

- *Automatic Scale* – Automatically adjusts the range of X and Y axis during simulation.
- *Manual Scale* – With this option you can specify the range for x and y axis. Only the data points that fit that range will be displayed.

## 12 Preferences



With the Preferences dialog, you can set the global properties of Cell Illustrator. The settings are stored as user preferences and apply also the next time you start the application. A change in the Preferences dialog is effective immediately and applies to new elements, canvas windows and simulations runs that are executed after the change unless the setting is one for the whole application, such as the grid size. In such a case, the setting applies to all (already existing and new) canvas windows. The *Restore Defaults* button restores the default (factory) settings for the selected branch of the option tree.

## 13 View Settings



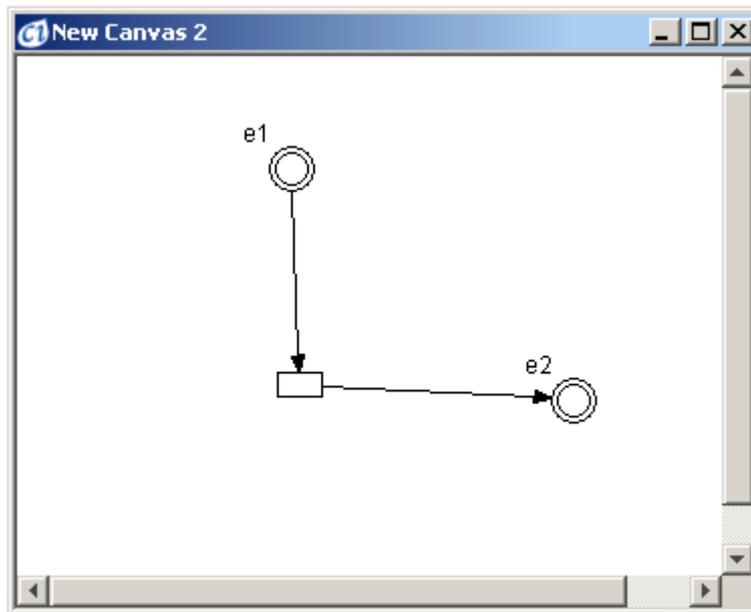
This dialog allows you to set global model visualization settings for the Cell Illustrator. The view settings are stored as user preferences and apply also the next time you start the application. A change in the settings results in an immediate update of all canvas windows.

### 13.1 Global settings

Options in this group allow user to change global view settings. These options apply to all canvases inside the CI workspace.

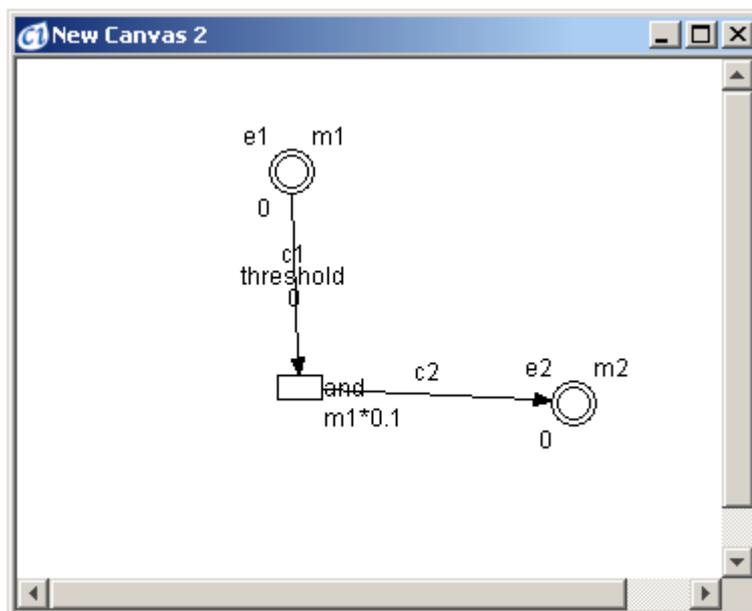
### 13.1.1 View Mode

In this mode CI displays names of entities only.



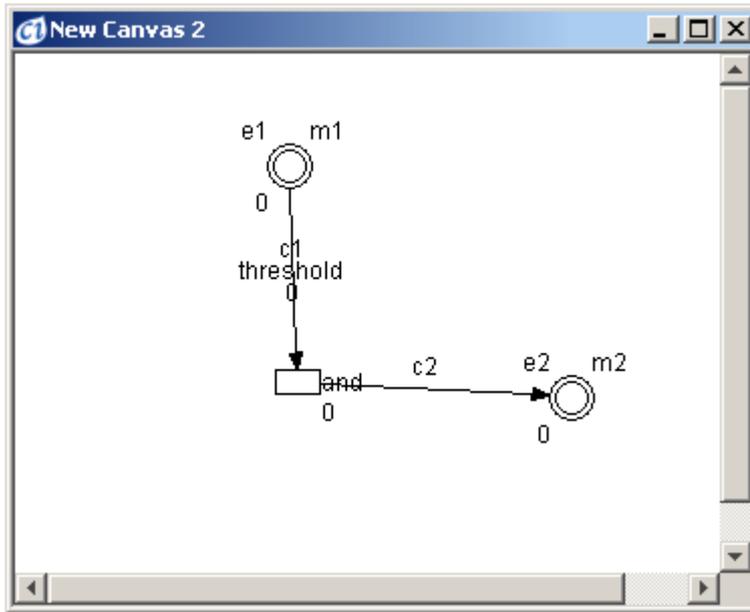
### 13.1.2 Edit Mode

In this mode CI displays all info about entities, processes and connectors, except processes names.



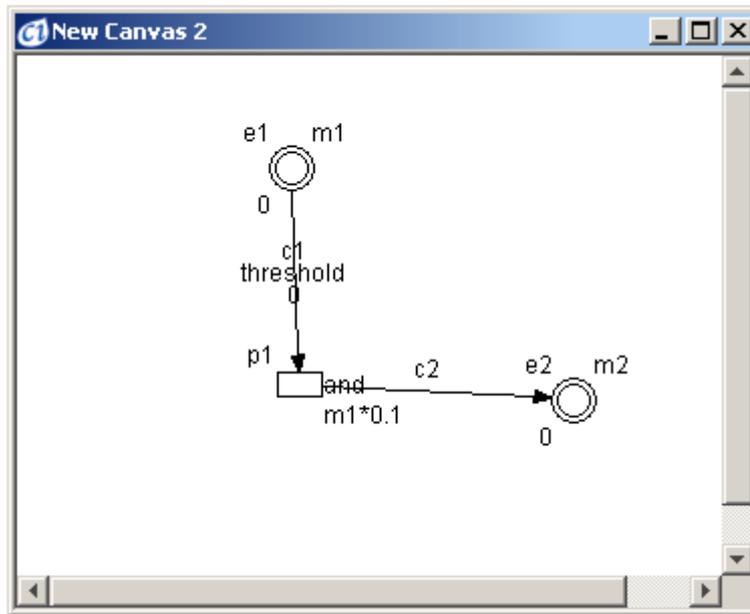
### 13.1.3 Simulation Mode

In this mode CI displays all simulation-related information



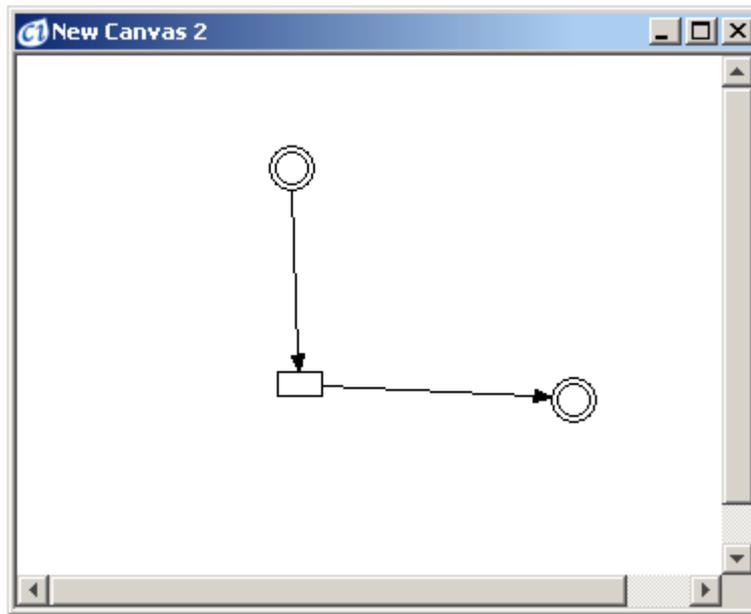
### 13.1.4 All Mode

In this mode CI displays all information about entities, processes and connectors.



### 13.1.5 None Mode

In this mode CI displays no information on entities, processes and connectors.



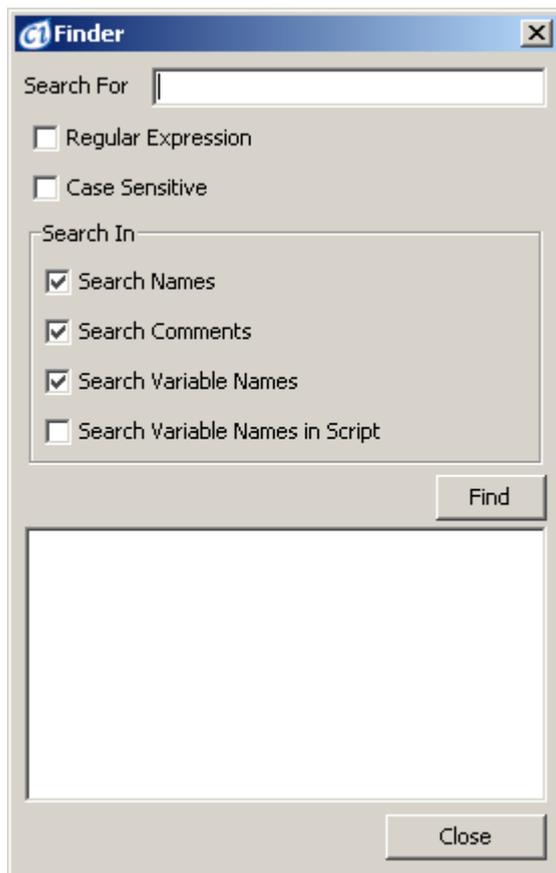
## 13.2 Depth Threshold

This option allows you to set depth threshold of active canvas. Every item on canvas has *Depth* parameter. Global *Depth Threshold* setting sets depth that elements can be selected to. E.g. if entity has depth of 60, and global *Depth Threshold* is set to 50, entity can't be selected (but is still visible on canvas). To be active, item must have *Depth* smaller than actual *Depth Threshold* value.

## 14 Finder

Using this dialog, you can locate elements (entities, processes and connectors) containing the specified text in one of their properties. The keyword search is performed by execution of the following steps:

- Enter a search string into the *Search For* edit box,
- Select search options using the checkboxes
- Select the properties to be searched for, in the *Search In* panel.
- Press the *Find* button.
- Left click an item in the *Search Result* list to select the elements
- Right click on the *Search Result* list to perform the operation on the discovered elements.



The *Finder* is a modeless dialog. After finding an element, the user can switch back to the canvas window and edit the element without closing the *Finder* window.

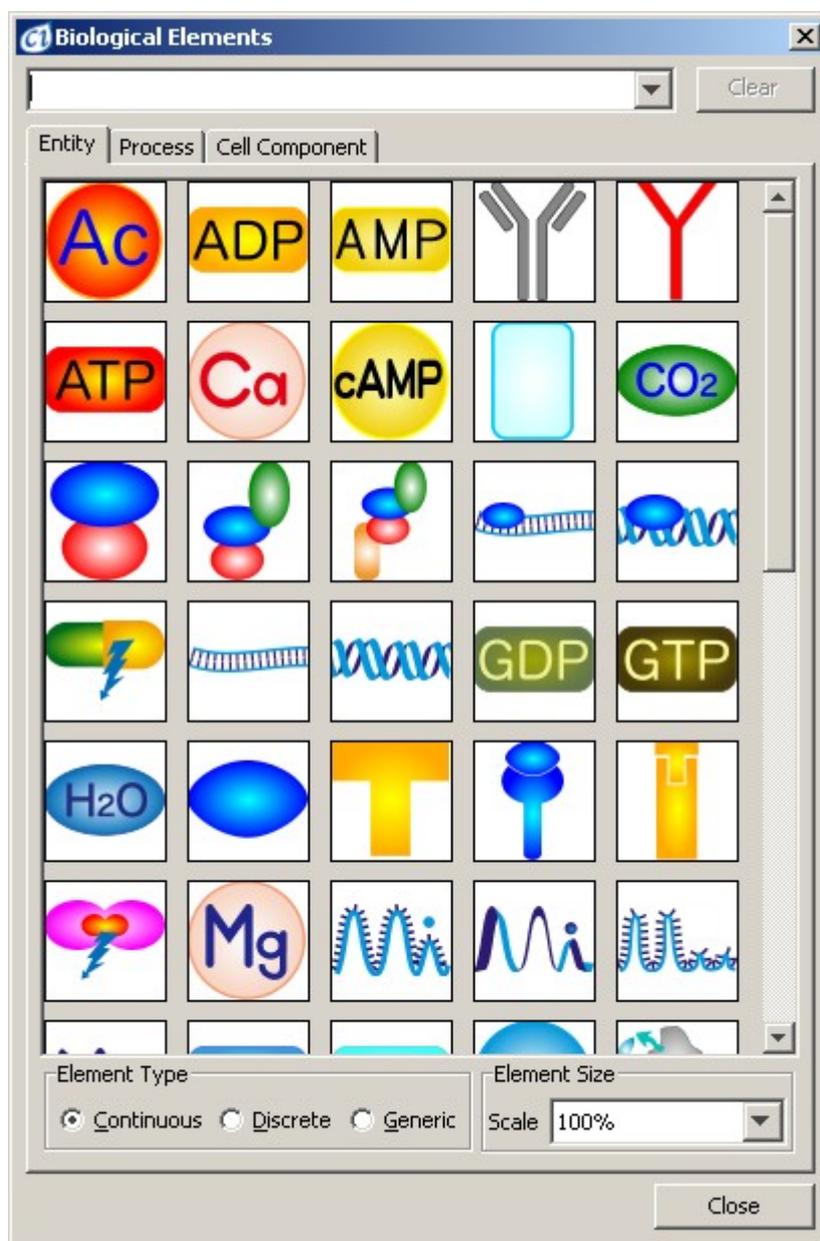
- Regular expressions can be used to find groups of similar elements.

- The following object types can be found: entity, connector, process and hierarchical objects. One cannot use Finder to search for a group, even if it contains objects matched by the search.
- You can search in the following element properties: element name, element comment, entity variable name, element scripts
- Elements found in the search process are displayed in the *Search Results* list box at the bottom of the dialog. Also, the number of found objects is displayed above the list box.
- Clicking an item in the *Search Results* list box selects the corresponding element in the workspace. CTRL+click (Apple+click on Mac) and SHIFT+click allow for selecting/deselecting multiple items.
- To select an object, the canvas that has been searched must be active. If the active canvas is changed after the search, the *Search Results* list is cleared.
- The *Close* button dismisses the dialog window.

## 15 Biological Elements

While you can use the menu options and toolbar buttons to add elements, biological pathways can be created faster and more intuitively by dragging and dropping appropriate elements from the Biological Elements dialog. You can use this dialog to:

- find a picture that represents a given biological entity, process or cell component
- add a new element to the canvas
- replace the image of an existing elements



To find a picture that represents a given biological entity, process or cell component:

- Go to the desired tab: *Entity*, *Process* or *Cell Component*.
- Enter one or more characters into the edit box
- The possible choices that start with the entered characters are displayed in the drop down list. Also the list of pictures is filtered, so that only the possible choices are displayed, while all other pictures are hidden
- Select the desired element from the drop down list. The corresponding picture is displayed.

To insert a biological element, proceed as follows:

- Select a picture in the *Element*, *Process* or *Cell Component* tab. The picture description and size will be displayed in a fly-over help string when you position the mouse cursor over the picture.
- Select the *Element/Process Type*
- Select the *Element Size* by defining the picture scale.
- Click on the chosen picture, drag it to the active canvas and drop it there by releasing the mouse button.

Pictures from the *Entity* or *Process* tabs are inserted as elements of the specified type: *Continuous*, *Discrete* or *Generic*. Pictures from the *Cell Component* tab are inserted as images and they do not have any impact on the simulation results.

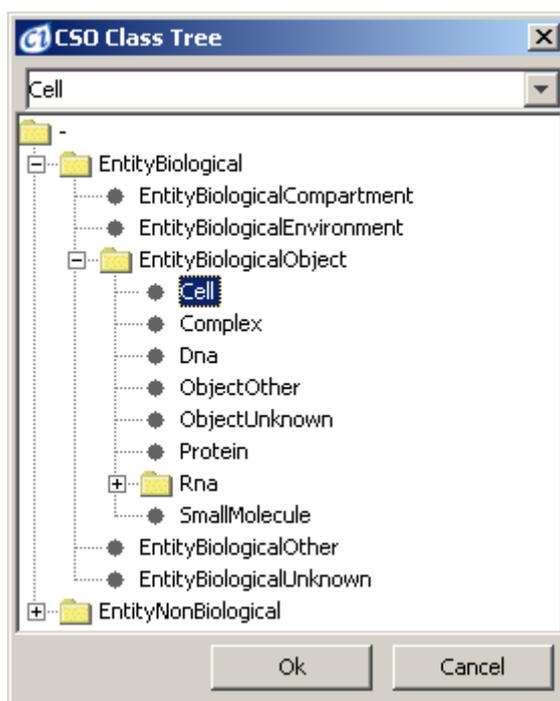
To replace the image of an existing element, proceed as follows:

- Select a picture in the *Element* or *Process* tab. The picture description and size will be displayed in a fly-over help string when you position the mouse cursor over the picture.
- Click on the chosen picture, drag it to the active canvas and drop it over the existing entity or process by releasing the mouse button.

Please note that pictures from the *Entity* can be used to replace entity elements only, while pictures from *Process* tab can replace process elements only. The replace function is not available for pictures from the *Cell Component* tab.

## 16 CSO Class Tree

The Cell System Ontology (CSO) is a dictionary that contains terms for the specific biological properties, such as biological class and location of the entity, process or connector. For each of these properties, there is a limited number of choices defined in the CSO Class Tree. This dialog box facilitates browsing/searching through the hierarchy of the terms and finding/selecting the proper one.



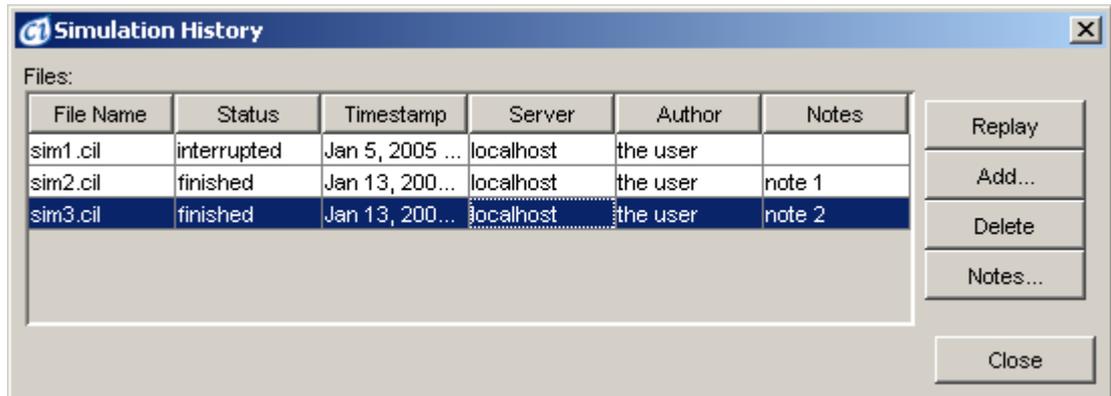
With this dialog you can:

- Select one element from the CSO hierarchy list of available choices
- Browse through the CSO dictionary
- Find a term in the CSO dictionary, the edit box at the top of the

To find a proper CSO term:

- Enter one or more characters into the edit box
- The possible choices that start with the entered characters are displayed in the drop down list.
- Select the desired element from the drop down list. This closes the drop down list and selects the corresponding term in the tree.

## 17 Simulation History



In this modeless dialog, you can view and manage the CI Log files (CIL) related to the model displayed in the active canvas. A CIL file is created automatically after each simulation in the log output folder of the model if at least one item or one process has been selected for logging. You can select the entities and processes that should be logged in the [Element Lists](#) dialog.

The dialog consists of the *Simulation History* table that contains a list of the CIL files and the set of buttons: *Replay*, *Delete*, *Add*, and *Notes*.

Each row in the *Simulation History* table represents one log file (CIL) and contains the following properties displayed in columns:

- File Name – the CIL filename
- Status - (running, finished, interrupted)
- Timestamp - date and time of the simulation
- Server – the simulation server; localhost identifies the internal CI engine.
- Author – the simulation author; the default author can be set in the [Preferences](#)
- Notes – simulation run annotations.

The CI logs are presented in the alphabetical order of their file names. The list supports multiple selections: zero, one or more items (CILs) can be selected in the list to mark the scope of *Replay* and *Delete* commands.

The button *Replay* opens the selected logs (one or more) in the main window of *CI Player* application. The main window of *CI Player* application becomes the active application and the selected simulation log is ready for a replay.

The command *Delete* deletes the selected CIL file(s) from the output directory and removes them from the history table as well.

The command *Add* allows facilitates including into the simulation history a log that was created on a different computer. The *Select File* dialog that appears after you click the Add button allows for selecting the CIL file. The file is copied into the output subfolder located in the folder where the original model file (.GON) resides.. After that the newly added file appears in the *Simulation History* table.

You can annotate a simulation run by double clicking on its Notes field in the table. Alternatively, you can select a log and press the *Notes* button. This opens a multi-line text entry dialog.

The Author column can be edited by double clicking on the field. All other properties(columns) are read-only and cannot be changed.

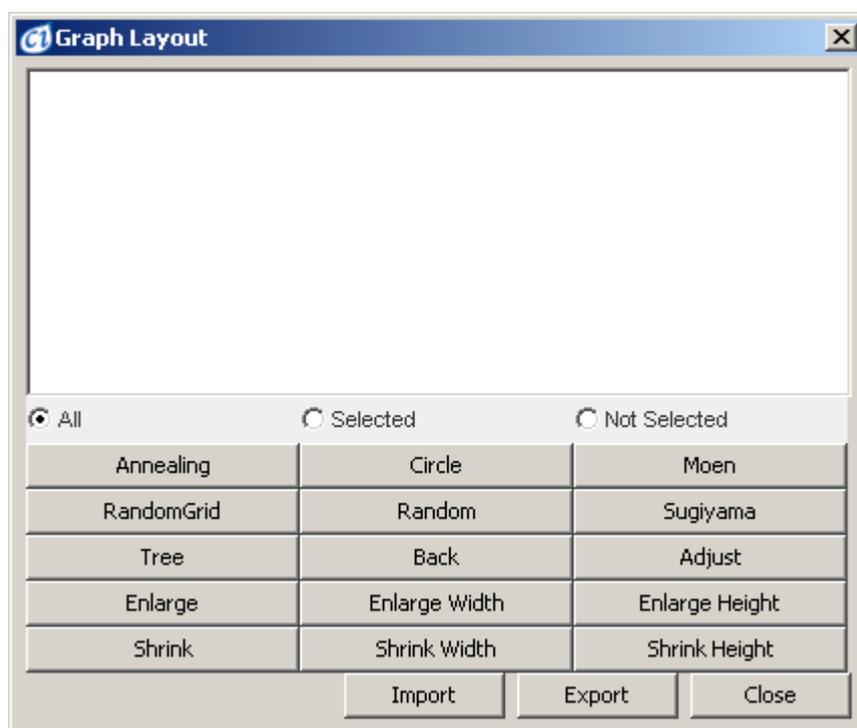
The *Close* button hides the Simulation History dialog..

## 18 Graph Layout

Using this dialog, you can “beautify” the graph layout of the model in the active canvas. This option can be especially useful when importing models from the BioPACS database or converting models from other formats (CellML, SBML)

To change the layout of a model you need to take the following steps:

- Open the graph layout dialog
- Import the model into the graph layout dialog box
- Run one of the available layout algorithms
- Export the new layout.



The buttons at the bottom of the dialog are used to perform the following commands:

- *Import* – imports the whole model on the canvas to the Graph Layout dialog box.
- *Export* – exports the graph from the Graph Layout dialog box to the canvas. This operation updates the positions of the elements in the canvas to the positions that have been set in the Graph layout dialog box.

- Each of the buttons *Annealing*, *Circle*, *GEM*, *Moen*, *Random*, *Sugiyama*, *Tree*, *etc.* starts the layout algorithm for the graph that is displayed in the Graph Layout dialog. Depending on the selected radio button, the layout algorithm can “optimize” the positions of *all* nodes, the *selected* nodes only or the *others*, *i.e.*, unselected nodes. The node selection should be done inside the small canvas with standard mouse operations.
- The *Enlarge* and *Shrink* buttons allow for linear scaling of the graph in the horizontal, vertical or both directions.

## 18.1 Graph Layout Algorithms

A brief description of each graph layout algorithm is given below.

### 18.1.1 Annealing Layout

This is an implementation of a simulated annealing layout. The idea of the algorithm is to minimize the total system energy. Simulated Annealing is a force-directed layout and is one of the more computationally expensive but generally effective layouts of this type. R.Davidson and D.Harel. “Drawing Graphs Nicely Using Simulated Annealing”, *ACM Transaction on Graphics*, 15(4):301–331, 1996.

### 18.1.2 Circle Layout

The circle layout arranges all nodes into a circle, with constant spacing between neighboring nodes. The performance of this layout is proportional to the number of vertices in the circle.

### 18.1.3 GEM Layout

This algorithm works by giving every node a position and a *temperature*. Then for every cell, repulsing and attracting forces are computed. Details of this algorithm are described in A.Frick, A.Ludwig, and H.Mehldau. “A Fast Adaptive Layout Algorithm for Undirected Graphs”, *Proc. Graph Drawing (GD’94)*, LNCS 894, 388–403, 1994.

### 18.1.4 Sugiyama Layout

The layout arranges the node with the Sugiyama layout algorithm. The algorithm is one of layered layout algorithms and it is only applicable to DAG (directed acyclic graph). A detailed description can be found in Kozo Sugiyama, “A

Cognitive Approach for Graph Drawing”, *Cybernetics and Systems*, 18(6):447-488, 1987

### **18.1.5 Random Layout**

The layout arranges the nodes at random positions. The layout area is  $(2\sqrt{n})^2$ , where  $n$  is the number of nodes.

### **18.1.6 Tree Layout**

The layout arranges the nodes into a tree structure. The root nodes are positioned at the top.

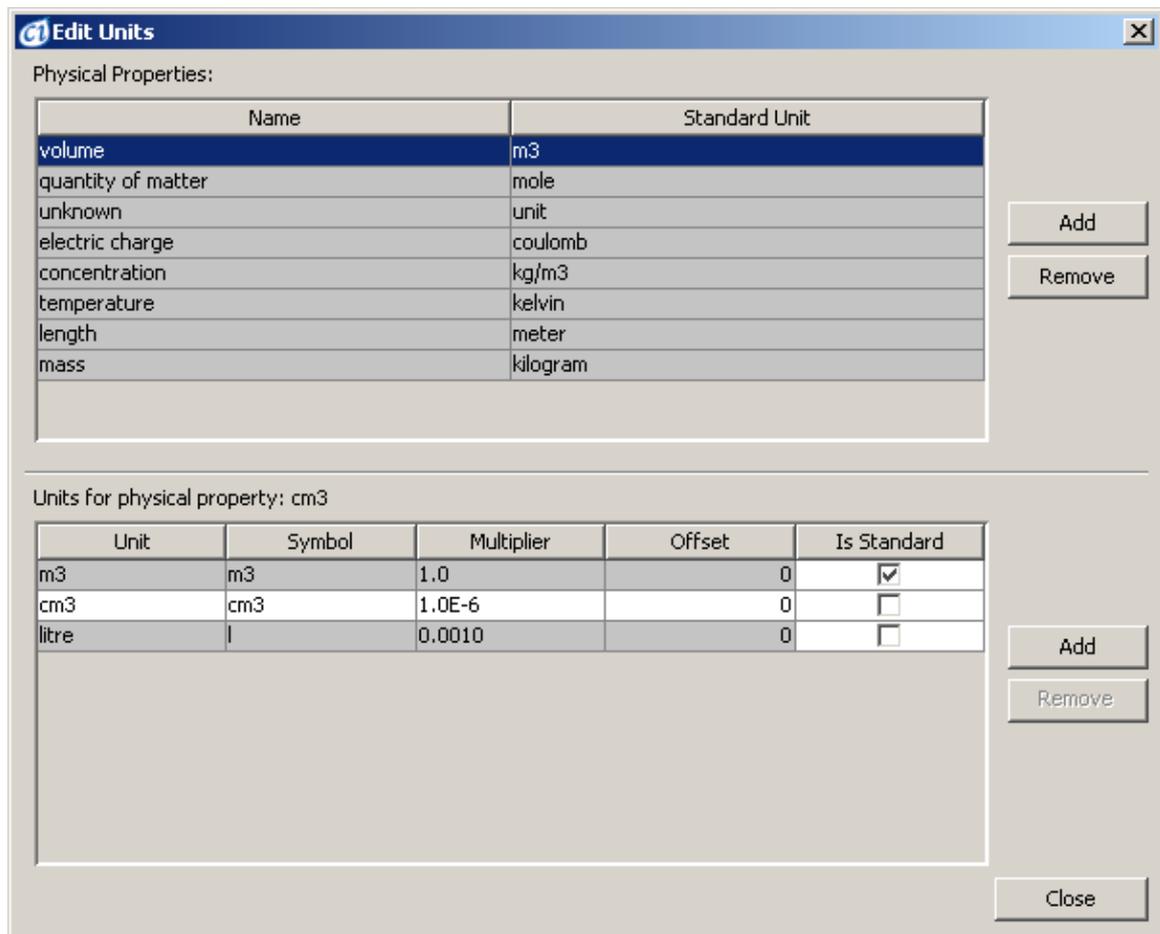
### **18.1.7 Moen Layout**

This Moen Layout makes some improvements over standard tree layout algorithms. The algorithm takes cell shapes into account and concentrates on producing as compact a result as possible. The nodes are ordered from left (root nodes) to right (child nodes). Details can be found in Sven Moen, “Drawing Dynamic Trees”, *IEEE Software*, 7(4):21-28, 1990

## 19 Edit Units

Cell Illustrator contains a units dictionary with a set of pre-defined physical properties and their units. The standard units are can be viewed in the *Edit Units* dialog box. Additionally, non standard units and non standard physical properties can be defined in the *Edit Units* dialog. These user defined units are specific to the active model and are stored in the model file. Therefore the units defined in this dialog are not system wide, i.e., they are not visible in other models.

Each physical property has one standard unit. All other units can be converted to the standard unit using the multiplier and offset properties. This means, that units defined for one and the same physical property are convertible between each other, while unit for two different physical properties are not convertible.



To add a new unit to your model:

- Select the desired physical property in the upper table. In the lower table you should see the list of all units defined for this physical property.
- Press the *Add* button and enter the *Name* of the unit and press OK. The new unit has been added to the lower table.
- Define the conversion rule by specifying multiplier and offset parameters. These parameter allow for the conversion of the new unit to the standard unit.
- The example below shows a new volume unit cm3 (cubic centimeter) that was defined by the user. The cubic centimeter is derived from the standard unit m3

(cubic meter) with the conversion parameters: multiplier equal to 1e-6 and offset equal to zero.

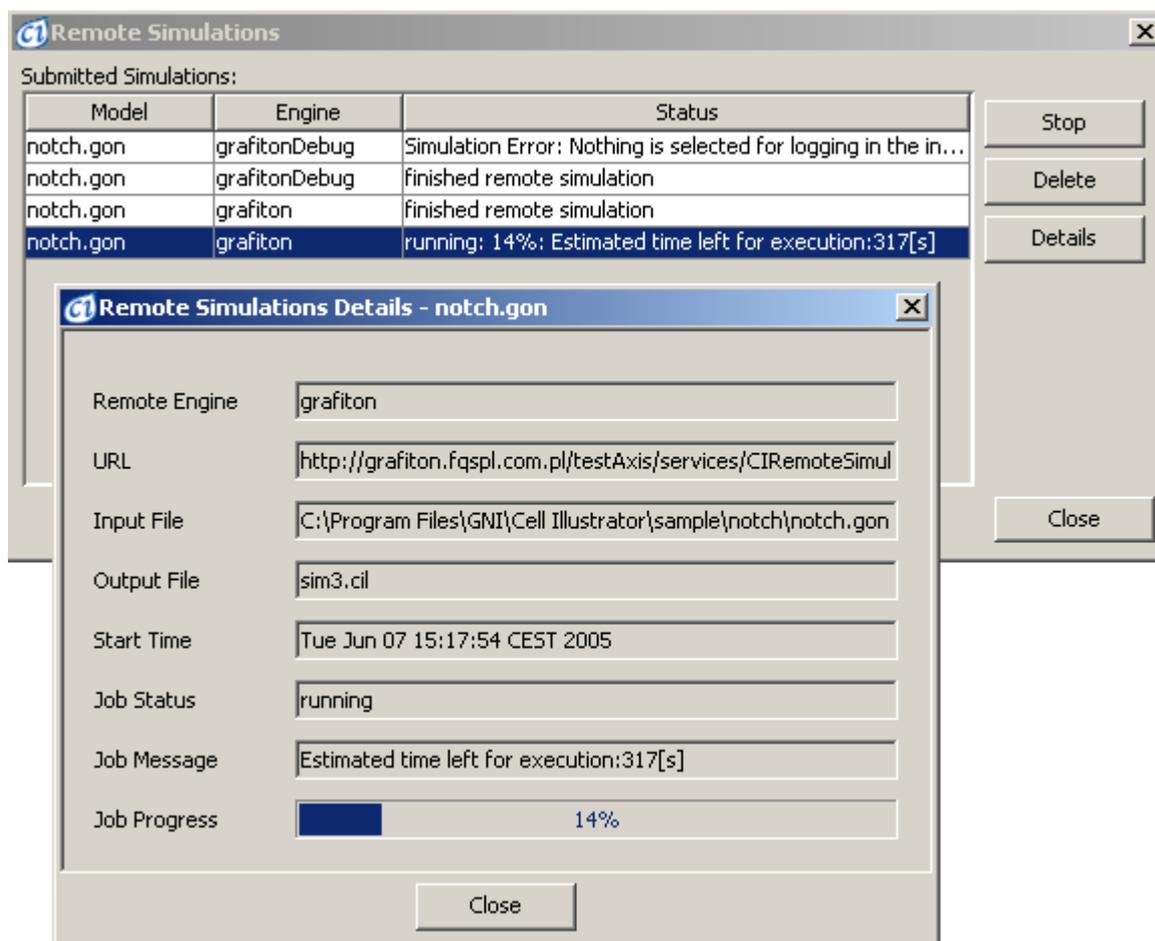
- The units defined in this dialog box are then available in the [Element Settings Dialog Box](#), in which the unit of each entity value can be selected.

**Note:** The simulation engine supports non-standard units, however it performs the calculation in standard units. The value of each entity expressed in standard units is the absolute value that is used by in the Petri Net model. This has the following consequences:

- Process speed should be always defined in standard units
- Entities representing two different physical properties, e.g. mass and volume can be connected by a process or used in one mathematical formula (script). The process or formula will operate on the absolute entity values expressed in standard units of each physical property.
- Non-standard units are converted to standard ones during initialization of the entity value, e.g. during the file open operation.
- You may view the absolute entity values by un-checking the menu item [View | Show User Units](#). Checking this item will display the entity values in user defined units.

## 20 Submitted Simulations

In this modeless dialog, you can view and manage the simulations submitted to CI server(s). The *Submitted Simulations* table lists all jobs that have been submitted to the server using the *Simulation | Send to Server* command. Each simulation job is described by the following properties: the name of the submitted input file (column *Model*), the name of the CI Server, where the simulation is executed (column *Server*), and a message that describes the simulation status and progress (column *Progress*).

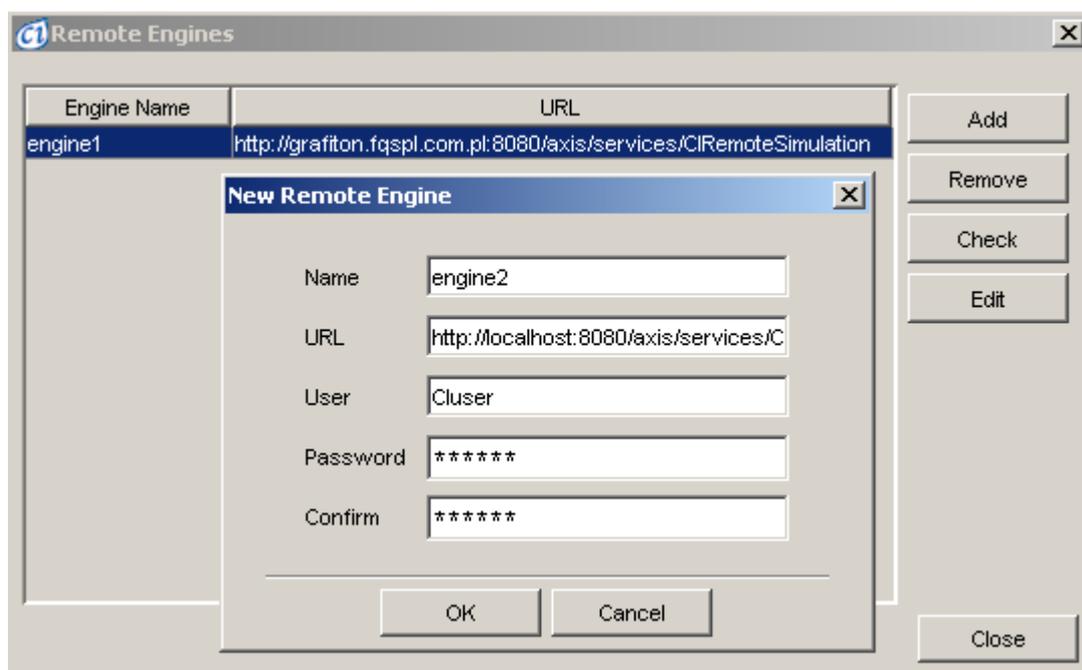


The dialog contains three buttons, which facilitate the management of the submitted jobs:

- *Stop* – interrupts a running simulation and download of the log files. If the selected simulation is not running, the command has no effect.
- *Delete* – remove the selected simulation from the table. After this command is executed the results of the remote simulations are lost.
- *Details* – opens the *Remote Simulation Details* dialog with more data on the selected simulation: server URL, input file path, output file name, etc. One *Remote Simulation Details* dialog can be opened for each simulation in the *Submitted Simulation* list.

## 21 Setup Servers

In this modeless dialog, you can view and manage the list of servers registered in the CI workspace. Each server is described by its name and URL. The name is a unique identifier specified by the user, while the URL is the HTTP address of the *CI Server* web service (see the **Cell Illustrator Server Installation Manual** for more information)



To register a new server, press the *Add* button. This opens the *New Server* dialog box, in which you need to specify the server properties: the name, URL, user and password. Click *OK*, to register the server in the CI workspace and add it to the server list.

The other buttons allow you to manage the list of registered engines:

- *Test* – checks if the selected server is accessible
- *Remove* – removes the selected server from the list
- *Edit* – facilitates the changing of the server properties, e.g. the URL, user name or password.

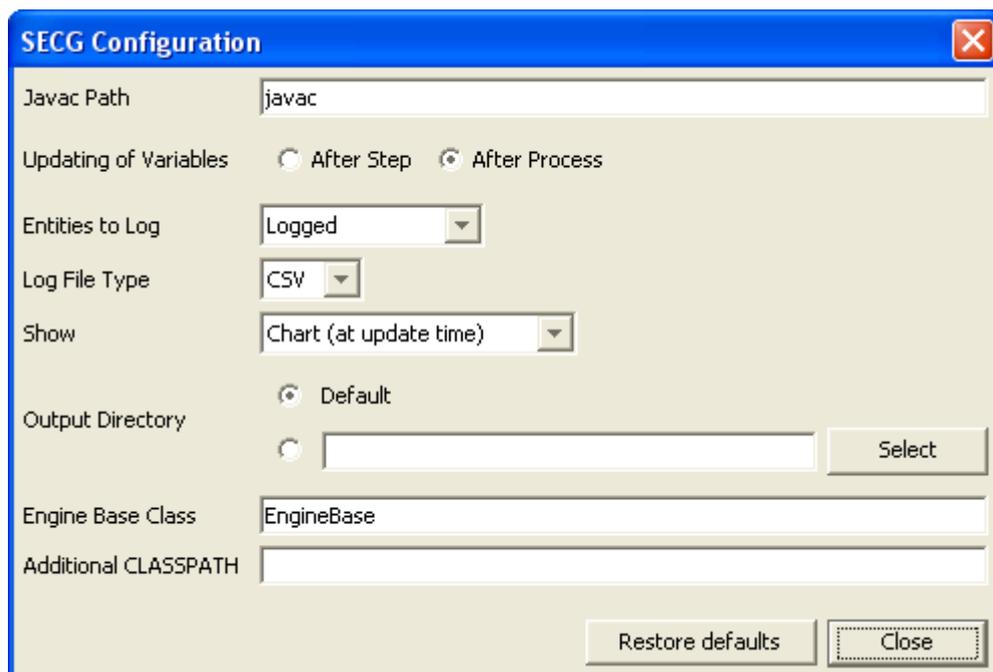
## 22 SECG Configuration

Simulation Engine Code Generator (SECG) is a simulation engine that enables you to simulate the selected model in a special way. SECG performs the simulation in the following steps:

- Generate the Java source code that represents the Petri Net model of the selected canvas
- Compile the source code using Java Compiler (javac)
- Execute the compiled program
- Save simulation log

Thanks to this approach large models can be simulated much faster than using the default simulation engine included in CI.

In *SECG Configuration* modeless dialog, you can setup parameters regarding running SECG simulation and exporting model to a source code.



Parameters available in this dialog can be divided into two groups. The first group include parameters, which specify how the source code of the engine is generated. The second group of parameters is related to the execution and results of SECG simulation

- Javac Path - the generated source code must be compiled in order to simulate the model. This parameter is the path to the javac compiler
- Updating of Variables - when this value is set to 'After Process' the change of the entity value is applied right after execution of this process, so the next

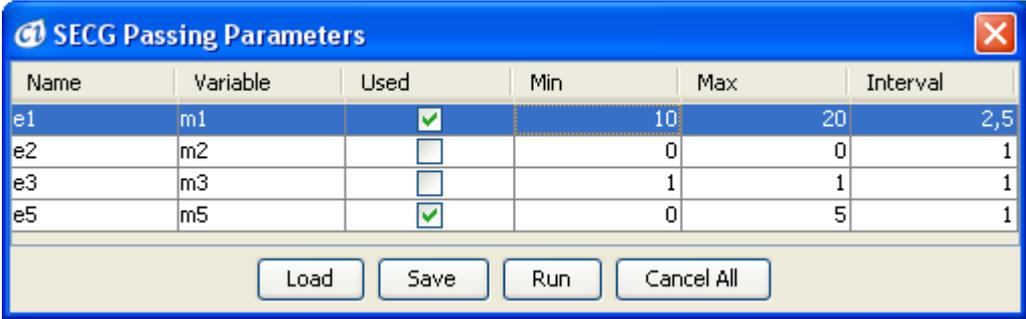
process uses the actual value of the entity even if both processes are executed at the time T (this causes sequential process execution). If the other option is selected the value of the entity is updated only after all processes at time T are executed (this gives some parallelism)

- Entities to Log – specifies which entities are going to be logged. There are 4 possibilities, most natural is that only entities marked with the log mark are going to be logged, other possibilities are that also entities used in charts will be logged or that all entities will be logged
- Log File Type – specifies the log file format.
- Show – specifies how to display the simulation results. The entities values can be shown in charts dialogs similarly as it is done in normal simulation. The charts can be drawn only after the whole simulation ends, or they can be redrawn after each chart update interval. The CSML option states that the resulting CI log file should be displayed in CI Player after the simulation is finished..
- Output Directory - running an engine first of all requires some temporary files to be produced and second of all can produce file with saved log, this parameter allows you to specify where these files are to be saved, it allows selecting the 'Default' directory which is the same directory to which are saved cil logs, or it can be some other directory.
- Engine Base Class, the generated engine has some module which handles running of the engine and other features like logging results, this parameter specifies the name of this module (class). This option is most relevant for running SECG simulation, note that the base class must be on the classpath when running simulation. Another example of engine base class can be RandEngineBase which randomizes the order in which processes are executed
- Additional CLASSPATH, when using a different base class or using more advanced code in scripts there might be needed for adding additional libraries, this parameter allows you to add additional jars and class folders to the classpath which will be used when compiling and running the simulation

## 23 SECG Passing Parameters

This dialog allows selecting the entities which should be treated as parameters in the passing parameters simulation. You can specify the parameter range and interval in a table with available entities.

For example, in the bellow window, the e1 and the e5 entities were selected to be parameters. The simulation will be run for each combination of the parameters. In this case entity e1 will have following values 10.0, 12.5, 15.0, 17.5, 20.0, and the entity e5 following 0, 1, 2, 3, 4, 5.

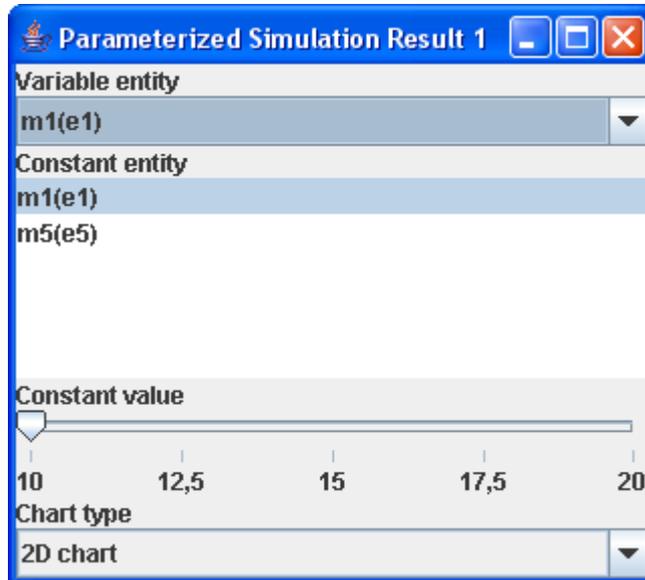


Name	Variable	Used	Min	Max	Interval
e1	m1	<input checked="" type="checkbox"/>	10	20	2,5
e2	m2	<input type="checkbox"/>	0	0	1
e3	m3	<input type="checkbox"/>	1	1	1
e5	m5	<input checked="" type="checkbox"/>	0	5	1

The parameter settings can be saved and load to a text file using the Load and Save buttons. The simulation is executed by pressing Run button. The last button with name Cancel All, cancels (stops) all SECG Passing Parameter simulations,.

## 24 Parameterized Simulation Results

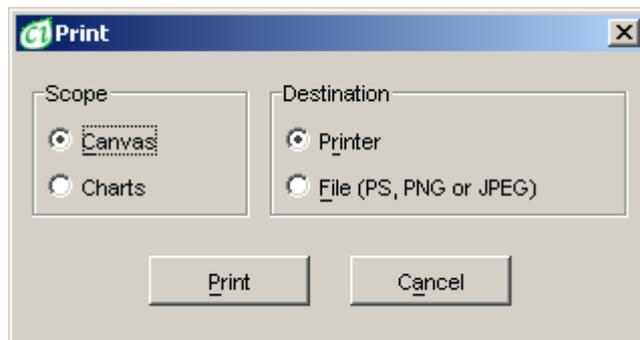
This dialog box is displayed after the SECG parameter simulation has finished. It enables you to select what should be viewed and how.



The *Chart Type* combo box allows specifying what kind of chart should be used - a 2D chart or a 3D grid or line chart.

In the 3D chart, the simulation results shows the dependency of selected entity values time series on one and only one parameter value, while other parameters are fixed (constant). Which parameter dependency is to be reflected on the charts is selected by choosing the entity in the *Variable Entity* combo box. The actual values of the other parameters are selected by choosing the entity in the list and selecting its value using the *Constant Value* slider.

## 25 Print Model

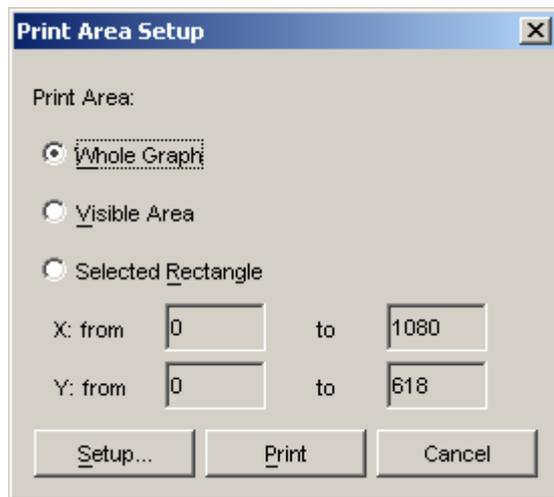


In the Print Model window, you can select the type of data to print and the destination for the print output. Either the model diagram or simulation charts can be printed. The output can be sent to the printer or an image file on a disk in PostScript, PNG or JPEG format.

In case *Printer* is selected, clicking on the *Print* button opens the *Print* dialog box. In this dialog, you can set the details of the Print job, e.g., the target printer from a list of available printers, the page size, orientation and the margin size.

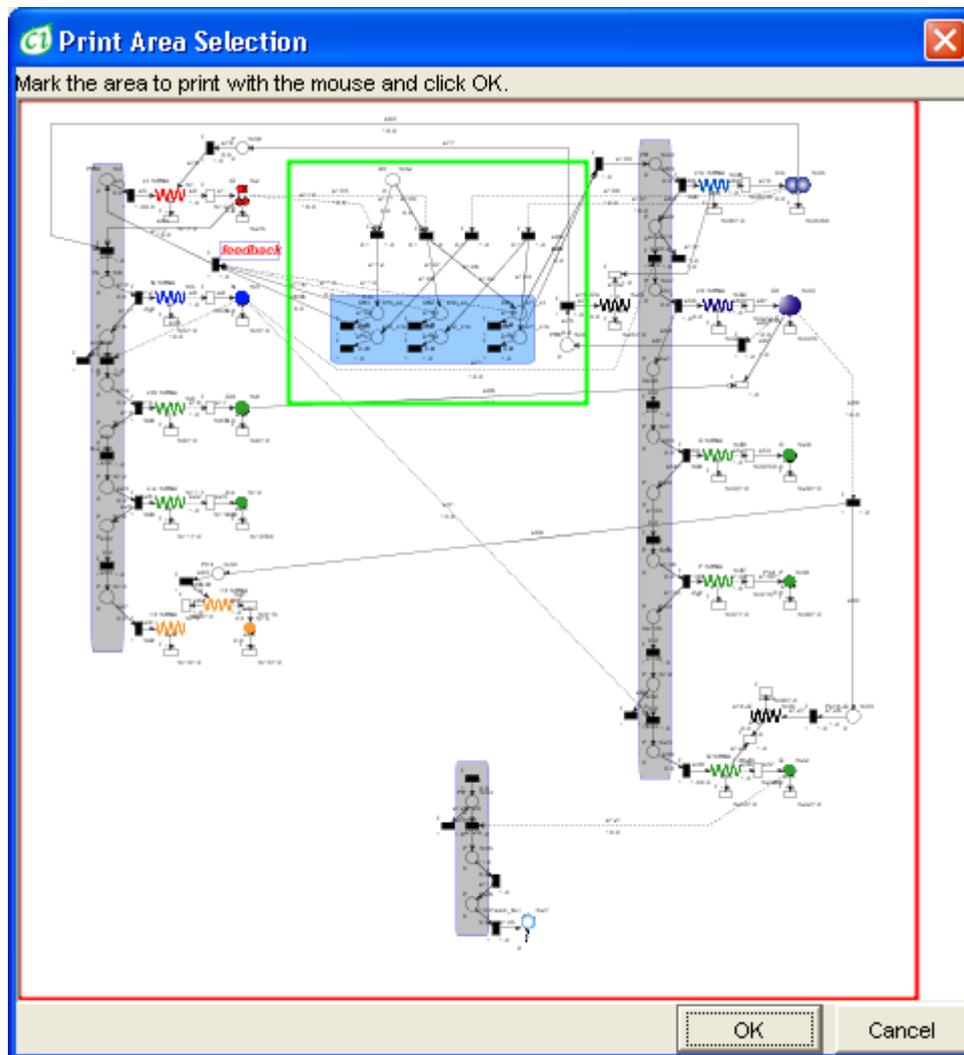
In case the *File* option is selected, clicking on the *Print* button opens the *File Save* dialog box. There you can select the desired file format (PostScript, PNG or JPEG) and the file name. Printing to a PostScript file is done using the service provided by your default printer. The quality of the output PostScript file depends on your printer setup. PostScript files created on computers connected to different printers might differ.

## 26 Print Area Setup



With the Print Area Setup dialog, you can specify which part of the model should be printed. Three options are available: *Whole Graph*, *Visible Area* and ***Selected Rectangle***. If the *Selected Rectangle* radio button is on, *From* and *To* edit boxes determine the portion of the model to be printed. The print area can also be selected graphically. The *Setup...* button opens the [Print Area Selection](#) window. After you made your selection press the *Print* button. This opens the [Print Model](#) dialog with additional options.

## 27 Print Area Selection



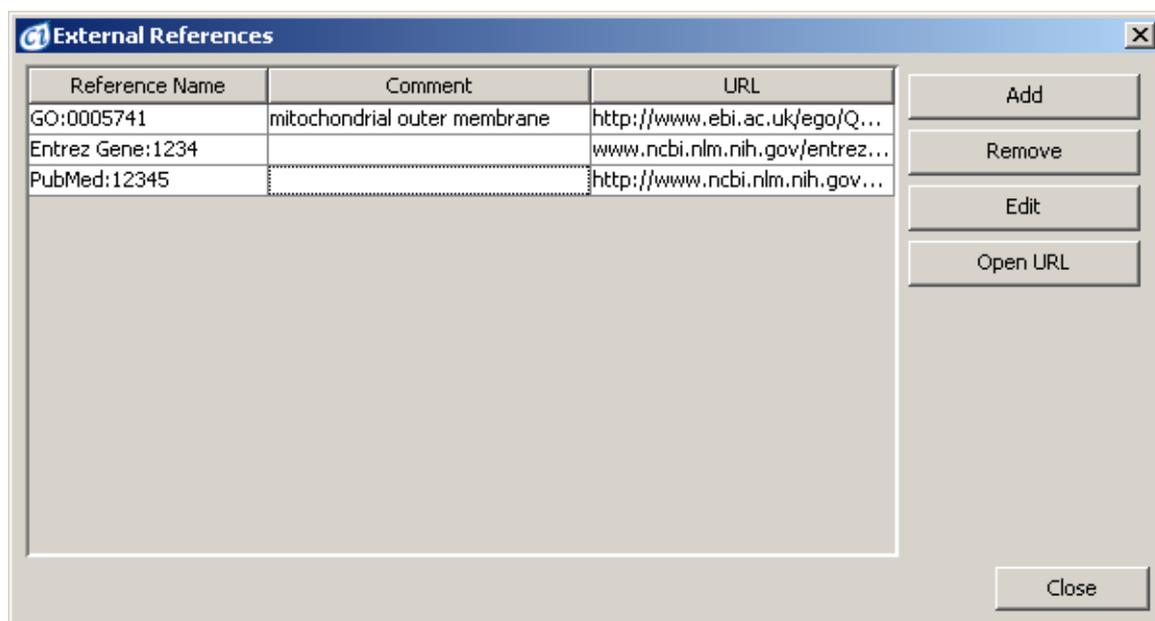
In the Print Area Selection window, you can select the area to be printed. Click on the model display and drag the mouse to mark the area for printing with a green rectangle.

The *OK* button confirms the selection and closes the window. The *Cancel* button dismisses changes to the print area and closes the window.

## 28 External References

With this dialog you can:

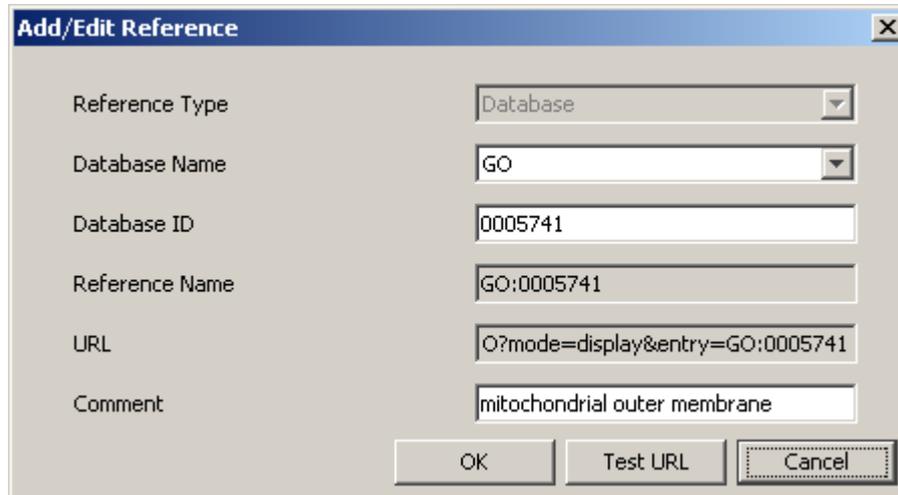
- create new references for the selected element
- edit/remove existing references



- *External References* is a modeless dialog box that displays the list of references associated with the currently selected element.
- *Add*, *Edit* opens the [Add/Edit References Dialog Box](#), in which you can specify the details of the reference
- *Open URL* opens the URL of the selected external reference in the web browser application
- The reference table displays the reference details in 3 columns: Reference Name, Comment and URL. You can edit any of those reference details by double clicking on the desired table cell.
- For database and publication references, the name and URL is generated automatically when the reference is defined. In some cases you might want to change the default name or URL, e.g. by adding a special, non-default parameter to the URL. Therefore editing of cells in the table is useful for the refinement of automatically generated URL and name attributes.
- Depending on the reference type, the comment property can be used for various purposes. E.g. for it can be the term that is defined by a vocabulary reference, or it can be a description of the relationship between the element and the reference.
- The database and publication references can be viewed/edited in two dialog boxes [External References Dialog Box](#) and in the *Biological Panel* of the [Element Settings Dialog Box](#).

## 29 Add/Edit References

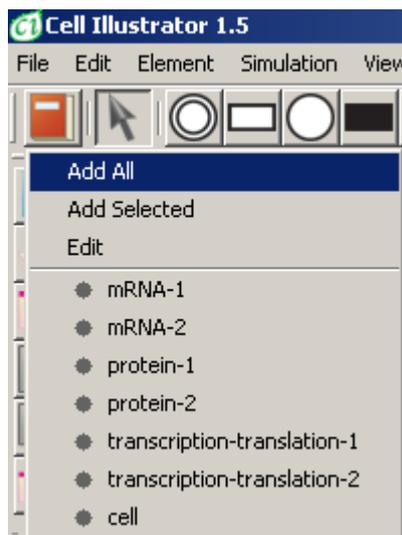
This modal dialog box enables you to create a new references to an external resource or to edit an existing one, by specifying the reference type and attributes.



- In *Reference Type* combo box you may select one of the available types: *Database*, *Publication* and *Simple*. The *Reference Type* is disabled, if the reference is opened for editing.
- For the *Simple References* you specify the *Reference Name*, *URL* and optionally the *Comment*. The attributes *Database Name* and *Database ID* are meaningless for simple references.
- For the *Database and Publication References* you specify the *Database Name* *Database ID* and optionally the *Comment*. The attributes *Reference Name* and *URL* are generated automatically basing on the *Database Name* and *ID*. The automatically generated attributes can be modified by the user in the [External References Dialog Box](#)
- *Test URL* opens the *URL* in the web browser application, which allows you to test whether the defined or generated *URL* is correct.
- Depending on the reference type, the comment property can be used for various purposes. E.g. for it can be the term that is defined by a vocabulary reference, or it can be a description of the relationship between the element and the reference.

## 30 Edit Parts Dialogs

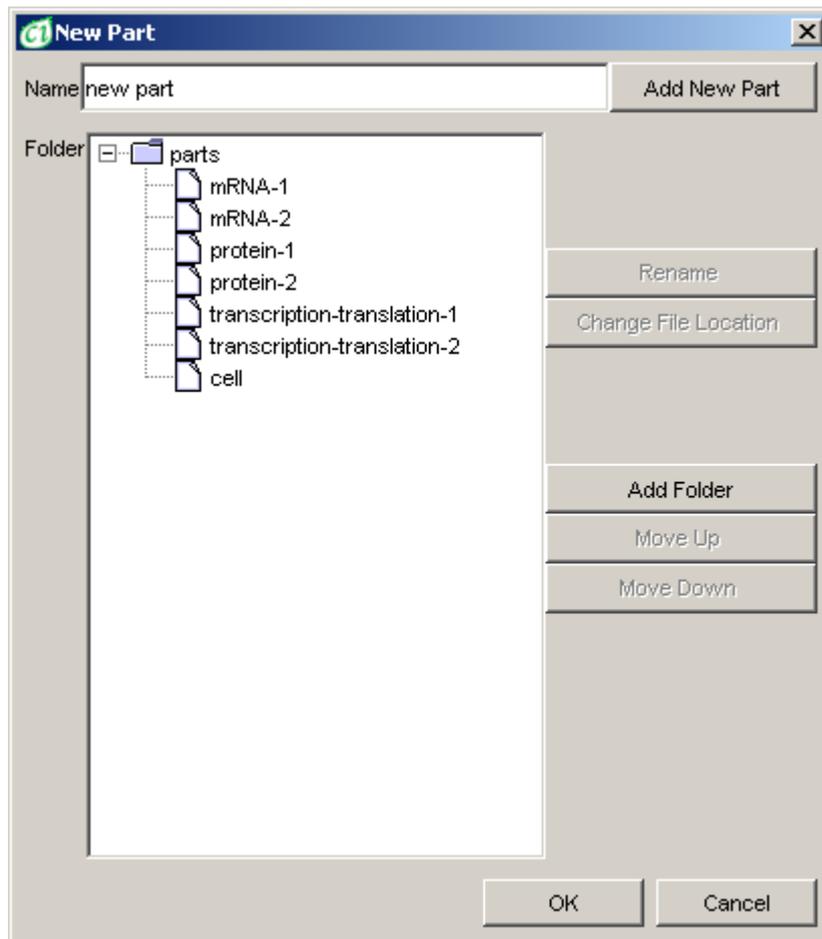
With Edit Parts, you can organize a repository of frequently reused models. Then, you can assemble more complex models out of lower-level “parts” stored in the repository. Cell Illustrator comes with several pre-registered parts to demonstrate this function.



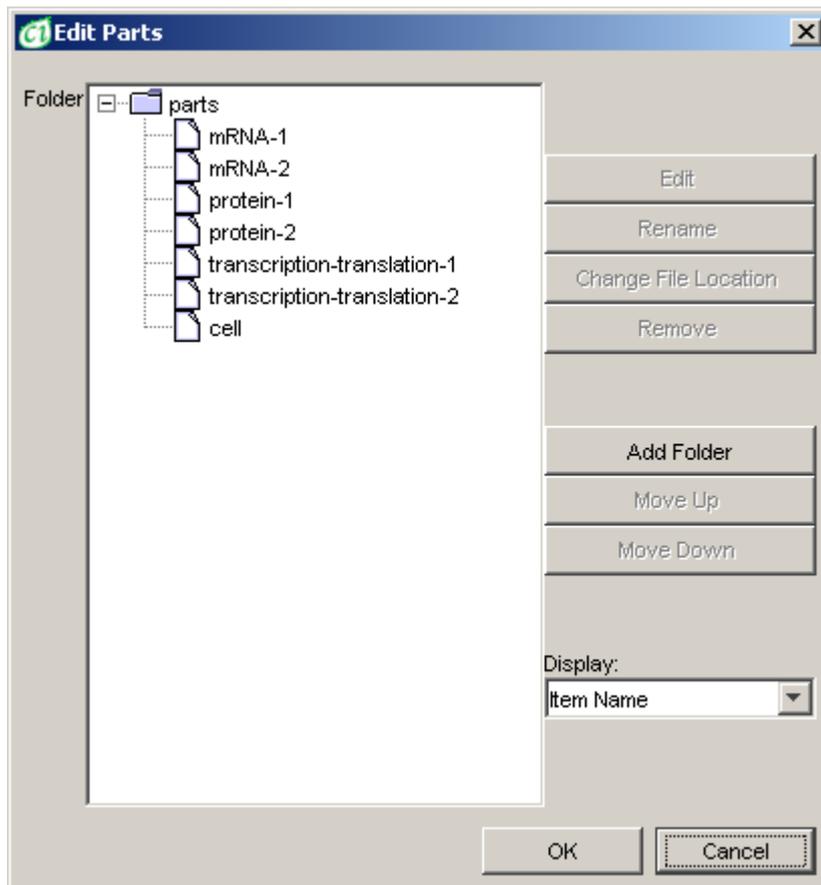
The *Edit Parts* drop-down menu is displayed after clicking the *Edit Parts* button on the Edit Toolbar. With this menu, you can:

- Add a new part to the repository by clicking *Add All* or *Add Selected*.
- Manage and organize the parts in the repository by clicking the *Edit* menu item.
- Insert a model part into the active canvas by clicking on its name.

The Add All command adds to the repository the whole model in the active canvas while the Add Selected inserts into the repository only the elements that are currently selected in the canvas. Both commands open the *Add New Part* dialog box shown below:



Clicking *Edit* opens the *Edit Parts* dialog shown below:



Models in the repository are organized into a tree of components. Each model is stored as a separate file in the location selected by the user. The component tree is stored in the *favorites.xml* file in *genomicobjectnet* subfolder of the user preferences folder. It contains references to those files. Renaming or moving a file to a different location invalidates its reference in *favorites.xml*.

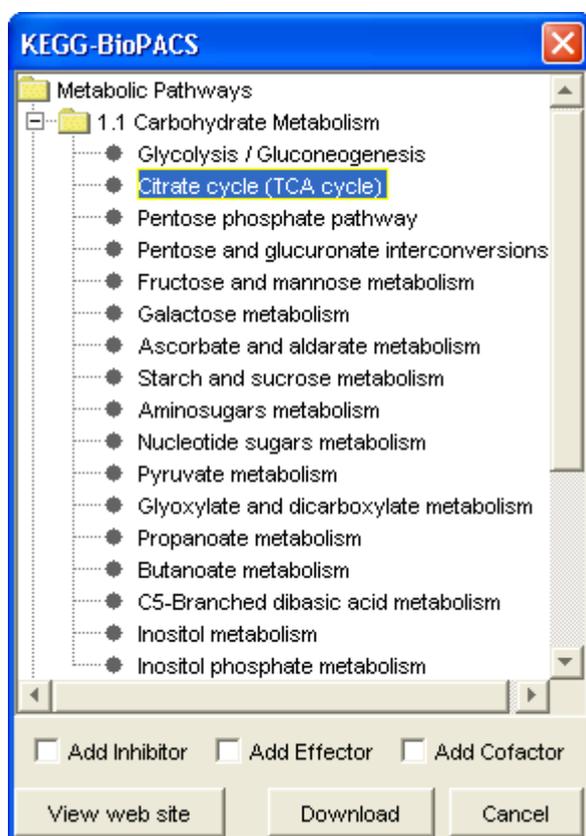
An item in the repository can be identified either by its name or by the name of the file where it is stored.

In the Edit Parts dialogs, the user can execute the following commands:

- *Add Folder* allows you to create a component group
- *Remove* deletes the references to selected components and/or groups from the list. The files that store the components are not deleted.
- *Move Up* moves a selected component or a group of components one position up in the list
- *Move Down* moves a selected component or a group of components one position down in the list
- *Rename* allows the renaming of a selected component or a group

- *Change File Location* saves a selected component into a specified file. The original file is not removed. The location of the component is updated in the list of components.
- Clicking the *Edit* button opens a selected component for editing in a new canvas window.
- The *OK* button saves the modifications to the list of components and closes the dialog, while the *Cancel* button closes the dialog without saving any changes.
- In the *Add All* and *Add Selected* mode, the *Add New Part* creates a new entry in the component hierarchy.
- In the *Add Selected* mode, after pressing *Add New Part*, the user is prompted to save the selected elements into a new file.

## 31 KEGG-BioPACS

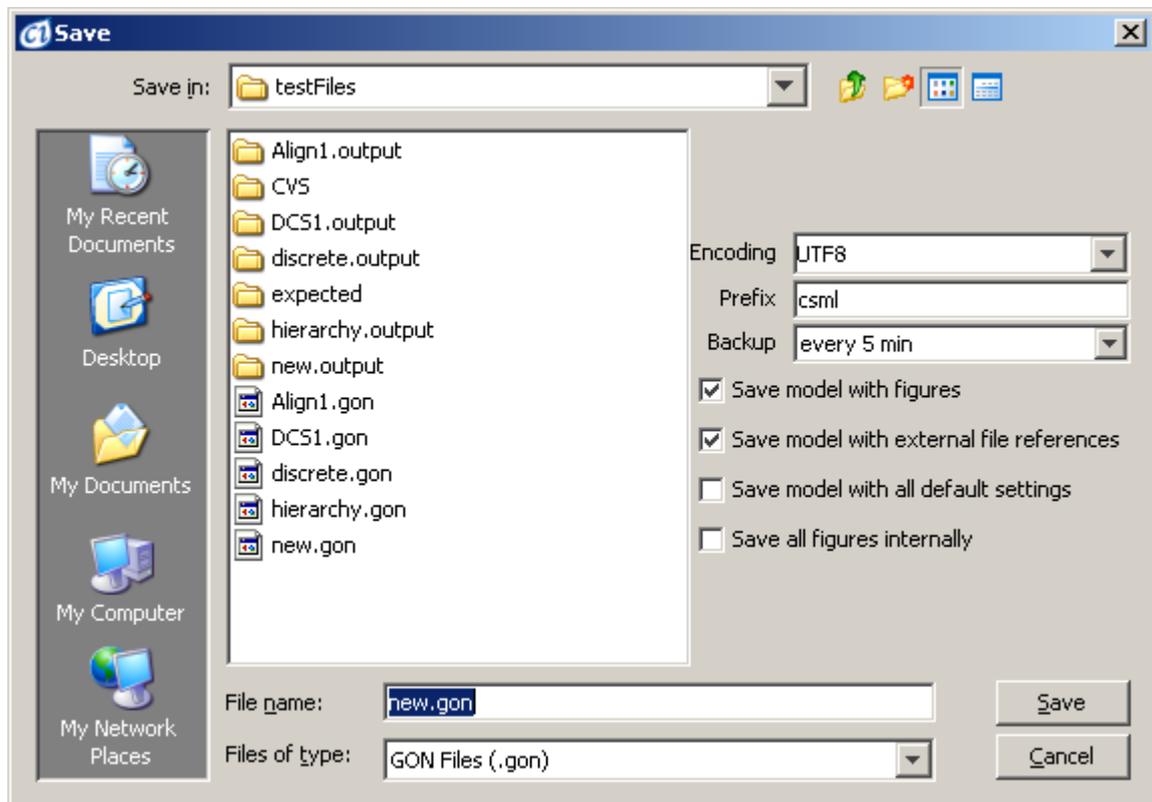


BioPACS is a Web system that converts metabolic pathway maps from the KEGG Web site to the XML file format used by CI. The KEGG-BioPACS dialog allows the selection of a metabolic pathway map in the KEGG Web site converts it with the BIOPACS converter to the XML file format used by Cell Illustrator and opens it in a canvas window:

- If the *Add Inhibitor* is turned on, all inhibitors of chemical reactions influencing the imported model that are present in the BioPACS are added.
- If the *Add Effector* is turned on, all effector molecules of chemical reactions influencing the imported model, present in the BioPACS, are added
- If the *Add Cofactor* is turned on, all cofactors of chemical reactions influencing the imported model, present in the BioPACS, are added

The *View Web Site* button opens the BIOPACS converter site in your default browser. The *Download* button starts a download operation for a selected model. The *Cancel* closes the dialog.

## 32 Save Dialog

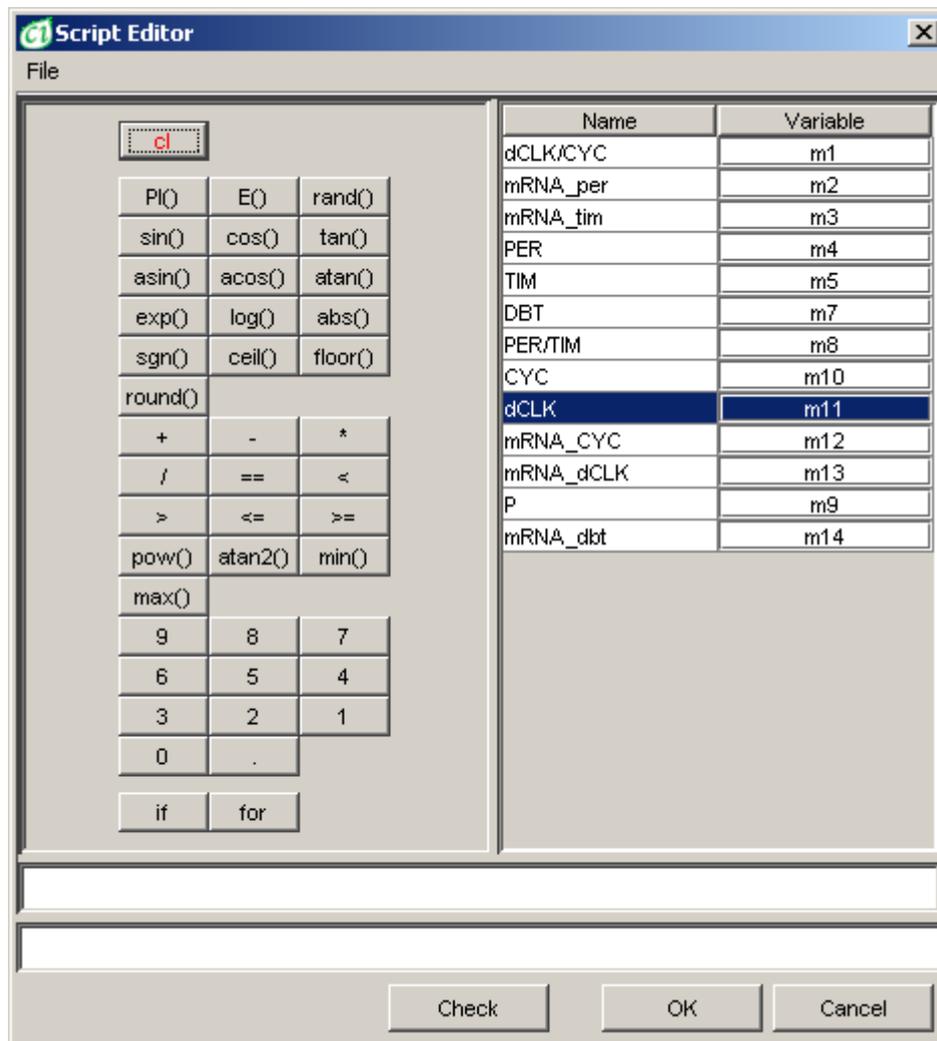


The Save dialog allows the saving of a model in an active canvas window to a file. The dialog has several options:

- *Encoding* determines the file encoding standard.
- *Prefix* specifies the prefix used in all XML tags in the file. The default value *csml* stands for “Cell System Markup Language”.
- If *Save net with figures* is not checked, the data on the position of model elements and their graphical representation will not be written in the file.
- If *Save net with external file references* is checked, the model that makes use of elements in other files will store references to those files. Otherwise, the contents of referenced files will be included in the output file.
- If *Save net with all default settings* is checked, each element in the canvas will be annotated with the current graphics settings. Use this option in case you want to preserve the way the model looks while passing it to a user who may have different display settings.
- If *Save all figures internally* is checked, all images on the canvas will be saved inside the model CSML file. Use this option in case you want to include all graphical files (JPEG, PNG, and SVG) inside your model file. This can be useful if you want to pass your model to another user. This will assure that the user will see all the graphics you have added to your model from external files.



## 33 Script Editor



An advanced user of Cell Illustrator may need to write a custom function to specify changes of a property value. With the Script Editor, you can write a Pnuts to define:

- *Threshold, Speed, Updater, and Firing Rule* property of a connector,
- *Activity, Speed and Delay* of processes as well as
- *Initial Value* of entities.

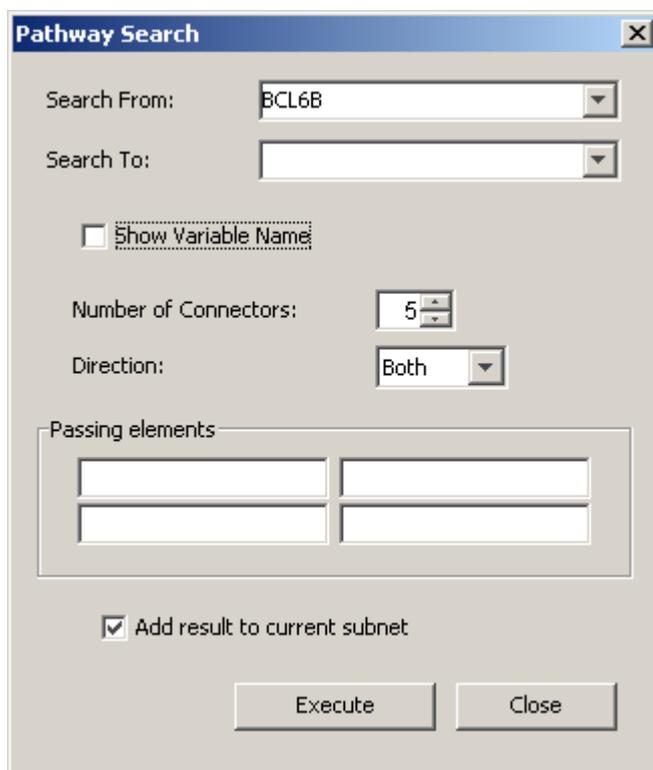
Pnuts is a script language for Java environment. The Pnuts Language Reference can be downloaded from the project website at <https://pnuts.dev.java.net/>.

At the top left in the dialog is a set of function buttons. At the top right is a table containing all entities in the model. In the middle, a script pad is placed where you can edit a script either by clicking on the function buttons and selecting entities from the table, or by typing in text. You can check whether the syntax of your script is correct by pressing the *Check* button. Error messages will appear in the bottom panel. Remember to press the Return key at the end of the script. The *OK* button saves the changes and closes the window. The *Cancel* button closes the window without saving any changes.

## 34 Pathway Search

Using this dialog, you can find subnetworks around the specified entity or entity-to-entity pathways. The pathway search is performed by the execution of the following steps:

- Select an entity in the *Search From* combo box.
- Select a target entity in the *Search To* combo box. This step is optional. Leave the *Search To* field empty, if you want to find a subnetwork around the specified entity.
- Specify the *Number of Connectors* to be searched for.
- Specify the search *Direction*.
- Specify the auxiliary options *Passing Vertices*
- Select whether to *Add results to the current subnet*.
- Press the *Execute* button. This will display the [Pathway Search Results](#)



The *Pathway Search* dialog consists of the following controls

### 34.1 Search From Combo Box

In this combo box you can select the starting entity for each search. This combo box contains list with all entities in the active canvas.

## 34.2 Search To Combo Box

In this combo box you can select the target entity for each search. This combo box contains the list with all the entities in the active canvas.

If this field is empty, the target entity can be any entity in the canvas and the search results will include all pathways beginning in the Search From.

If this field is not empty the search results will include only those pathways that start in the *Search From* entity and end in the *Search To* entity.

Use this field, if you want to find a pathway between two entities (entity-to-entity pathways) only. Otherwise, if you want to find a subnetwork around the starting entity leave this field empty.

### 34.2.1 Show Variable Name

This options changes the information displayed in the entity lists in the *Search From* and *Search To* combo boxes. If the option *Show Variable Name* is selected, then each entity is represented as a pair *Entity Name* and *Entity Variable Name* in the entity list. Otherwise only the *Entity Name* is displayed in the entity list.

This option is useful when handling ambiguous situations. In some cases, two entities may have the same *Entity Name*, but they will possess different *Variable Names*.

### 34.2.2 Number of Connectors

In this field you specify the number of connectors to be searched for. To search for the nearest neighbors only, specify 1. To search for the nearest neighbors plus their nearest neighbors specify 2. The larger the number of connectors the more search results you will receive.

### 34.2.3 Direction Combo Box

In this combo box you specify the search direction. You may choose one of the following 3 possibilities:

- Forward - to search for output (target) entities/processes only.
- Reverse - to search for input (source) entities/processes only.
- Both to search for any connected entities/processes.

### 34.2.4 Passing Element

A *Passing Element* is an entity or process that must be included in the *Search Results* pathways. You may define up to 4 *Passing Elements*, by specifying their names in the edit boxes.

### **34.2.5 Add Results to Current Subnet**

Select this option to maintain the current subnet. If this option is checked the current subnet will be preserved after finishing the pathway search.

### **34.2.6 Execute Button**

This starts the search with the specified options. The discovered pathways are displayed in the *Pathway Search Results* dialog box.

## 35 Pathway Search Results

This dialog box displays the list of pathways that have been discovered during the [Pathway Search](#).

	0		1		2
1	B	←	p37		
1	B	←	p35		
1	B	←	p1		
2	B	←	p37	←	C
2	B	←	p35	←	A

Total: 5

Close

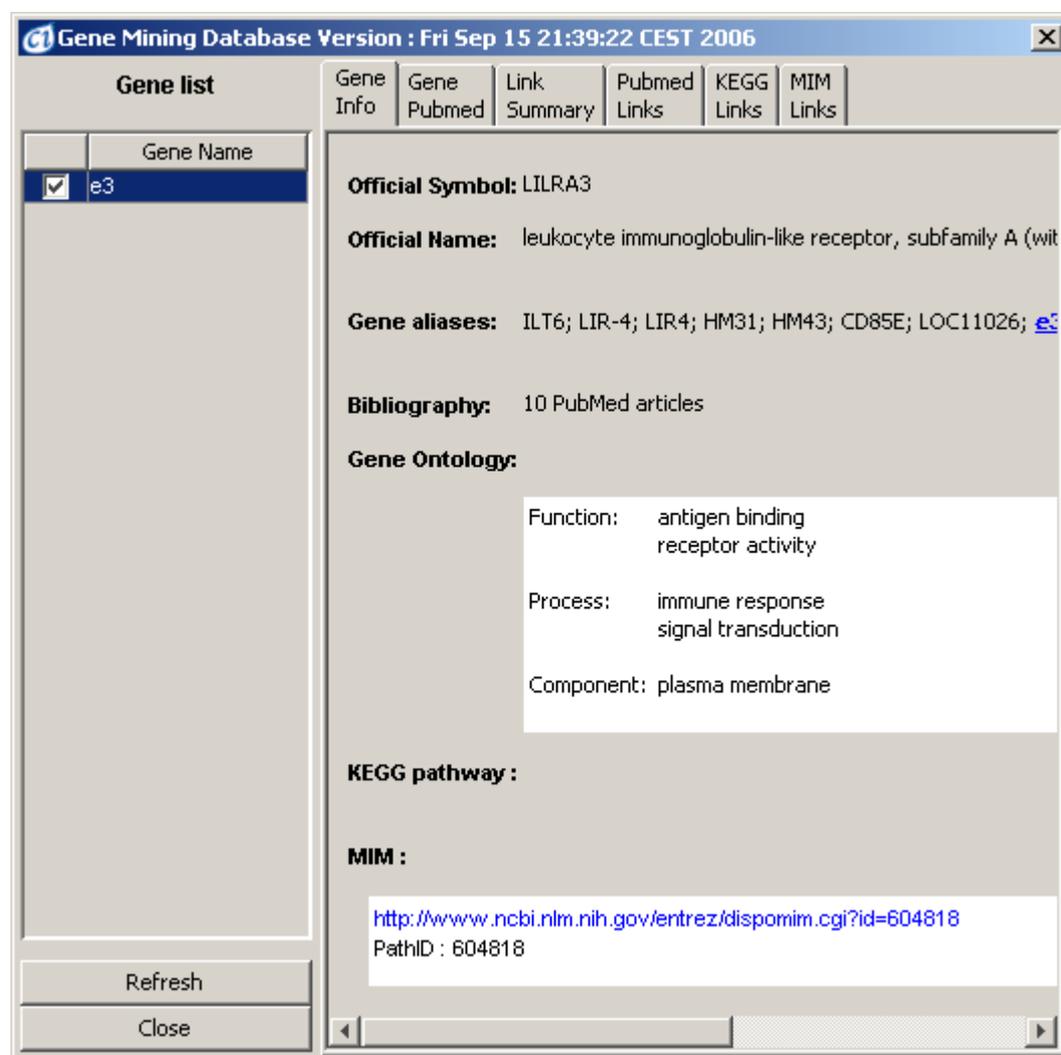
Each pathway is displayed in one row and described by the following properties:

- column 1: pathway length – the number of connectors in the pathway
- column 2: the first entity in the pathway – the entity specified in the Search From field
- column 3: connector direction – the direction of the connector between the first entity (column 2) and the connected process (column 4)
- column 4: the first process in the pathway
- column 5: connector direction – the direction of the connector between the first process (column 4) and the second entity (column 6)
- column 6: the second entity in the pathway
- etc.

Click a row in the table to add the corresponding pathway to the subnet. CTRL+click (Apple+click on Mac) and SHIFT+click allow for the addition or removal of multiple items to the subnet.

## 36 Gene Mining

This dialog box displays the detailed information concerning the selected genes retrieved from the PubMed, KEGG and MIM databases. You can extract this information either for a selected subset of genes or for all the genes in the network.



The set of genes upon which gene mining is performed depends on the canvas selection at the time of the execution of the [Analyze | Gene Mining](#) command in the following way:

- if a gene subnetwork exists on the canvas, then gene mining is performed upon the genes of this subnetwork
- otherwise, if the normal selection is not empty then gene mining is performed upon the set of selected genes
- otherwise, if none of genes in the network is selected, the gene mining is performed on all genes in the network.

The Gene Mining dialog box uses an internal database which is periodically updated. CI checks at each startup for the new version of this database and ask you

whether you want to download the newer file from the server. You may enable/disable this check in the [Preferences Dialog Box](#).

### **36.1.1 Gene List**

Gene Mining searches for articles concerning selected genes and for links between these genes. The set of genes that has been analyzed in Gene Mining is displayed in the Gene List panel. Selecting a gene in this list, displays the information about this gene in the following described six panels:

### **36.1.2 Gene Info**

Displays the main information about the gene selected in the Gene List: gene name, official name, aliases and number of PubMed articles, gene ontology, information about gene functions, processes and components

If information about an MIM or KEGG Pathway is present for the selected gene, you may click on the hyperlink to open it in the web browser.

A gene can be represented by its official symbol or an alternate symbol (alias) on the canvas. The symbol used on the canvas is highlighted in blue and underlined in the Gene Info panel. Clicking on it opens detailed information about this gene symbol from Entrez Pubmed database in the web browser.

This information is especially useful when the gene alias is used on the canvas. In such cases you can check in the Entrez Pubmed database, whether the gene alias is unique or ambiguous. If it is ambiguous, the Entrez Pubmed database displays you all possible official symbols for this gene alias.

### **36.1.3 Gene Pubmed**

In this panel you can observe the Pubmed article list concerning the selected gene. Each article includes the following details: authors, title, journal and publication date. You may also display the article abstracts by selecting the checkbox of each article.

### **36.1.4 Link Summary**

For a selected gene, this tab lists all related genes in the analyzed set as well as the number of PubMed, KEGG and MIM identifiers that the gene has in common with other genes in the analyzed set.

### **36.1.5 PubMed Links**

For a selected gene, this tab lists Entrez PubMed entries that link this gene to one or more genes in the analyzed set. You can expand each entry to see the full abstract. The list of related genes is displayed next to each link.

### 36.1.6 KEGG Link

For a selected gene, this tab lists KEGG pathways that link this gene to one or more genes in the analyzed set. The list of related genes is displayed next to each link. Click on the http link to access the WWW site with information on a particular MIM identifier.

### 36.1.7 MIM Links Panel

For a selected gene, this tab lists MIM identifiers that link this gene to one or more genes in the analyzed set. The list of related genes is displayed next to each link. Click on the http link to access the WWW site with information on a particular MIM identifier.

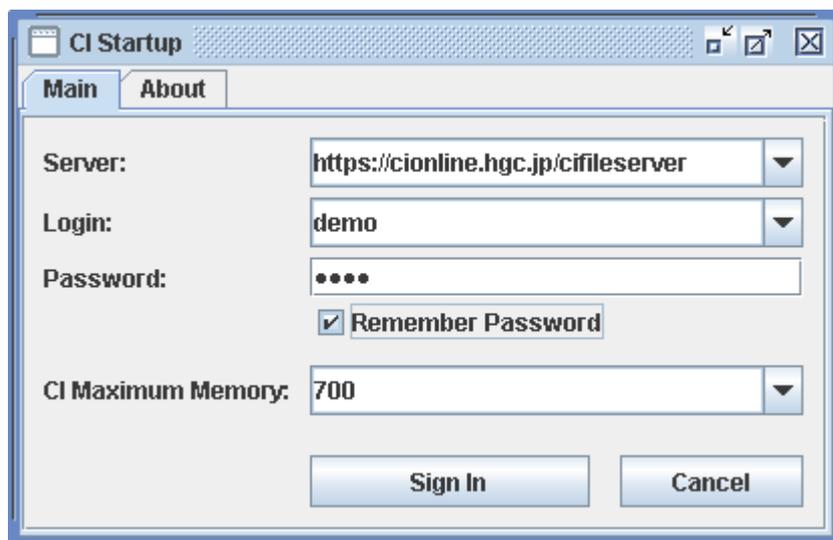
**Note:** You may use the shortcut keys Tab and SHIFT+Tab to navigate between the panels. The Tab key switches you one panel forward (to the right), while SHIFT+Tab one panel backward (to the left).

### 36.1.8 Refresh Button

This button starts the gene mining process for the selected subnet on the active canvas. It has the same meaning as the [Analyze | Gene Mining](#) command.

## 37 CI Online Login Dialog

This dialog box is displayed when the authentication on the CI Online sever is required. After a successful login the user data is displayed in the CI title bar in the form user@server e.g. [demo@cionline.hgc.jp](mailto:demo@cionline.hgc.jp). Depending on your account status, you might access remote data and services available on the CI Online server, such as: [#Project Manager Dialog](#), [#CSMLDB Search Dialog](#).



Before you login the CI Online Server, you need to register and obtain the account name and password. Then you enter this data in the Login dialog box:

- *Server* – the address of CI Online Server
- *Login* and *Password* – your login data

The other options in the Login dialog are:

- *Remember Password* – select this option to store your login data on the local computer. This will speed up the login when the dialog will be displayed the next time.
- *CI Maximum Memory* – the maximum memory (heap space) for the CI-Online process. Increase this value if you plan to open large pathway models.

**Note:** You may login only once in one CI window. If you want to login as another user, you need to close the CI window and start CI again.

## 38 CSMLDB Search Dialog

The *CSMLDB Search Dialog Box* is an interface that allows for submitting queries to the remote CSMLDB database. To access the remote CSMLDB database, the user must be logged in to the CI Online server.

Using this dialog you can search in the CSMLDB database for molecules (entities) and for reactions (processes) and import them into active canvas.

To find a biological entity or process in CSMLDB:

- Go to the desired tab: *Entity*, *Process*.
- Enter the search string, one or more characters, into the *Search For* edit box
- Choose the search options filtering, sorting results
- Press the *Find* button. And wait until the search results are displayed in the table. During this the *Find* button changes to *Cancel*
- Browse through the search results or narrow the search by applying additional criteria.

To insert a biological element, proceed as follows:

- Select the desired element(s) in the results table.
- Check the option *Merge*, if you want to merge entities with the same *TranspathDB ID*. Otherwise uncheck this option
- Click on the chosen row(s), drag it to the active canvas and drop it there by releasing the mouse button. You may also release the mouse over an empty space in the CI workspace; this will create a new canvas and drop the selected elements there.
- Alternatively, press the *Import* button to add the active elements to the active or a new canvas.

## 38.1 Molecule Search – *Entity* tab

The screenshot shows the 'Search CSMLDB Academic' window with the 'Entity' tab selected. The search criteria are as follows:

- Search For: p53
- Search In:  Name,  ID
- Type: (empty dropdown)
- Order by: (empty dropdown)
- Max rows: 50

Results are displayed in a table with columns ID, Name, and Type. The first 11 rows are shown:

ID	Name	Type
G000583	p53(m)	---mRNA
G001075	p53(h)	---mRNA
G009085	TP53BP1(h)	---mRNA
G009976	TP53(r)	---mRNA
G010150	TP53(b)	---mRNA
G010151	P53(pg)	---mRNA
G010153	TP53(z)	---mRNA
G010157	TP53(c)	---mRNA
G010158	TP53(x)	---mRNA
G010159	P53(ca)	---mRNA
G013616	TP53BP2(h)	---mRNA

At the bottom of the window, it states 'Found 457 Molecules for "p53".' and '100%'. There are also checkboxes for 'With merge' (checked) and 'Create new canvas' (unchecked), along with 'Import' and 'Close' buttons.

Molecule search is performed by the execution of the following steps:

- Enter a search strings into the *Search For* edit box. You may enter several strings separated by semicolon.
- Select the properties to be searched for using the check boxes in the *Search In* panel.
- Choose the entity type to be search for,
- Specify results order,
- Specify max results number per page,
- Press *Find* button

Search may take up to several seconds. If you want you can cancel search and make another query, but you are restricted to maximum of 4 running queries at one time. If 4 queries are still running on server, message box will appear when trying to run next search.



The *Molecule Search* dialog consists of the following controls:

### 38.1.1 Search For

In this field, you can specify part of the name or id of entity. The CSMLDB database will be searched for all entities that contain given name in their id and/or name depending on the settings in *Search In* box.

You may specify several search strings separated by semicolon (;). In this case the results will be the sum of each single string search. It means all entities will be matched that include at least one of the specified strings.

If this field is empty, CSMLDB will search for any entity satisfying other criteria.

### 38.1.2 Search In

In this field you specify, which entity property name, id, or both should be matched during the search.

If none of options is selected search will not be performed.

### 38.1.3 Type

In this combo box you can select the desired entity type. This will limit the search result to the entities of the selected type. The type are equivalent to CSO Entity Types.

If this field is empty entity type will not be used as a search criterion.

### 38.1.4 Order By

In this combo box, you can select how results should be ordered: by entity name or entity id.

### 38.1.5 Max Rows

In this field you can specify the maximum number of rows to be displayed on a single page. The smaller the value, the faster search. Default value is 50.

## 38.2 Reaction Search – *Process* tab

In this panel, you can search for all processes that contain an entity with given name/id.

Search CSMLDB Academic

Entity Process

Search For  Find

Search In:  Name  ID

Relation:  Input  Output

Type:

Order by:  Max rows:

Displaying results 1-50 of 749

ID	Name	Reaction	Type
XN000004307_0	XN000004307	cso30:c:P...	--binding
XN000004308_0	XN000004308	cso30:c:P...	--binding
XN000004309_0	XN000004309	cso30:c:P...	--binding
XN000004932_0	XN000004932	cso30:c:P...	---unknown activation
XN000005230_0	XN000005230	cso30:c:P...	---unknown process
XN000005278_0	XN000005278	cso30:c:P...	--binding
XN000005281_0	XN000005281	cso30:c:P...	--binding
XN000005304_0	XN000005304	cso30:c:P...	--binding
XN000006228_0	XN000006228	cso30:c:P...	---DNA binding
XN000006228_1	XN000006228	cso30:c:P...	-transcription
XN000006229_0	XN000006229	cso30:c:P...	---DNA binding

Found 749 Processes for "p53". 100%

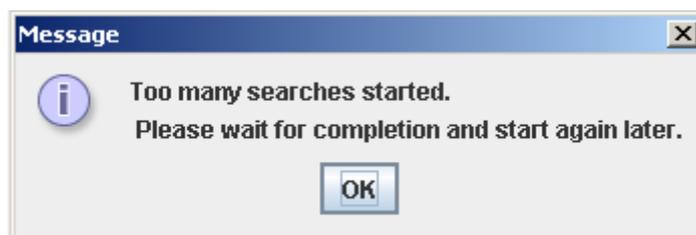
With merge  Create new canvas

Reaction Search is performed by the execution of the following steps:

- Enter a search string into the *Search For* edit box. You may enter several strings separated by semicolon.
- Select the properties to be searched for using the check boxes in the *Search In* panel.
- Choose relation type between entity and process: input or output,
- Choose the process type to be search for,
- Specify results order and maximum number of rows per page,
- Press *Find* button

Search may take up to several seconds. If you want, you can cancel search and make another query, but you are restricted to maximum of 4 running queries at

one time. If 4 queries are still running on server, message box will appear when trying to run next search.



The *Reaction Search* dialog consists of the following controls:

### 38.2.1 Search For

In this field you can specify part of the name or id of entity. The CSMLDB database will be searched for all processes that are connected with an entity containing given name in their id and/or name (depending on the settings in *Search In box*).

You may specify several search strings separated by semicolon (;). In this case the results will be the sum of each single string search. It means all entities will be matched that include at least one of the specified strings.

If this field is empty CSMLDB will search for any processes satisfying other criteria.

### 38.2.2 Search In

In this field you specify, which entity property name, id, or both should be matched during the search.

If none of options is selected search will not be performed.

### 38.2.3 Relation

In this field, you can limit the search to input or output entities only. If none of options is selected, search will not be performed. If both are selected, the search results will include entities connected to the process by input as well as output connectors.

### 38.2.4 Type

In this combo box you can select the desired process type. This will limit the search result to the processes of the selected type. The type are equivalent to CSO Molecular Events Types.

If this field is empty, process type will not be used as a search criterion.

### 38.2.5 Order By

In this combo box, you can select how results should be ordered: process name or process id.

### 38.2.6 Max rows

In this field you can specify maximum rows number to be displayed at single page. The smaller the value, the faster the search. Default value is 50.

## 38.3 Import Button

You can import some or all search results into the active CI canvas, or into new canvas.

To do this, you have to select one or more search results in Search Results Table, and press *Import* button.

For Molecule Search, all selected entities with their external references will be imported.

For Reaction Search, all selected processes with all connectors and entities associated with them, as well as all their external references will be imported.

## 38.4 Import Options

The Import options consist of three checkboxes: *Merge*, *Auto-Layout* and *Create new canvas*.

If option *Create new canvas* is selected, object will be opened in new canvas. Otherwise it will be added to the active canvas.

If option *Merge* is selected, new object will be merged with the elements existing in the active canvas.

If both options *Create new canvas* and *Merge* are selected, new object will be merged with the elements from active canvas and all object will be opened in new canvas.

If option *Auto-Layout* is selected, a special layout is applied to the imported elements.

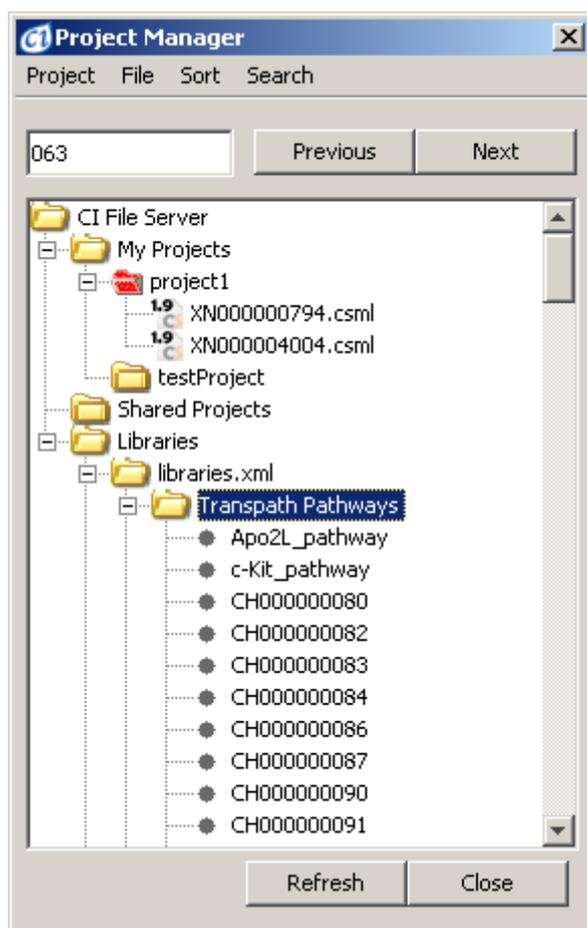
When importing elements by *Drag and Drop* the option Create New Canvas is ignored.



## 39 Project Manager Dialog

*CI Project Manager* is a user interface to pathway models stored on *CI Online Server*. To access the remote *CI Online Server*, the user must be logged in.

CI Project Manager allows user to create, store, organize and share CSML models (e.g. pathways) and other data on a remote server. Additionally you can access public and proprietary pathway libraries using the Libraries section. Project Manager Dialog consists of menu containing *Project*, *File*, *Sort* and *Search* groups, simple search panel, and graphical file browser.



To find a pathway in project tree:

- Enter the search string, one or more characters, into the edit box
- Press the *Next/Previous* button to select the next/previous item that matches the search string.
- Browse through the search results or narrow the search by applying additional criteria.

To insert a biological element, proceed as follows:

- Select the desired element(s) in the project tree
-

- Click on the chosen tree item, drag it to the active canvas and drop it there by releasing the mouse button. You may also release the mouse over an empty space in the CI workspace; this will create a new canvas and drop the selected model there.
- Alternatively, choose the *Open* or *Insert into Active Canvas* from the File or context menu.

## 39.1 File Browser – Project Manager Tree

File browser contains 3 sections: My Projects, Shared Projects and Libraries.

### 39.1.1 My Projects

My Projects folder contains user's projects. User has full privileges to projects stored in this folder. To create new project user has to right-click *My Projects* and select *New Project* from the context menu.

Projects are displayed as yellow folder icons (as “testProject” in figure above). If you share project with other users – its icon is red (as for “project1” in figure above).

### 39.1.2 Shared Projects

Shared Projects folder contains projects that other users share with you. Depending on your privileges, you can read and/or write to these projects. You cannot delete shared project.

**Note:** The project owner can delete any of his projects. In such case, you will lose all information that you have created in shared project.

### 39.1.3 Libraries

Libraries folder contains files that can be imported into your models. You cannot in any way modify contents of this folder.

**Note:** Access to some libraries (such as Transpath) requires a special license-CI Online module.

## 39.2 Top menus

Top menus contain actions that can be performed by Project Manager. Options are active only in proper context. Additionally, all actually available options can be found in context menu that opens after right-click on item *Project Manager Tree*.

### 39.2.1 Project menu

Project menu contains options applicable to projects. It is active only for My Projects folder.

### 39.2.1.1 Upload

This allows you to upload local model to the server.

### 39.2.1.2 Upload from canvas

This allows you to upload model from active canvas to the server.

### 39.2.1.3 Remove

This command allows you to remove project from server.

### 39.2.1.4 Share this project

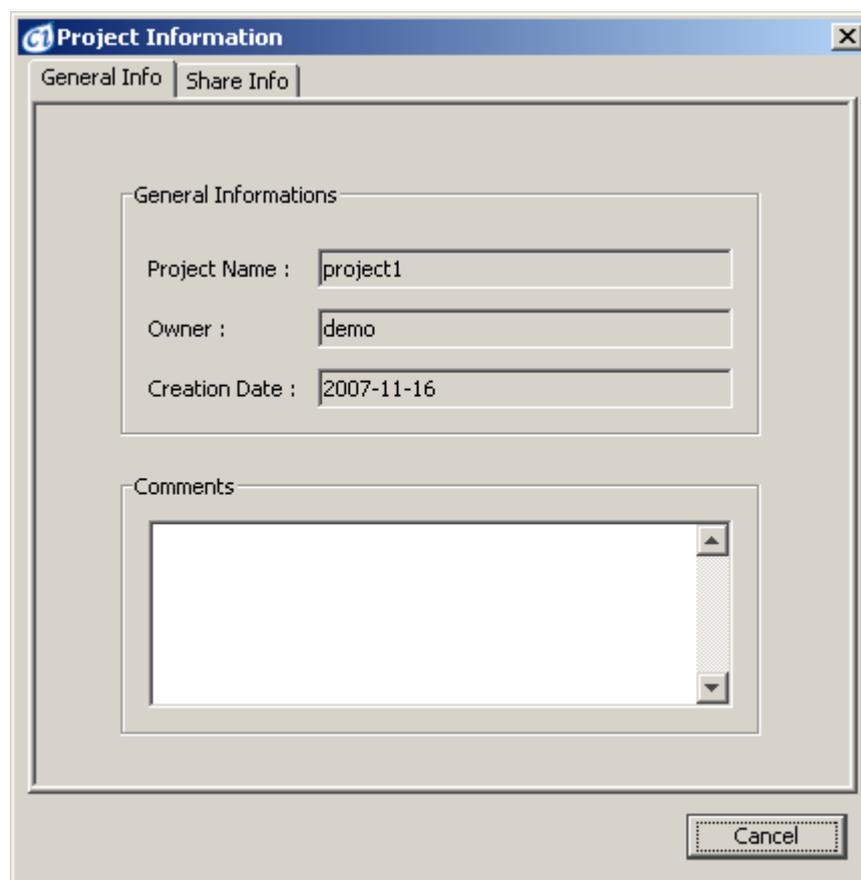
This command allows you to share project with other users. Selecting this option opens dialog, when you can add or remove users that you share project with. When there is at least one user in share list, project icon turns red.

### 39.2.1.5 Rename

This command allows you to rename project.

### 39.2.1.6 Information

This command shows Project Information dialog:



### 39.2.2 File menu

This menu is active only when file is selected in file browser. Some actions may be inactive in Libraries and Shared projects folders.

#### 39.2.2.1 Open

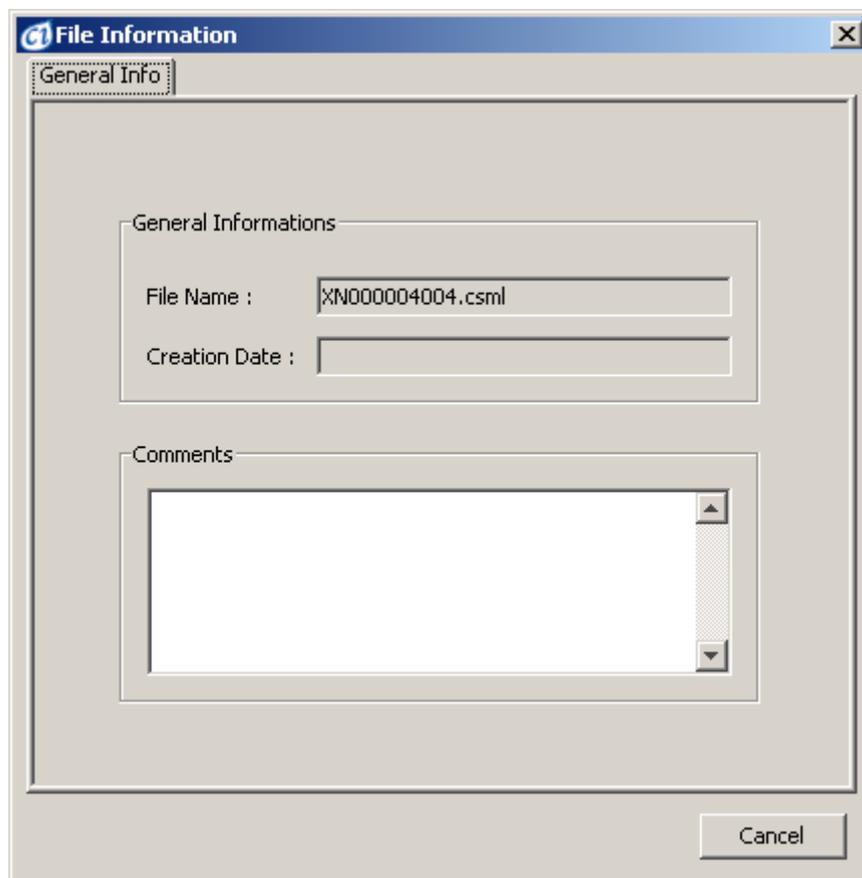
Opens file into new canvas.

#### 39.2.2.2 Save as

This option allows user to save file from Project Manager to local disk.

#### 39.2.2.3 Information

Displays File Information dialog:



#### 39.2.2.4 Insert into active canvas

This option imports selected file into active canvas

#### 39.2.2.5 Remove

This option allows user to remove file from Project Manager. User can remove files only from “My Project” folder.

### **39.2.2.6 Rename**

This option allows user to rename file. User can rename files from “My Projects” folder only.

### **39.2.3 Sort**

In this menu you can set files order: by name or by creation date

## **39.3 Simple Search Panel**

*Simple Search* panel allows the user to find files containing given string. To find an item in the *Project Manager* tree: specify the filename to be search for (or part of it), press the *Previous* or *Next* to select the next/previous search results.

## 40 About Cell Illustrator

About Cell Illustrator is a modal dialog that contains four tabs: *Version*, *License*, *Serial Number* and *3<sup>rd</sup> Party Components*.

- *Version* contains the version number and the copyright information.
- *License* leads to the End User License Agreement text from the license file.
- *Serial Number* sheet displays the license serial number and the customer data contained in the license file.
- *3<sup>rd</sup> Party Components* sheet displays information about software components used in Cell Illustrator.