

CADLIVE Ver.2.15

Operation Manual

2004.4. Kyushu Institute of Technology

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1 . CADLIVE

CADLIVE is a system for constructing large-scale biological networks (metabolic and gene regulatory networks) using GUI (Graphic User Interface) and saving them as regulator reaction equations in a database in the format compatible to a simulator. It has been developed by H. Kurata at the Kyushu Institute of Technology together with staffs at Mitsui Knowledge Industry Co., Ltd.

2 . System Requirements

Hardware Configuration:

CPU : Pentium3 500MH z or higher
Memory : 128MB or more (256MB or more recommended)
HDD : 1Gb or more recommended

Software Configuration:

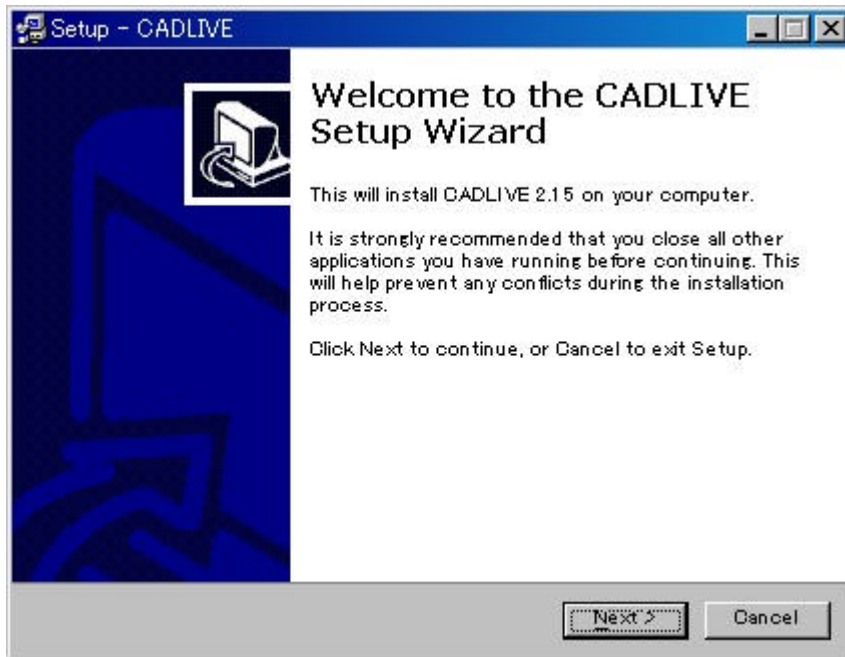
Windows 98, NT4.0, 2000, XP
Java™ 2 Runtime Environment 1.3

3 . Installation

3 - 1 Installing CADLIVE

Double-click the cadlive2.15.exe. icon.

Follow the on-screen instructions to install CADLIVE directly below the C drive.
(Installation will be completed by pressing the NEXT button and Install button.)



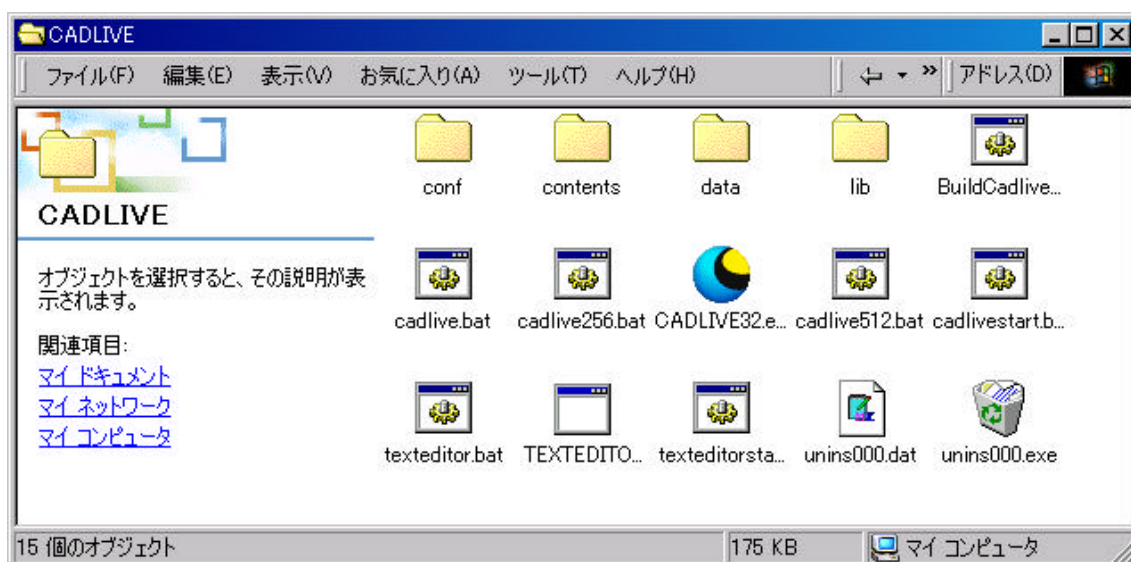
To uninstall CADLIVE, double-click the unins000.exe icon installed on the directory. Once CADLIVE is uninstalled, all the existing files as well as the existing network data will be deleted. If you need the network data, make sure to save it as backup on another directory before uninstalling.

4 . Start-up

4 - 1 Start-up of CADLIVE

Select CADLIVE from the Program menu or double-click the "CADLIVE32.exe" on the directory (C:¥CADLIVE) where CADLIVE is installed.

Note that CADLIVE needs more than 4000 kB memory allocation.

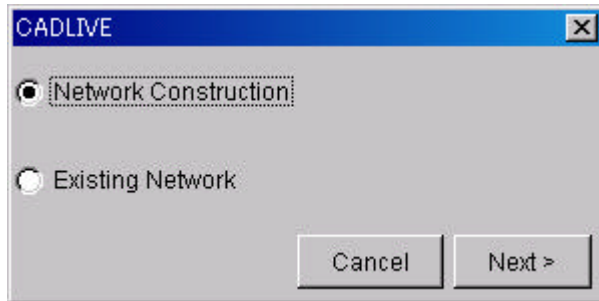


Start-up Screen



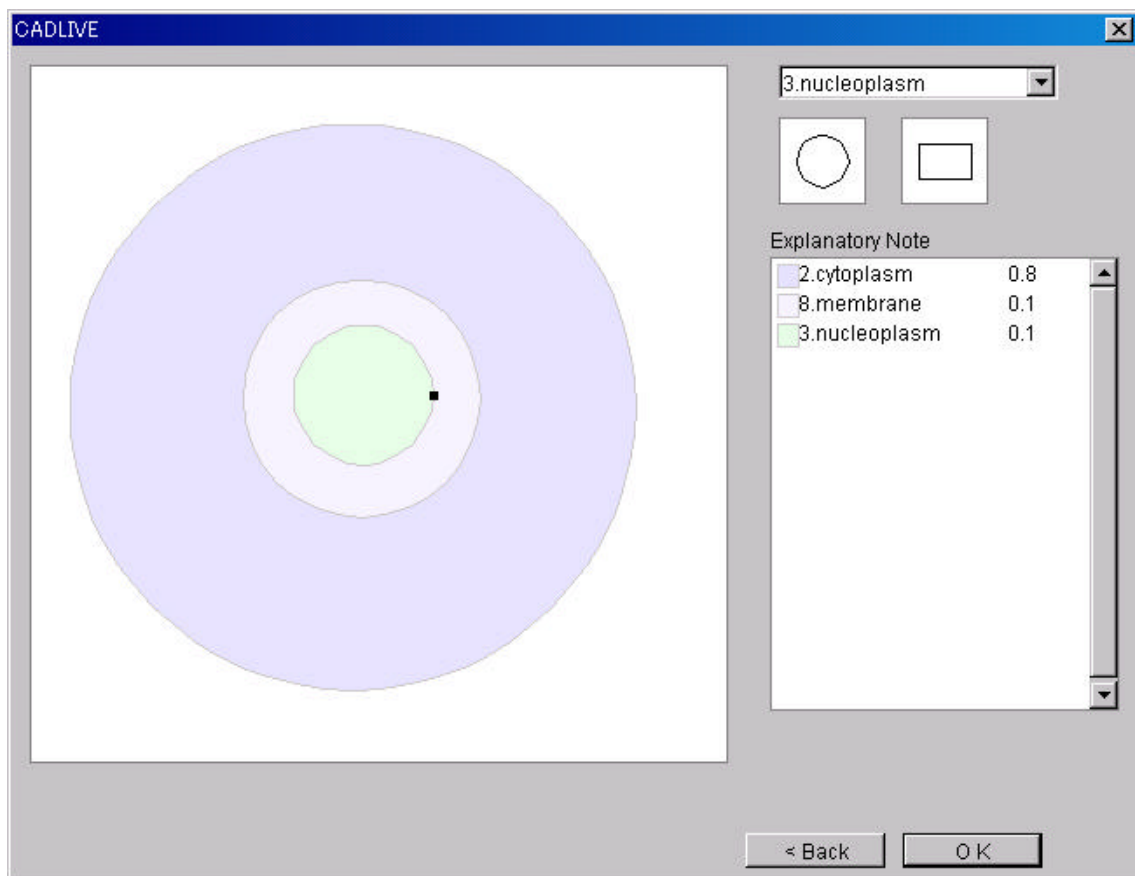
4 - 2 Creating a New Network

- OpeningDialog box



Select "Network Construction."
Click the [Next>] button.

- Component layout using the Cell Comp Dialog box



Select Components from the select box for editing cellular components.

*There are nine types of Components: Environment, Cytoplasm, Nucleoplasm, ER, Mitochondria, Golgi, Chloroplast, Membrane and Others.

*If "Others" is selected, its name can be edited arbitrarily.

Select the form (circle or rectangle).

If the panel is clicked, the object will be placed in the designated form of the designated Component.

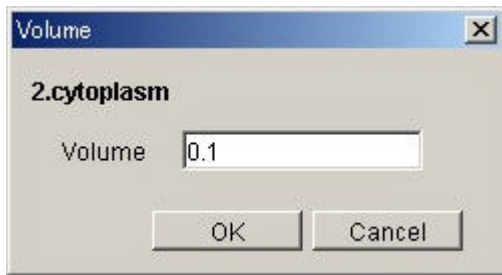
*By dragging the object, it can be moved to a new location.

*By dragging the toggle button on the object, its size can be changed.

*When two objects are overlapped, the overlapping object will have priority over the other. The overlapped part will then be invalid.

* By right-clicking on the object and selecting Delete, the object will be deleted.

- VolumeDialog



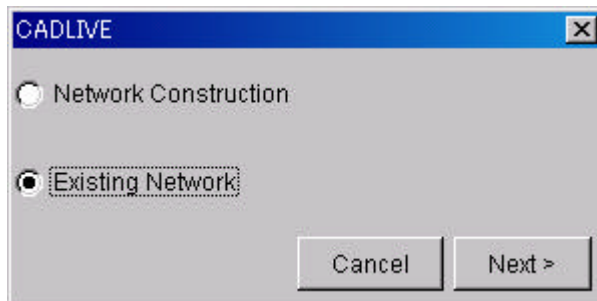
In order to define the Volume of Compartment, select the specified Compartment and click the Volume on the right-click menu. Put an appropriate value in the Volume box and click the [OK] Button.

* Regarding Compartment whose name is the same, setting the value of Volume reflects all the values of Compartment Volume.

After finishing placing all objects, click the [OK] button.

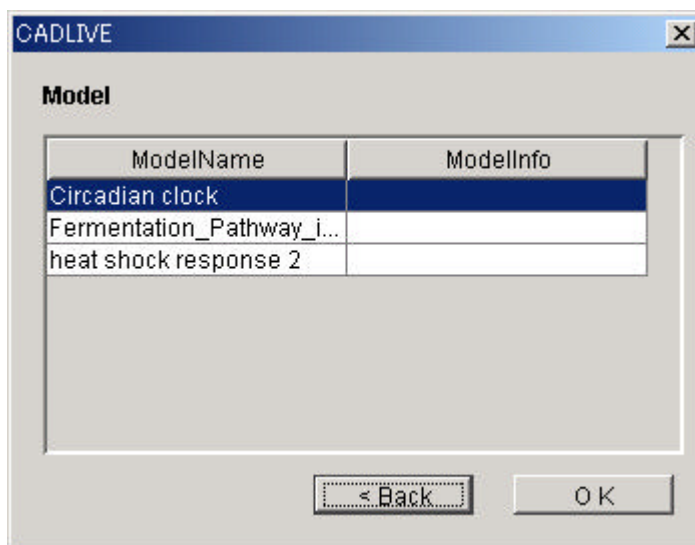
4 - 3 Loading the Existing Network

- OpeningDialog



Select the Existing Network
Click the [Next>] button.

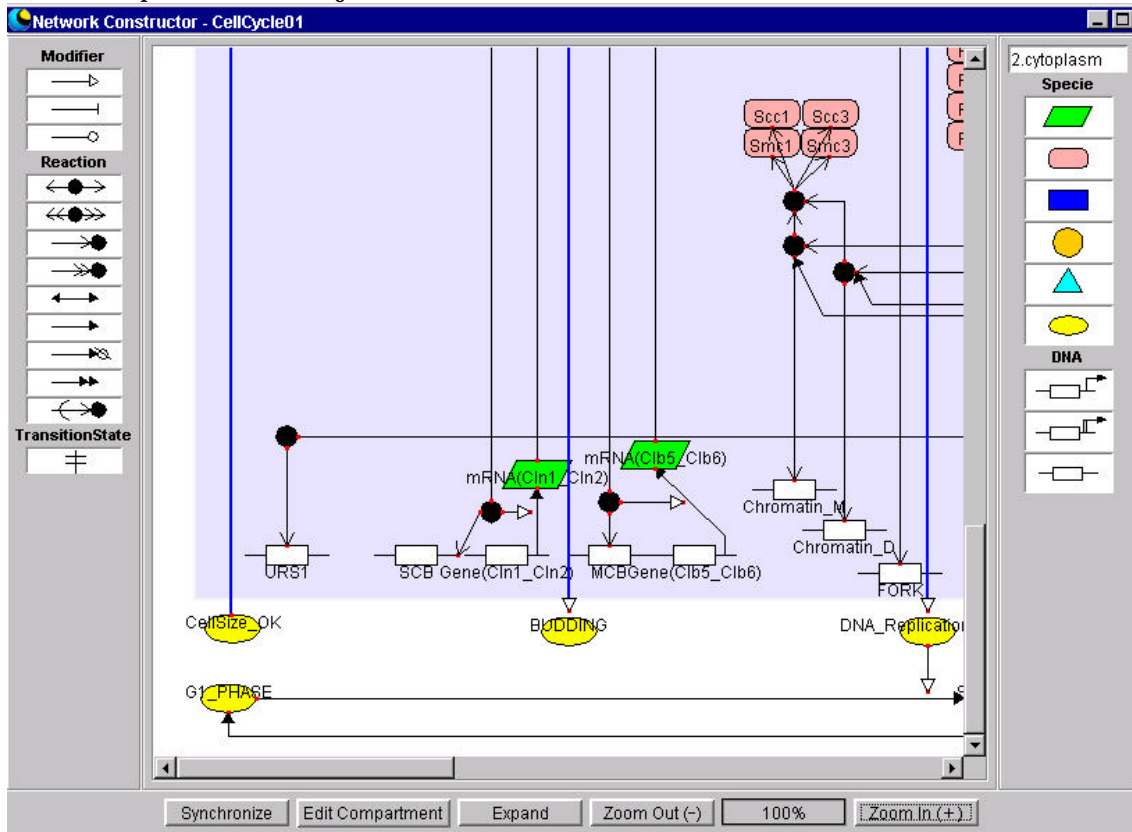
- OpenNetWorkDialog



ModelName and ModelInfo will be displayed in a list.
Select the ModelName of the network to load.
Click the OK button.

5 . Network Constructor

5 - 1 Explanation of Objects on the Network Constructor



5 - 1 - 1 Panel

This is the field used to position and draw Symbols. One sees the Components that have been selected from the Component Dialog box.

5 - 1 - 2 Specie Palette

This palette is used to position RNA, protein, metabolite, environmental factor, ion signal, or others.

5 - 1 - 3 Reaction Palette

This palette is used to position binding, binding_with_stoichiometric_changes, homo_association_or_modification, homo_association_or_modification_with_stoichiometric_changes, reversible_conversion, irreversible_conversion, transitionState, degradation, transport, or translation.

5 - 1 - 4 Modifier Palette

This palette is used to position activator, inhibitor, or enzyme.

5 - 1 - 5 Gene Palette

This palette is used to position transcription, protein_synthesis, or regulatory regions of a gene (enhancer, promoter, other).

5 - 1 - 6 Compartment Display Box

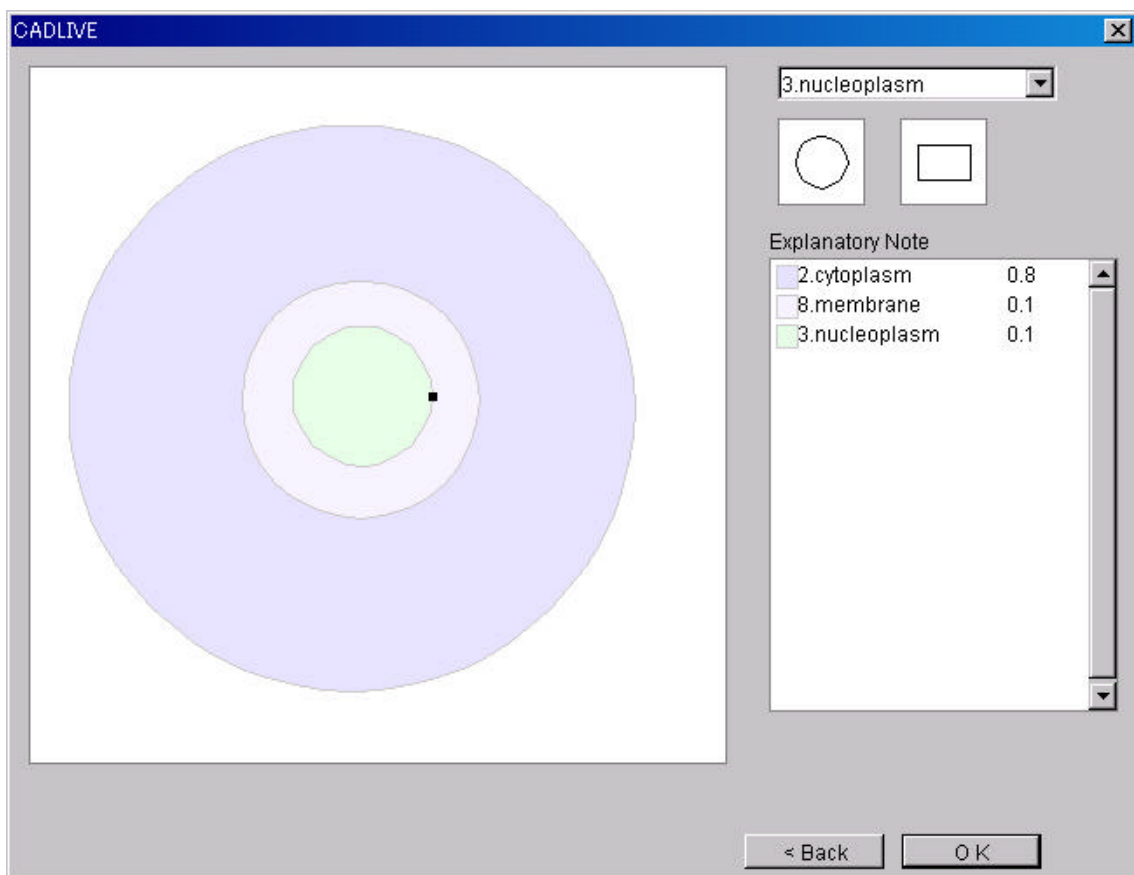
This box displays the Component that is selected in the panel.

5 - 1 - 7 Synchronize Button

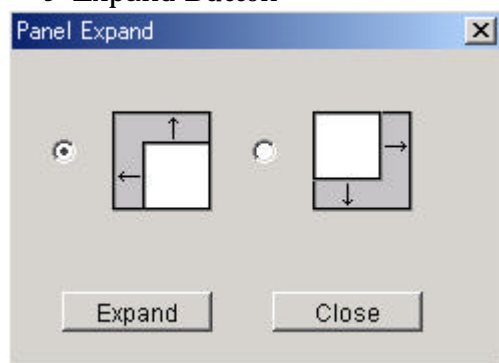
Clicking this button will synchronize data on the Network Constructor with the other Windows.

5 - 1 - 8 Edit Compartment Button

Clicking this button will display the Window to reedit Compartment.

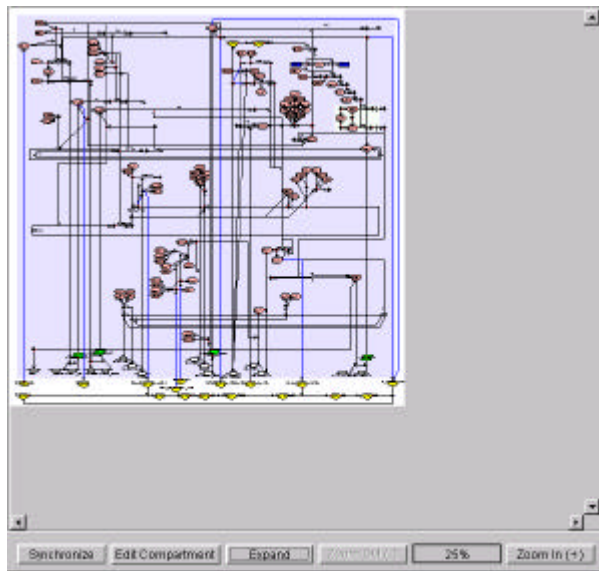


5 - 1 - 9 Expand Button



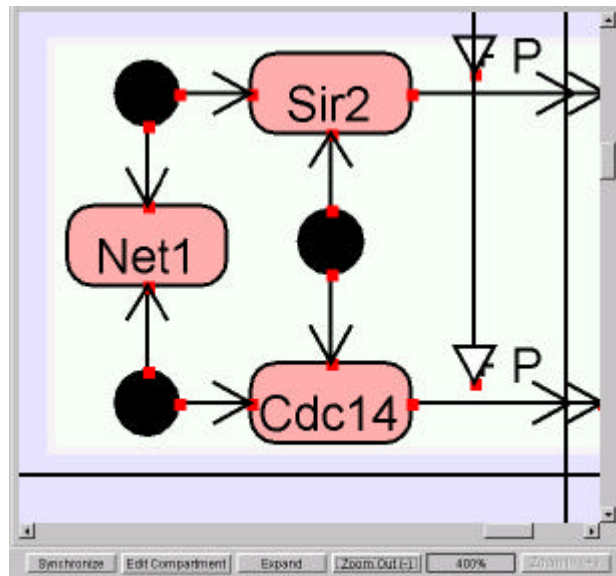
Clicking this button will expand the drawing area of the panel in the upper left or lower right direction. Since the area of the environment is enlarged, one can change the size of area of cellular compartments of interest.

5 - 1 - 10 Zoom Out Button



Clicking this button will reduce the viewing area of the panel (Individual Symbols will be reduced accordingly.) The area can be zoomed out up to 25%.

5 - 1 - 1 1 Zoom In Button



Clicking this button will expand the viewing area of the panel (Individual Symbols will be enlarged accordingly.) The area can be zoomed in up to 400%.

5 - 1 - 1 2 Zoom Magnification Display Box

The box displays the current zoom magnification.

5 - 2 Positioning the Symbol

5 - 2 - 1 Positioning the Specie

The Specie is an element that expresses a biomolecule and can become a node of biological networks.







- Positioning the Specie

Click any Specie to be positioned on the Specie palette, making it "selected."

Click the Specie once again at the location that you want to position it in the panel.

The Specie will be positioned in the panel.

The Specie data that is set in the spreadsheet of the Data Editor is displayed at the same time as the Specie is placed on the panel.

Specie		
	RNA	Denotes RNA
	rotein	Denotes Protein
	etabolite	Denotes Metabolite
	vironmental_factor	Denotes Environmental Factor
	n_signal	Denotes Ion Signal
	thers	Denotes Others

"DNA" denotes DNA.

* Use Gene ([5 - 2 - 4](#)) for layout.

"complex" denotes a complex.

* Position Complex using binding, homo_association_or_modification.
([5 - 2 - 2](#))

"modified" denotes a modified substance.

* Position Modified substance, use binding_with_stoichiometric_changes,
homo_association_or_modification_with_stoichiometric_changes
([5 - 2 - 2](#))

"text_option" denotes text data necessary for detailed reactions.

* Position text_option using Option ([5 - 2 - 7](#)) of Reaction.

"small_molecule" denotes small compound.

* Position small_molecule_option using Option ([5 - 2 - 7](#)) of Reaction.

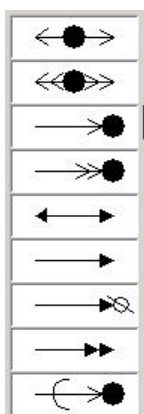
5 - 2 - 2 Positioning the Reaction

Reactions are the elements that are described as lines of biological networks, denoting various biochemical reactions and formations of complexes.

• Positioning the Reaction

Click any Reaction to be positioned on the Reaction palette, making it "selected."

Click the Reaction one more time at the location where you want to position it on the panel. The reaction is placed on the panel. By dragging either node of the reaction onto the Symbol of the Specie, reaction can be connected with the specie. Both ends of the arrows turn red in color when the specie is successfully connected to the reaction. The reaction data appear in the spreadsheet of the Data Editor in the timing of connecting the reaction arrow to the Specie that satisfies the reaction equation.



binding denotes the reaction that forms a complex.

binding_with_stoichiometric_changes

denotes the reaction that forms a complex with a chemical process (stoichiometric).

homo_association_or_modification

denotes the association of identical molecules.

homo_association_or_modification

_with_stoichiometric_changes

denotes the modification of small molecules.

reversible_conversion denotes reversible conversion.

irreversible_conversion denotes irreversible conversion.

degradation denotes degradation reaction.

translation denotes translation reaction.

transport denotes transport reaction.

*If Transport is used, a Specie identical to its reactant will automatically be registered in the Compartment where the specie is transported.

elimination

denotes eliminating a molecule from the complex.

elimination_with_stoichiometric_changes

denotes eliminating a molecule from the modified molecule.

* Use Option ([5 - 2 - 7](#)) for elimination and elimination_with_stoichiometric_changes.

reversible_conversion_regarding_multicomponent

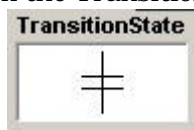
denotes reversible conversion regarding multiple species.

irreversible_conversion_regarding_multicomponent

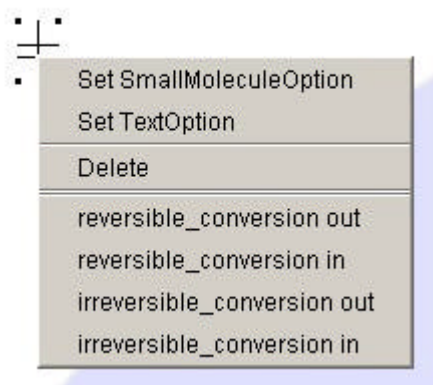
denotes irreversible conversion regarding multiple species

*Position reversible_conversion_regarding_multicomponent and irreversible_conversion_regarding_multicomponent using the Symbol of TransitionState.

Click the Transition State on the Reaction palette, making it "selected."



Click it once again at the location that you want to position it in the panel. Transition State will be positioned in the panel.



If Transition State is right-clicked, Set SmallMoleculeOption, Set TextOption, Delete, reversible-conversion out, reversible-conversion in, irreversible-conversion out, irreversible-conversion in will be displayed. Thus, when creating reversible_conversion_regarding_multicomponent, use reversible-conversion out and reversible-conversion in, and when creating irreversible_conversion_regarding_multicomponent, use irreversible-conversion out and irreversible-conversion in.

transcription
protein_synthesis

* Position transcription and protein_synthesis using Gene. ([5 - 2 - 4](#))

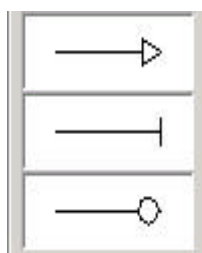
5 - 2 - 3 Positioning the Modifier

The Modifier is an enzyme that catalyzes reaction, or a regulator that activates or inhibits a reaction. Regulators can also express the reaction for activation or inhibition of the Specie or another Modifier.

• Positioning the Modifier

Click Modifier on the Modifier palette, making it "selected."

Click it once again at the location that you want to position it in the panel. Modifier will be positioned in the panel.



activation

inhibition

enzyme

denotes Activation

denotes Inhibition

denotes Enzyme Reaction

* Enzyme can be connected only to protein, complex, modified

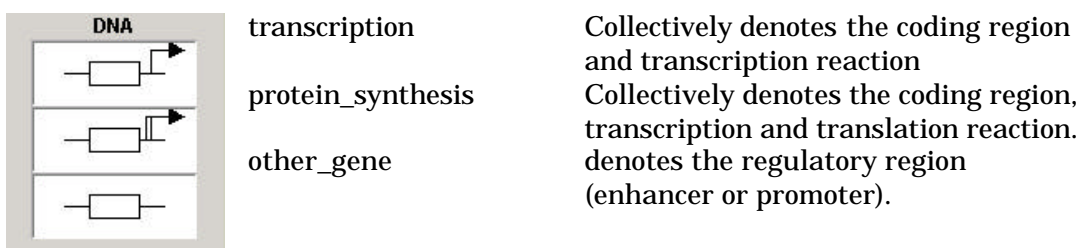
5 - 2 - 4 Positioning the Gene

Functions of Gene are Specie elements such as DNA and transcription, as well as reaction elements such as protein synthesis.

- Positioning the Gene

Click Gene on the DNA palette, making it "selected."

Click it once again at the location that you want to position it in the panel. Gene will be positioned in the panel.



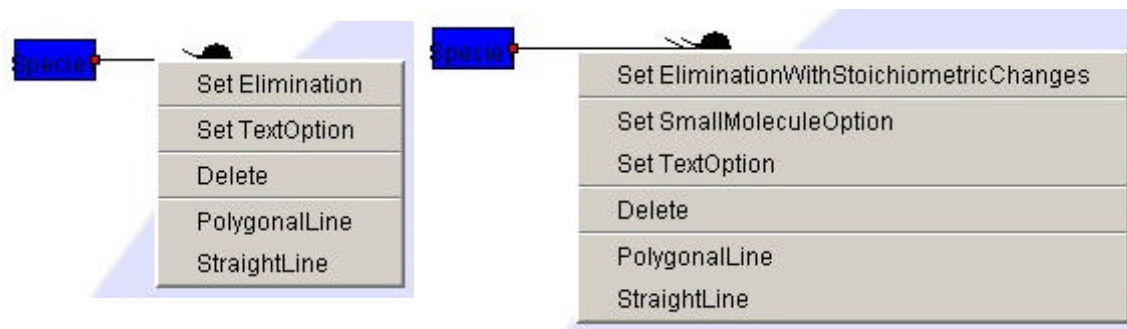
* Transcription is connected only to RNA.

* "protein_synthesis" is connected only to protein. When using protein_synthesis, RNA will be registered as Specie while transcription and translation will be registered as Reaction.

5 - 2 - 5 Positioning the Option

- Positioning the elimination, elimination_with_stoichiometric_changes

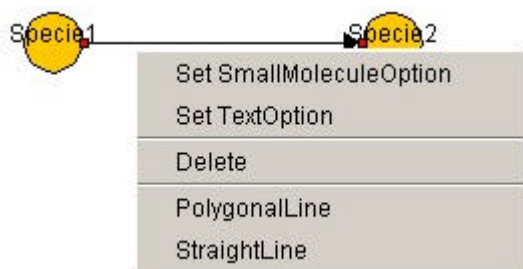
Right-click homo_association_or_modification or homo_association_or_modification_with_stoichiometric_changes, and select SetElimination or SetEliminationWithStoichiometricChanges.



- Positioning the Text Option

Right-click the arrow for Reaction

(binding, binding_with_stoichiometric_changes, homo_association_or_modification, homo_association_or_modification_with_stoichiometric_changes, elimination, elimination_with_stoichiometric_changes, reversible_conversion, irreversible_conversion, reversible_conversion_regarding_multi_component, or irreversible_conversion_regarding_multi_component) to open Text Option and select Set Text Option.



Input Option data by following the Text Option Dialog box.

*Input the number of Species on the Reactant side of Reaction to which Text Option will be added(can be selected from numbers from 2 to 10, or Poly, Hyper or Hypo.)

*Input the number of Specie on the Product side of Reaction to which Text Option will be added (can be selected from numbers from 2 to 10, or Poly, Hyper or Hypo.)

*Input the Specie data to which Text Option will be added.

If the data is "+," it will be registered in Reactant.

If it is "-," it will be registered in Product.

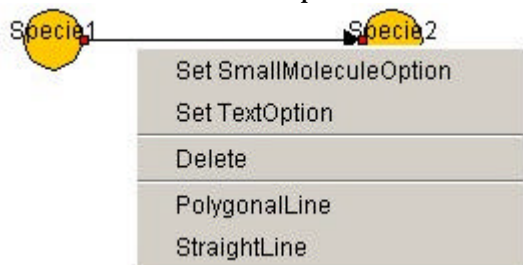
However, it will always be positive in Homo_association_or_modification or

Homo_association_or_modification and it will always be negative in

Elimination, Elimination_with_stoichiometric_changes

The number of Text Option of Specie can be selected from numbers between 2 and 10, or Poly, Hyper or Hypo. The name input in the lower box will be registered as Specie Name.

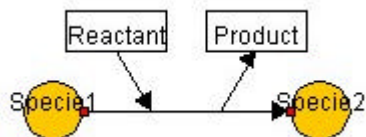
• Layout of Small Molecule Option



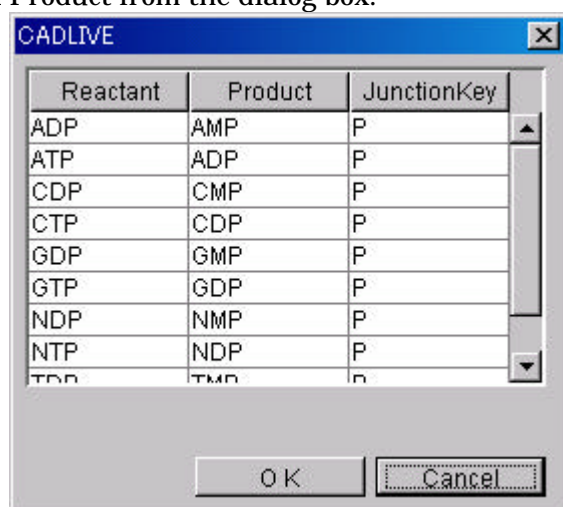
Right-click Reaction that can position SmallMoleculeOption and select "Set SmallMoleculeOption."

In order to add Option to ReversibleConversion, IrreversibleConversion,

reversible_conversion_regarding_multi_component or irreversible_conversion_regarding_multi_component, the specie name before and after the reaction can be edited. The default is Reactant and Product as follows.



To set up SmallMoleculeOption regarding Homo_association_or_modification_with_stoichiometric_changes, select Reactant and Product from the dialog box.



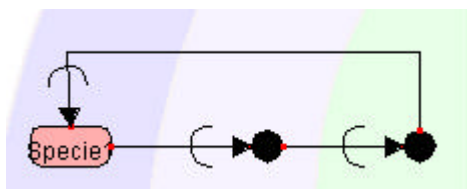
The substance in JunctionKey will be added to Modified.

• Positioning the Option Transport

By right-clicking on the Transport and selecting SetOptionTransport, users are able to draw the reversed transport.



Since Option transport is able to connect not only to the transported Reactant but also to the related Specie, users are able to draw the transportation between multiple compartments.



5 - 3 Moving the Symbol

5 - 3 - 1 Moving the Specie

By dragging the Symbol viewing area of the Specie, it can be moved. However, TextOption and SmallMoleculeOption cannot move individually. They move according to the movement of the added Reaction.

5 - 3 - 2 Moving the Reaction

By dragging one end node of Reaction, one can rotate, expand and contract Reaction using the opposite node as an axis. However, TransitionState will move in line with the Specie. The Reaction connected to the Specie moves in accordance with the movement of its connecting end of the Specie.

5 - 3 - 3 Moving the Modifier

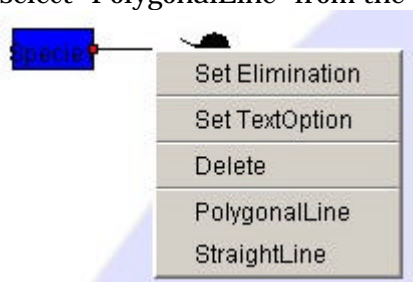
By dragging one end node of the Modifier, one can rotate, expand or contract the Modifier using the other end node as an axis. However, TransitionState will be moved in line with the Modifier. The Modifier connected to Specie, Reaction or another Modifier move in accordance with the movement of its connecting end of the Symbol.

5 - 3 - 4 Moving the Gene

By dragging the Symbol viewing area of the Gene, it can be moved. By dragging the one end node of the Gene, one can rotate, expand and contract Reaction using the Specie as an axis. The Reaction area of the Gene connected to Specie can move following the movement of its connecting end of the Specie.

5 - 3 - 5 Bending the Symbol

To draw a polygonal line, right-click the line segment you want to change, and select "PolygonalLine" from the Popup menu.

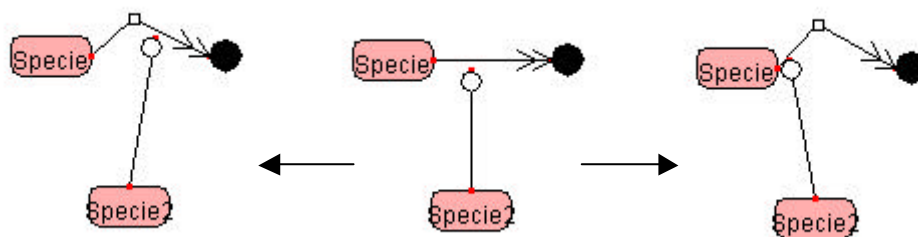


A handle () will appear in the center of the designated line. By dragging the handle, a polygonal line can be drawn. A polygonal line can be bent up to four times.



To make the polygonal line back to a straight line, right-click the line segment and select StraightLine from the Popup menu.

If there is Modifier attached to that line segment, right-click to draw a polygonal line on the Reactant side. Modifier will move towards the Product side. Likewise, if one draws a polygonal line by right-clicking on the Product side, Modifier will move towards the Reactant side.



Right-clicking on the Reactant side

Right-clicking on the Product side

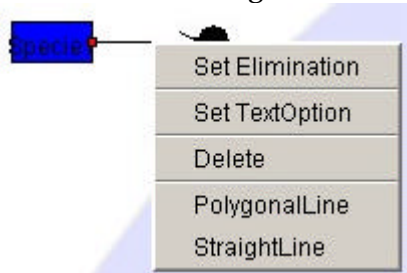
5 - 4 Deleting the Symbol

5 - 4 - 1 Deleting the Specie



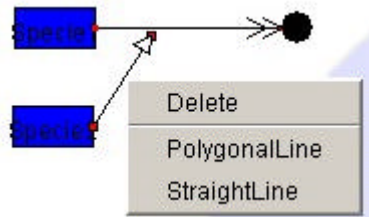
By right-clicking on the Symbol viewing area of the Specie and selecting "Delete," the Specie can be deleted. To delete TextOption or SmallMoleculeOption, right-click the Reaction viewing area where Option has been positioned, and select "DeleteTextOption" or "DeleteSmallMoleculeOption." Also, if one deletes the Reaction where Option has been positioned, Option will be deleted as well.

5 - 4 - 2 Deleting the Reaction



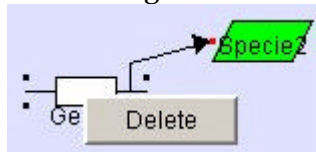
By right-clicking on the Reaction and selecting "Delete," Reaction can be deleted. If both end nodes are connected, Reaction can be deleted by right-clicking the line and selecting "Delete."

5 - 4 - 3 Deleting the Modifier



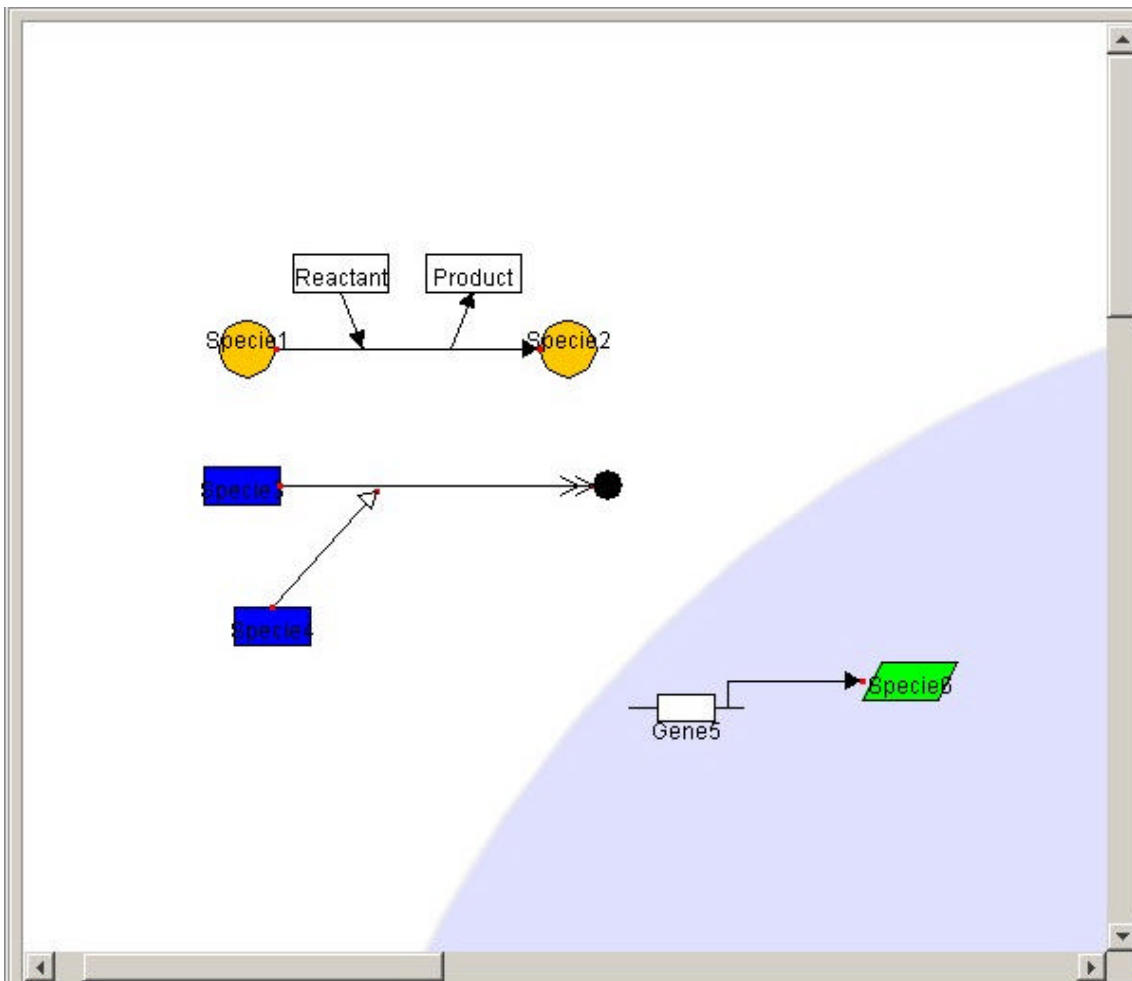
By right-clicking on the Modifier and selecting "Delete," Reaction can be deleted. If both end nodes are connected, Modifier can be deleted by right-clicking the line and selecting "Delete."

5 - 4 - 4 Deleting the Gene



By right-clicking the Specie viewing area of Gene and selecting "Delete," Gene can be deleted. However, one cannot do so by right-clicking the Reaction area.

5 - 5 Connecting the Symbol



5 - 5 - 1 Connecting the Reaction, Modifier and Specie

By dragging the either node of the Reaction and Modifier onto the Symbol of the Specie, Reaction and Modifier can be connected with the Specie.

Both ends of the arrows turn red in color when the Specie is successfully connected to the Reaction.

5 - 5 - 2 Connecting the Gene and Specie

By dragging the end node of Transcription and Protein_synthesis onto the Symbol of Specie, DNA (Transcription, Protein_synthesis) and Specie can be connected.

5 - 5 - 3 Connecting the Modifier and Reaction

By dragging the tip of Modifier onto the Reaction or another Modifier 's line, Modifier, Reaction, or another Modifier can be connected.

6 . Data Editor

6 - 1 Explanation of Objects on the DataEditor

Data Editor - CellCycle01							
ListOfSpecies							
SpeciesName	SpeciesClass	BindingSite	Compartment	MassBalance	TotalAmount	Decomposition	InitialAmount
Bck2	protein		cytoplasm	on	variable	on	
Cdc28	protein		cytoplasm	on	variable	on	
Cln3	protein		cytoplasm	on	variable	on	
Pcl1_Pcl2	protein		cytoplasm	on	variable	on	
Pho85	protein		cytoplasm	on	variable	on	
Cln1_Cln2	protein		cytoplasm	on	variable	on	
Cib5_Cib6	protein		cytoplasm	on	variable	on	
Mbp1	protein		cytoplasm	on	variable	on	
Swi4	protein		cytoplasm	on	variable	on	
Swi5	protein		cytoplasm	on	variable	on	
Swi6	protein		cytoplasm	on	variable	on	
Cdc28Cln3	complex		cytoplasm	on	variable	on	
Cdc28Cln1_Cln2	complex		cytoplasm	on	variable	on	
ListOfReactions							
ReactionName	ModifierReactionEquation	Layer	ReactionType	IsConvertible	IsTotal		
#414	Swi4.Swi6-P(Swi6).SCB->> Gene(Cln1_Cln2)-> m...	protein	transcription	true	true	Swi4.Swi6-P(Swi6)	
#416	Mbp1.Swi6-P(Swi6).MCB->> Gene(Cib5_Cib6)-> m...	protein	transcription	true	true	Mbp1.Swi6-P(Swi6)	
#417	Bck2->> #416	protein	activation_of_modifier	false	true		
#418	Cdc28.Cln3-> Swi4.Swi6 + P(Swi6) = Swi4.Swi6-P...	protein	homo_association_of...	false	true		
#419	Bck2->> #418	protein	activation_of_modifier	false	true		
#420	Cdc28.Cln3-> Mbp1.Swi6 + P(Swi6) = Mbp1.Swi6-P...	protein	homo_association_of...	false	true		
#421	Net30.Skp1.Cdc34.Cdc53-> Cln3-P + Ub = Cln3-P...	protein	homo_association_of...	true	true	Net30.Skp1.Cdc34	
#422	Cln1.Skp1.Cdc34.Cdc53-> Cln1_Cln2-P + Ub = Cln...	protein	homo_association_of...	true	true	Cln1.Skp1.Cdc34	
#423	Cdc28.Cln1_Cln2->> Swi4.Swi6-P(Swi6) + Swi4.Sw...	protein	elimination_with_stoichi...	false	true		
#424	Cdc28.Apc1_Apc2.Cdc27.Apc4.Apc5.Cdc16.Cdc23.A...	protein	homo_association_of...	true	true	Cdc28.Apc1_Apc2	
#425	Cdc28.Cln1_Cln2-> Skt1 + P = Skt1-P	protein	homo_association_of...	true	true	Cdc28.Cln1_Cln2	
#426	Pcl1_Pcl2Pho85-> Skt1 + P = Skt1-P	protein	homo_association_of...	true	true	Pcl1_Pcl2Pho85	

6 - 1 - 1 Specie Spreadsheet

This is the spreadsheet used to display, input and edit attribute data of the Specie and BlackBox positioned by NetworkConstructor. Before inputting texts, make sure that the input cell is "selected." After inputting text, press the return key to define it.

6 - 1 - 2 Reaction Spreadsheet

This is the spreadsheet to display, input and edit attribute data of Reaction positioned by NetworkConstructor. Before inputting text, make sure that the cell to input data in is "selected." After inputting text, press the return key to define it.

6 - 1 - 3 Save Button

Network data created and edited by NetworkConstructor or DateEditor will be saved in the model folder on the XML database (C: ¥CADLIVE¥data)

It is the same function as the Save in the File menu.

6 - 2 Explanation of Specie Items

- SpecieName

The Specie positioned will be given as a temporary name in the system, which can be edited by DataEditor.

*The name connecting the SpecieName with colons like "A:B:" is given as a Complex; the name connecting SpecieName with hyphens like "A-B-" is given as a Modified. Such generated Specie name cannot be changed. However, the name of RNA generated by ProteinSynthesis can be edited.

- SpecieClass

Material denotes material attributes of the Specie generated by NetworkConstructor.

DNA

RNA

protein

metabolite

environmental_factor

ion_signal

complex

modifier_complex (Enzyme-substrate complex: Specie that is automatically created by the system, cannot be edited by users)

modified (Modified Substance)

text_option (Specie Generated by a text_option)

small_molecule (Specie Generated by a small_molecule_option)

others

- BindingSite

It selects the classification of the DNAs that neither encode any protein nor RNAs as a material attribute.

enhancer : activating factor binding site of DNAs

promoter : inhibiting factor binding site of DNAs

other : non-specific binding sites of DNAs

The default is other. Depending on the selection box, the displayed content can be changed.

- Compartment

Component denotes location attributes of the Specie generated by NetworkConstructor.NetworkConstructor.

environment

cytoplasm

nucleoplasm

ER

mitochondria

golgi

chloroplast

membrane

other

- MassBalance

Select MassBalance attribute in the ListOfSpecies.

off : It does not require any mass balance equation.

on : It requires a mass balance equation.

When the SpecieClass is RNA, Protein, Metabolite, Complex or Modified, the default will display "on," if not, the default will display "off." The viewing content can be changed using the selection box.

- TotalAmount

Select TotalAmount attribute in the ListOfSpecies.

constant : constant in a differential equation

variable : variable in a differential equation

If the SpecieClass is DNA, metabolite, environmentl_factor, ion_signal, small_molecule and other, the default "constant" will appear. If not, the default "variable" will appear. Depending on the selection box, the displayed content can be changed.

- Decomposition

Select Decomposition attribute in the ListOfSpecies.

on : generates the decomposition term in a mathematical model

off : does not generate the decomposition term in a mathematical model

When the SpecieClass is RNA, Protein, Metabolite, Complex or Modified, the default will display "on," if not, the default will display "off." The viewing content can be changed using the selection box.

- InitialAmount

Input the initial value of species.

6 - 3 Explanation of the Reaction Items

- **ReactionName**
The Reaction name is displayed that is attached by the symbol “#” preceding Reaction ID.
- **ModifierReactionEquation**
The regulator reaction equations corresponding to the map are displayed. (They appear in the order of Modifier Specie, ModifierType, ReactantReaction Specie, Reaction, and ProductReaction Specie.)
- **Layer**
Select the reaction layer.
metabolic : reaction at the metabolic layer
protein : reaction at the protein interaction layer
gene : reaction at the gene expression layer
The default is given according to **ReactionType**.
The viewing content can be modified using the selection box.
- **ReactionType**
Reaction attributes generated by NetworkConstructor are displayed.
binding
binding_with_stoichiometric_changes
homo_association_or_modification
homo_association_or_modification_with_stoichiometric_changes
elimination
elimination_with_stoichiometric_changes
reversible_conversion
irreversible_conversion
reversible_conversion_regarding_multicomponent
irreversible_conversion_regarding_multicomponent
transport
option_transport
transcription
translation
degradation
activation_of_specie
inhibition_of_specie
activation_of_modifier
inhibition_of_modifier
- **isConvertible**
Select if a simulator converts the reaction into mathematical equations or not.
true : It is convertible.
false : It is not convertible.
The default is true.
Depending on the selection box, the displayed content can be changed.
Note that the reaction that is not able to generate any regulator reaction equation is “false” and it cannot be changed by users.

- isTotal

Select the method for calculation of modifier by a simulator.

 true : the modifier is the Total amount

 false : the modifier is not the Total amount

The default is true. Depending on the selection box, the displayed content can be changed.

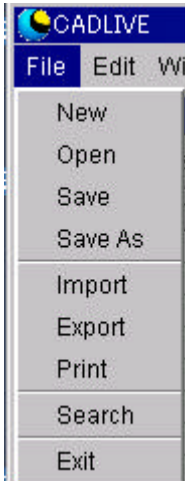
- ChemicalReactionEquation

Displays chemical reaction equations of the Reaction.

The reaction whose attribute of "isConvertible" is "false" does not create any ChemicalReactionEquation.

7 . Explanation of Menu Items

7 - 1 File Menu



7 - 1 - 1 New

Start the NewDialog box.

Positioning the Component in the dialog box. ([4 - 2](#))

7 - 1 - 2 Open

Start the OpenFileDialog box.

Loading the Existing Network Data in the dialog box. ([4 - 3](#))

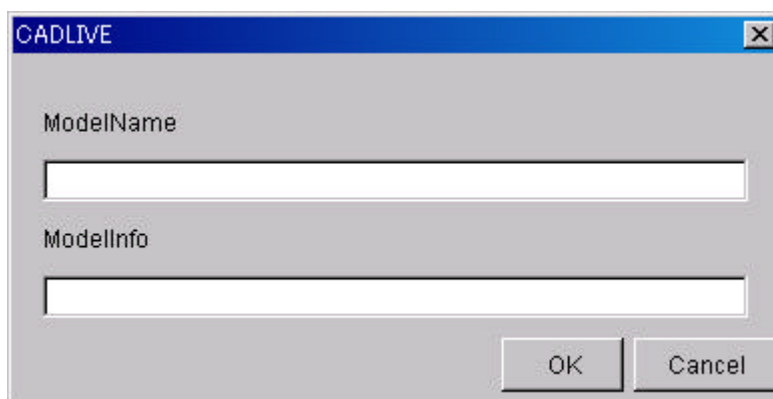
7 - 1 - 3 Save

Save the network data created and edited by NetworkConstructor or DateEditor on XML. If the network is newly created, it will be always saved as "SaveAs."

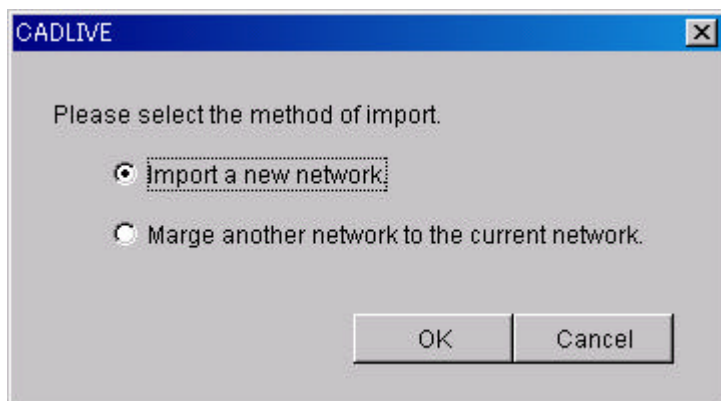
7 - 1 - 4 SaveAs

Network data can be saved as ModelName.

The input content is ModelName and ModelInfo as follows.



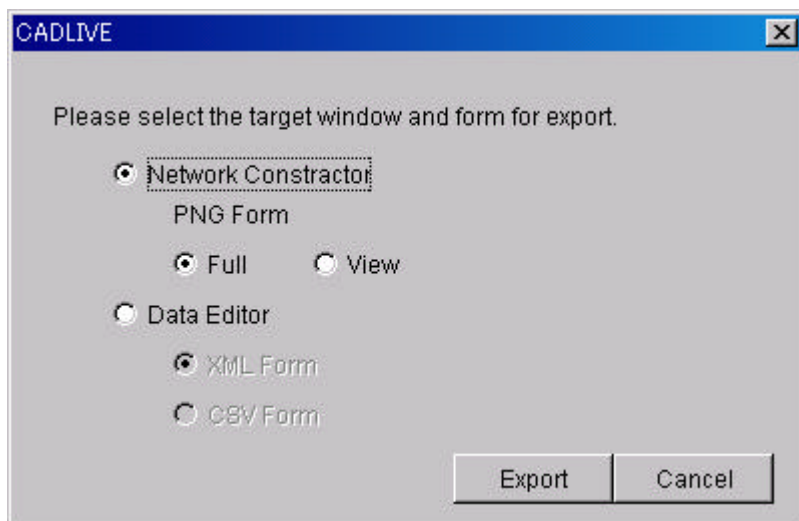
7 - 1 - 5 Import



Load the XML file that is created by another launched CADLIVE by selecting from dialog.

- Important a new network : a new XML file will be imported.
- Merge another network to the current network : the XML file designated for the currently-edited network will be added.

7 - 1 - 6 Export



The NetworkConstructor panel will be exported as a PNG image.

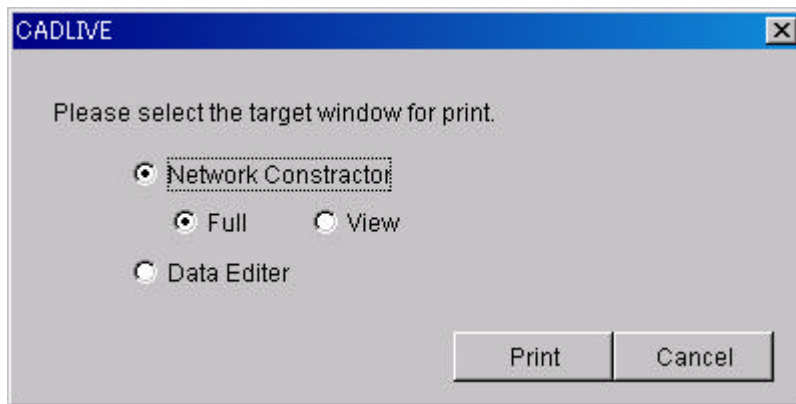
Full : The whole panel of NetworkConstructor will be exported as a PNG image.

View : The panel area of NetworkConstructor will be exported as a PNG image.
Specie data and Reaction data of the network viewed in DataEditor will be exported as a PNG image.

XML Form : will be saved in the XML format.

CSV Form : will be saved in the CSV format (comma-delimited text format)

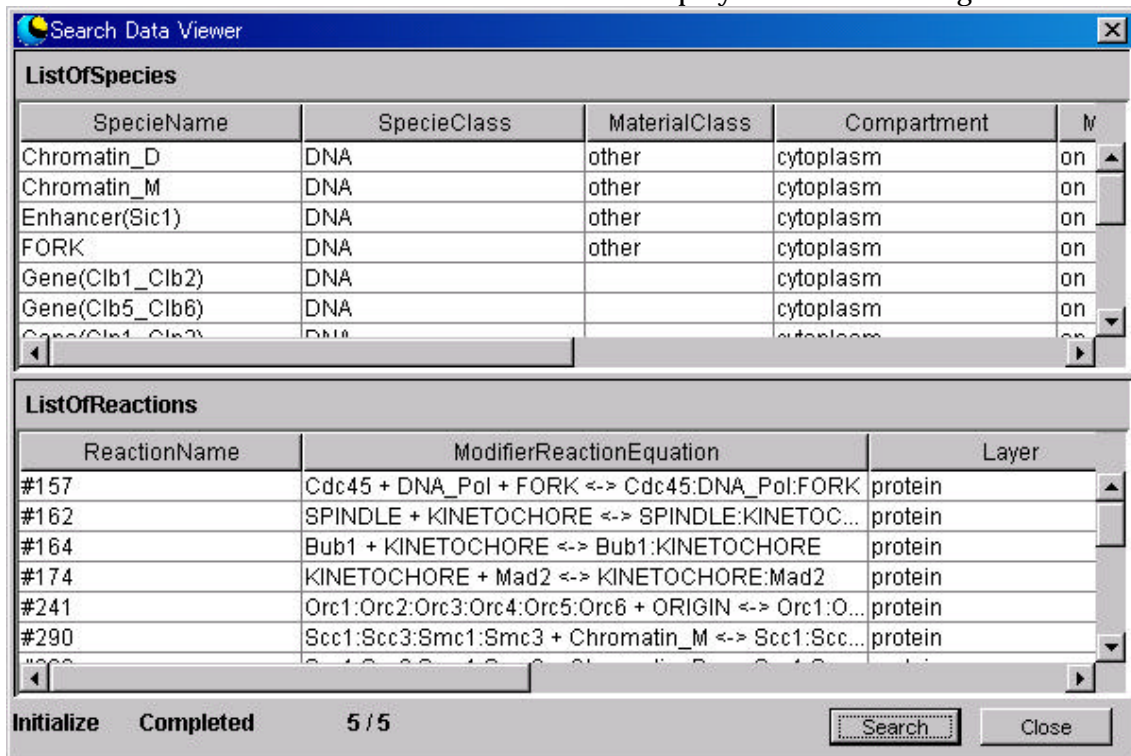
7 - 1 - 7 Print

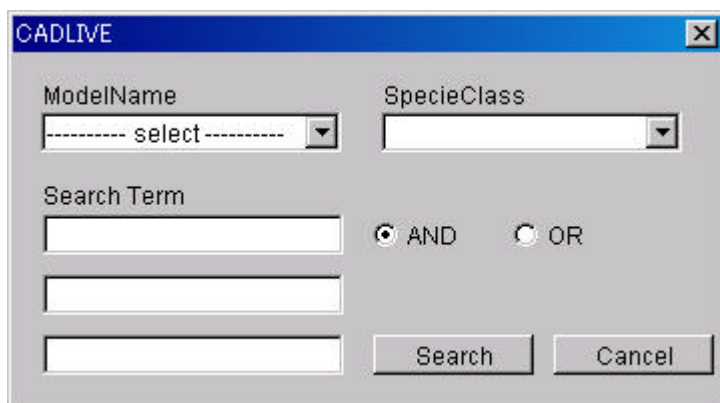


- Printing the NetworkConstructor screen
 Full : The whole panel area of NetworkConstructor will be printed on one page.
 View : The panel viewing area of NetworkConstructor will be printed on one page.
- Printing the DataEditor screen
 The spreadsheet of DataEditor will be printed.

7 - 1 - 8 Search

Press the Search button on SearchDataEditor to display the Search Dialog box.





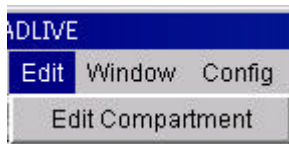
- **ModelName**
Select the ModelName to search.
- **SpecieClass**
Select the SpeciesName of species to search.
With no input data all SpeciesClass are target [/object].
- **SearchTerm**
Up to 3 SearchTerms can be input to search.
- **And/Or Radio Button**
Select whether the character line input in SearchTerm will be searched on the "And" or "Or" condition.
- **Search Button**
Search the Reaction and Specie applicable to the conditions input from XML networks and display them in spreadsheets of SearchedReaction and Searched Specie.

7 - 1 - 9 Exit

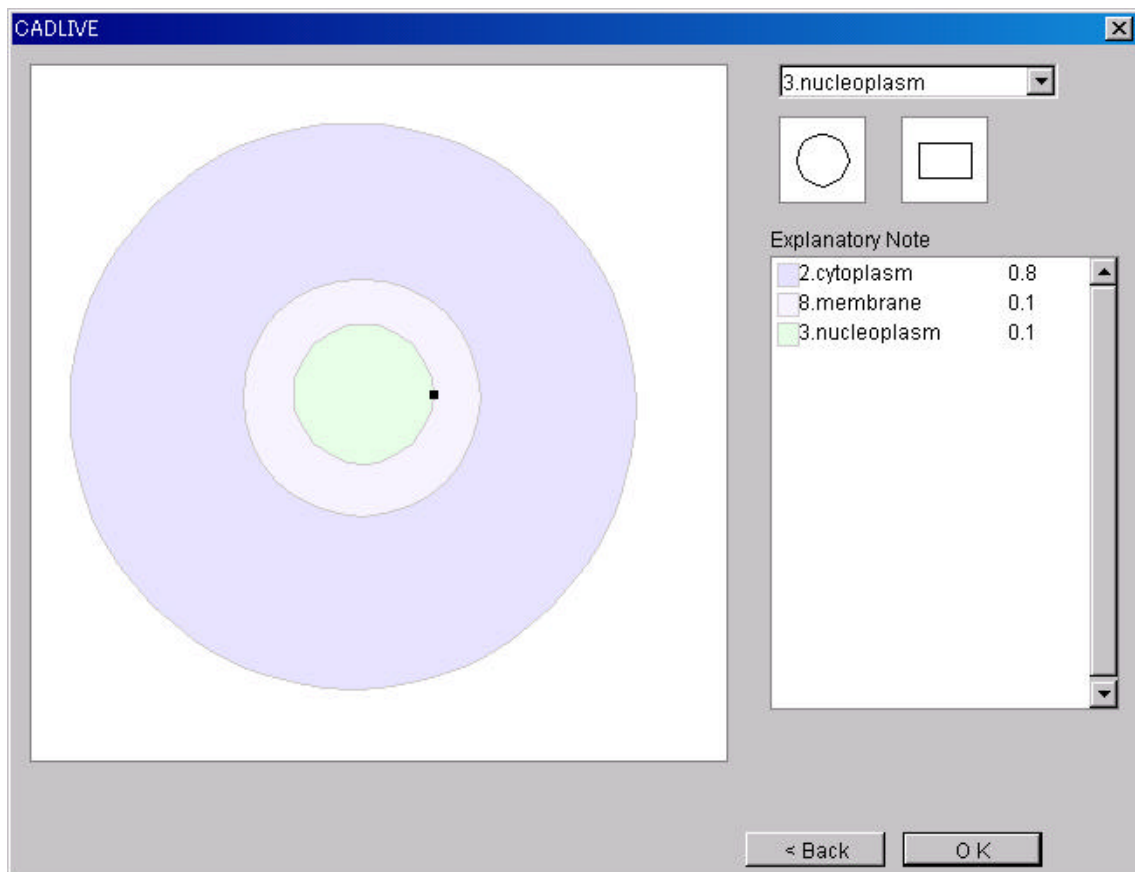


You are exiting CADLIVE.

7 - 2 Edit Menu

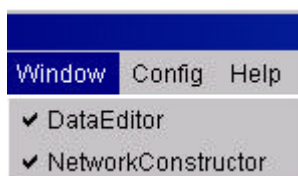


7 - 2 - 1 EditCompartment



The Window is displayed to reedit the Compartment.

7 - 3 Window Menu



7 - 3 - 1 DataEditor

When the DataEditor screen is visible, the menu is set to "Invisible." When it is invisible, it is set to "Visible." The check mark is displayed when the screen is visible.

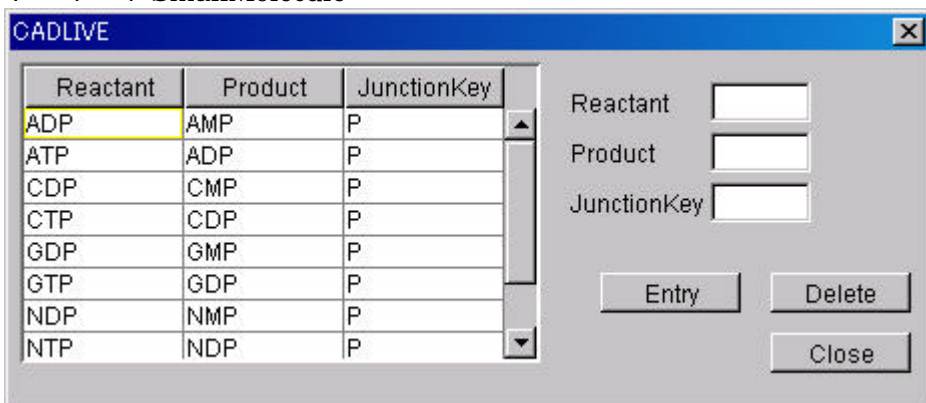
7 - 3 - 2 NetworkConstructor

When the NetworkConstructor screen is visible, the menu is set to "Invisible."
When it is invisible, it is set to "Visible." The check mark is displayed when the screen is visible.

7 - 4 Config Menu



7 - 4 - 1 SmallMolecule



Configure Specie and JunctionKey, which are viewed when SmallMoleculeOption is added to the homo_association_wih_stoichimetric_change reaction.

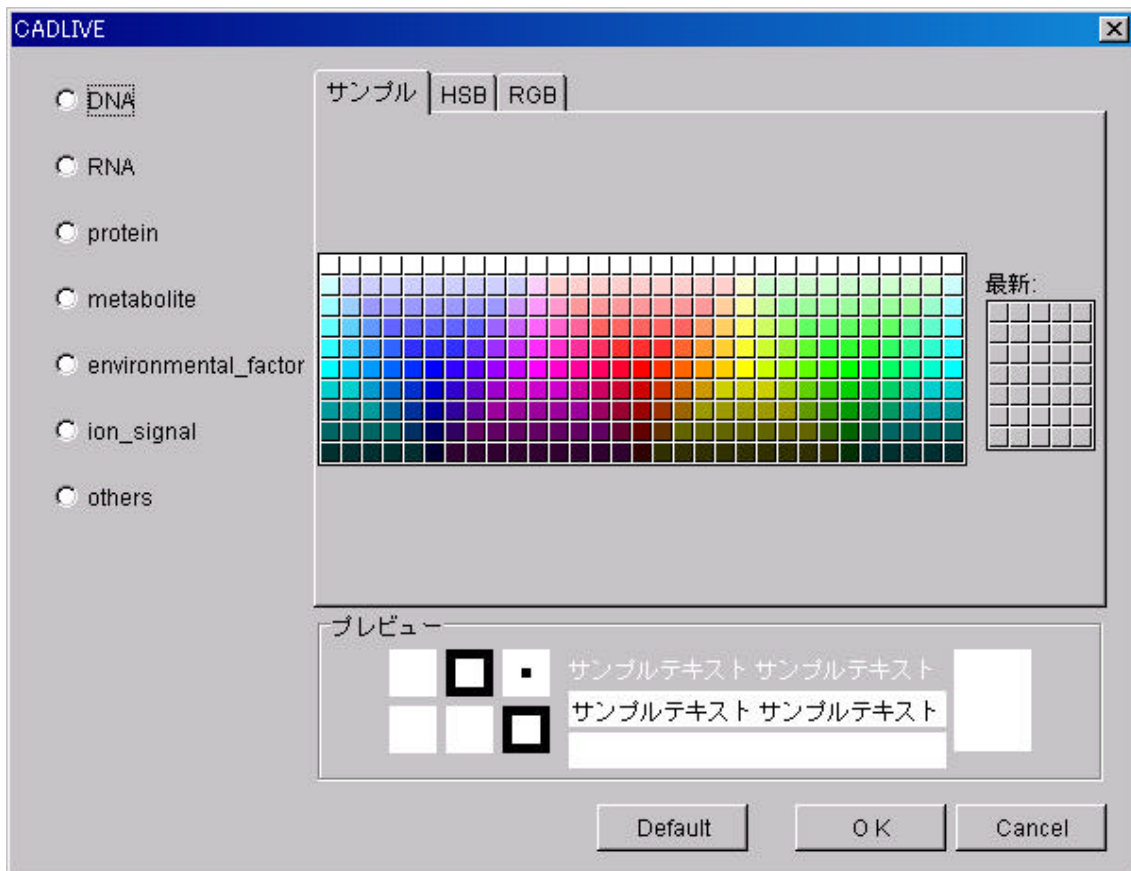
- Configuration

Input a character line in Reactant, Product and JunctionKey, and press the Entry button.

- Deletion

After selecting the viewed Specie and JunctionKey, press the Delete button.

7 - 4 - 2 SymbolColor



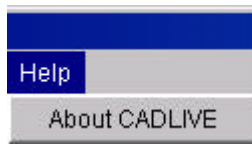
The viewing color of the Specie can be changed.

- Configuration

After selecting the Specie to configure on the left, select the color from the right and define it by pressing OK. A plural number of Species can be configured simultaneously.

To set color as the initial color, press the Default button after selecting the Specie on the left.

7 - 5 Help Menu



7 - 5 - 1 About CADLIVE

The version information of CADLIVE is displayed.

