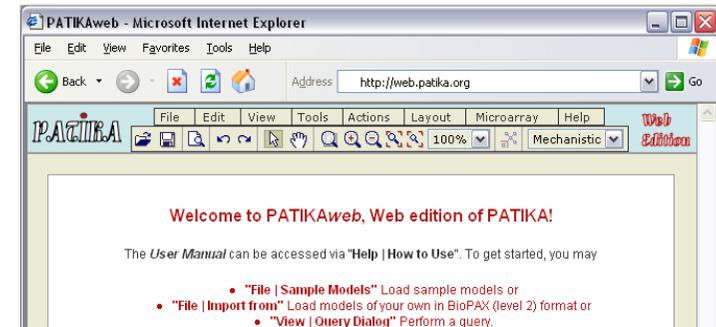# A QUICK START GUIDE TO USING

PATİKA*web*

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*Simply point your browser to **web.patika.org** to get started; after license agreement you get the following Welcome screen.*


Start by loading an existing pathway model; either a model of your own in BioPAX or PATIKA (".pmdl") format, or a sample model. Below is the result of loading sample model Citrate (File | Sample Models | Citrate).


Bioentity view
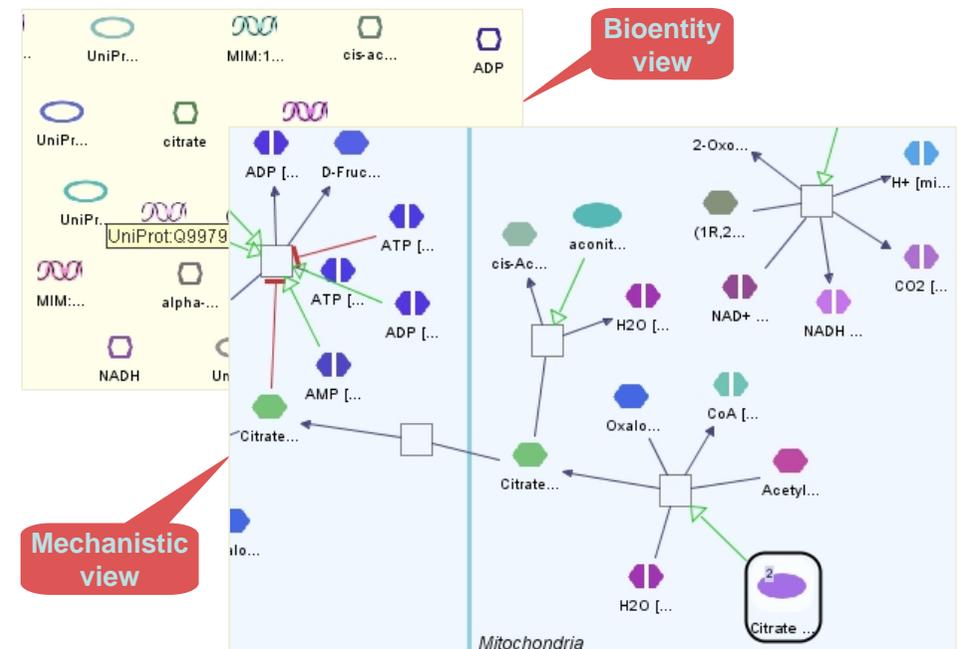
Mechanistic view

In Mechanistic view, right-click on mitochondrial protein state of "aconitase 2" (in green) and select "Find Neighbors in Database"; neighbors of aconitase 2 are brought from DB and highlighted. Notice how this links the previously disconnected transition (in yellow) to the rest of the pathway through "(1R,2S)-1-hydroxypropane-1,2,3-tricarboxylate" (cyan)!
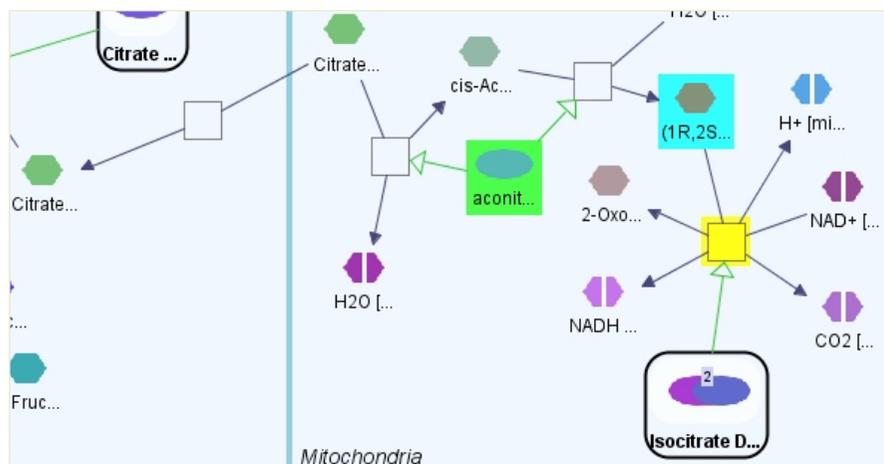
Now start the Query applet by selecting "View | Query Dialog"; click on "New Query" button to create a new "Paths-of-Interest" query, whose source is a field query for all mechanistic nodes whose names contain "caspase-8" and target is a similar field query for those whose names contain "bax". Also set limit to 8 and execute this query!
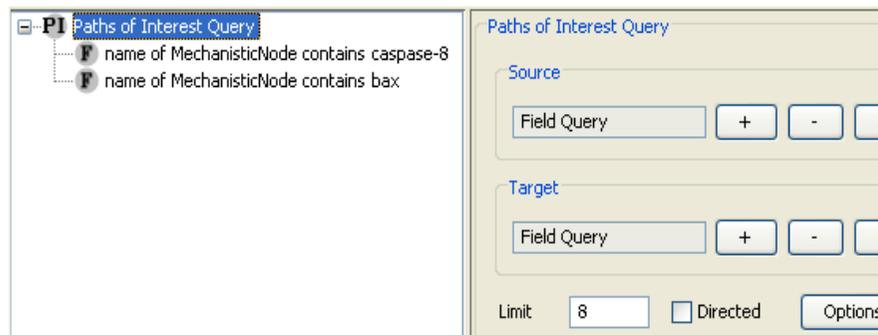
The result should be composed of mechanistic level objects only. Click on "Display". The result should contain 3 regular abstractions (compound nodes whose upper-left corner is tagged with an "R"). Select all three (use ctrl for multiple selection) and issue "Edit | Delete Selected from Model". The view should look like the following, where paths between source (green) and target (cyan) objects are highlighted with yellow.
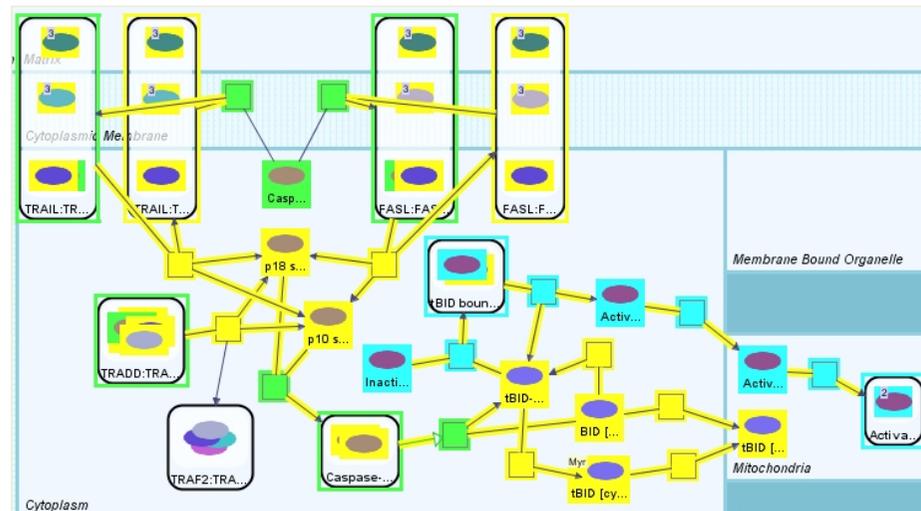

You may save the current model as a static image ("File | Save as Image"), persist for later use ("File | Save Model") or export to a standard format such as BioPAX ("File | Export to").

Now perform "Actions | Collapse All"; multi-compartment spanning compound nodes are not allowed to collapse, so the view is not simplified much. Let's expand these back by performing an undo ("Edit | Undo").

Now let's apply layout. Experiment with each of the layout parameters ("Layout | Properties") to see if you can obtain a layout you like better.

Now suppose we want to focus on the events in Cytoplasm. Using the select tool, select all objects in Cytoplasm (double selection acts as de-selection) and perform "Edit | Crop to Selected". This removes all but selected objects (and their dependents) from the model. Let us now also remove the isolated protein "Caspase-8 precursor" by first selecting it and then performing "Edit | Delete Selected from Model".
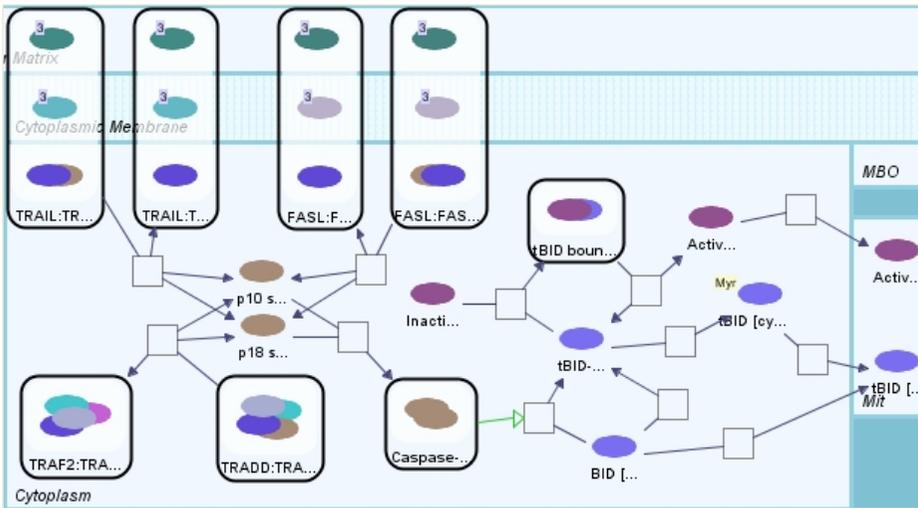
Another facility you may make use of in PATIKAweb is the microarray data analysis component.

You may convert and load microarray experiment data and visualize the gene expression levels on top of your pathway models.

You may also perform clustering on the loaded microarray data. The results may be visualized using the highlighting mechanism (one color per cluster) or abstractions (one compound node per cluster).

Please refer to *User's Guide* and *tool Web site* reachable from **Help menu** for detailed instructions.