

# Pathway Modeler (v. 1.0.0)

Pathway Modeler is an open source Cytoscape application created to aid in modeling the upstream and downstream signaling effects of small molecule binders in a biological pathway. A user may perturb a given system through multiple steps and observe the affected pathway under these various conditions.

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## Installation:

1. Download the latest JAR file from <https://github.com/HelloAarya/cytoscape-pathways>
  2. Open Cytoscape. Click on **Apps > App Manager > Install from File**
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## Function Guide:

- Pathway Modeler functions are located in Cytoscape under **Apps > Pathway Modeler**

**Node Analysis:** An algorithmic analysis that models how a selected activated or inactivated node (or nodes) will affect their nearest neighbors. May be performed in one step (nearest neighbors) or two steps (nearest neighbors + neighbors of nearest neighbors).

### Compound Label:

- Activated – Gives selected nodes a value of one.
- Inhibited – Gives selected nodes a value of negative one.
- Reset – Gives selected nodes a value of zero.

### Edge Label:

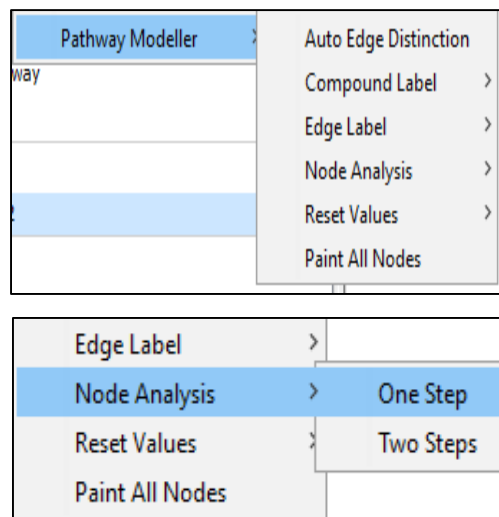
- Activating – Gives selected edges a value of one.
- Inhibiting – Gives selected edges a value of negative one.
- Reset – Gives selected edges a value of zero.

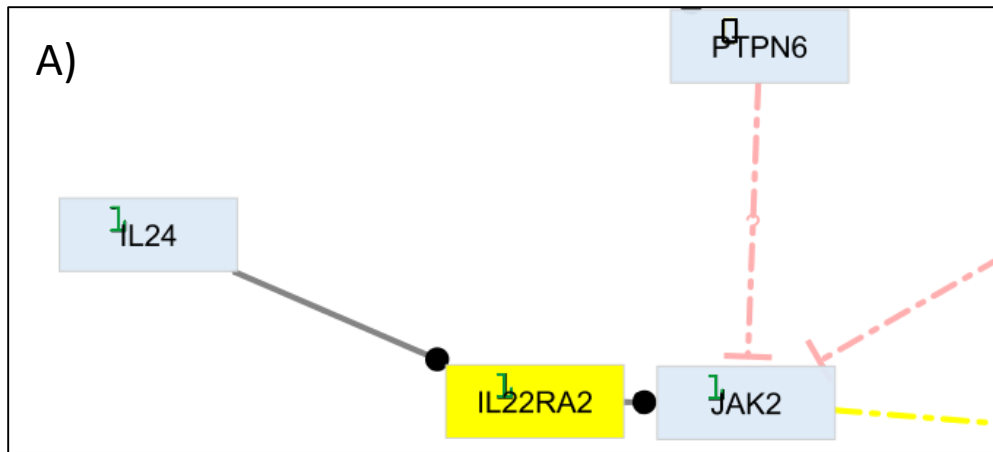
### Reset Values:

- Reset Nodes – Resets all node values to zero.
- Reset Edges – Resets all edge values to zero.
- Clear Images – Erases all painted images made by the Paint All Nodes function.

**Auto Edge Distinction:** This purely visual feature takes any edge that has previously been allocated a value of activating (+1), inhibiting (-1), or null (0) and gives it a corresponding circle, T, or diamond interaction symbol. Furthermore, if the pathway is taken directly from a KEGG source (like KEGGScape), edges are automatically changed based on provided information.

**Paint All Nodes:** This function gives any node labeled with an integer value, previously set by Node Analysis or Compound Label tabs, a corresponding image of the value. Users may use this to visually model the effects of a perturbed pathway.





**Example A:** JAK2 pathway modeled after a one-step node analysis is performed on IL22RA2. Because both the node is activated and its edge is an activating edge, the node JAK2 is given a value of 1, signifying its activation.

**Example B:** PTPN6 is a protein that dephosphorylates JAK2, signified by the pink dashed inhibiting edge. When the node is activated by excess extracellular IL24, a one-step node analysis models how it dephosphorylates JAK2, setting the JAK2 node to zero (neither activating nor inhibiting other nodes).

