Detailed Instructions for using Powerplay

There are 2 ways to use Powerplay
1. Browser Applet (recommended for all users, should work in any browser with Java)
http://www.ent.orst.edu/loop/pplay.aspx

2. Download (allows you to save models, doesn't work on Mac OS)
http://esapubs.org/Archive/ecol/E083/022/suppl-1.htm

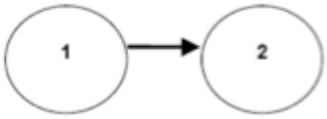
Instructions are for the Applet version. If you download it, it might be a little different.

Building the model:
Use the circle tool to create the components of the ecosystem by clicking it and then clicking to make circles in the workspace. Rename the components by right clicking and selecting "edit" from the dropdown menu. Use the positive and negative connection tools by clicking and holding on one circle then dragging to another. To create a self-limiting closed loop, just click once on a single circle using the negative connection tool. You can erase things with the trash tool. When finished, click "loop analysis."

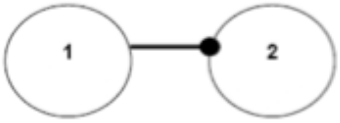
Editing the community matrix:
Your model will be listed in matrix form as an input in the text box. The matrix is formatted such that each row represents incoming interactions on a given component (either -1, 0, or 1). Each column represents the outgoing interactions of that component, or effects it has on other components. You can easily make changes to your model from here by changing these values. Clicking "Show Matrix" will show an updated version of the model that accounts for any changes you made. You can also go back to the model-building applet, but you will have to rebuild the model from scratch.

Checking stability:
Click "Stability." If your system passes both Hurwitz Criterion then it is stable. If it does not, you will be unable to use the model for predictive analysis. You will need to go back and make changes to the model to make it stable. Often, adding a self-limiting closed loop or two can help stabilize the network.

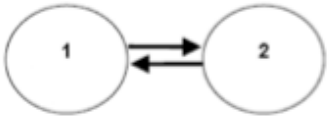
Making predictions:
Click "Prediction." Click one of the column headers to simulate a positive or negative perturbation to that specific component of your system. The model will be displayed with large red circles for components that are positively affected and small yellow for those that are negatively affected.



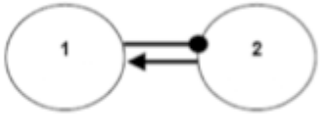
Positive (sunlight, cyanobacteria)



Negative (oceanic CO2, urchins)

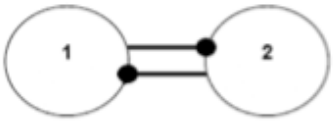


Symbiosis/Mutualism



Predator/prey

Density dependence



competition