Transformations

Video Script

Associated with "03_BioCyc-Groups_Transformations_121113.mov"

Transformations are a powerful way of computing a new column for a group, containing objects that are related to a starting set of objects. For instance, we can use a transformation to see the reactions catalyzed by the enzymes encoded by our gene group. That's accessed by this other menu, which shows the transformations that apply to these genes.

We'll pick the "reactions of gene" transformation. Note that the reactions are of the gene's products. Each cell of this new column shows zero, one, or more reactions catalyzed by the gene product, depending on whether the product of a given gene is an enzyme, and on how many reactions that enzyme catalyzes. Let's now delete that reaction column before our next example.

Now we'll look at the first way to find related pathways using transformations. First we'll pick the transformation to find pathways of our genes. Now we see for each gene it lists the pathways containing reactions catalyzed by enzymes encoded by a gene from our group. Clicking on a pathway takes us to the information page for that pathway. Again, each new cell shows zero, one, or more pathways. Since some genes may be in the same pathway, the list of pathways in this column may contain duplicates. If we want to create a new group that contains a non-redundant list of all the pathways in this column, we can click on the "+" at the top of the column to create the new group. The resulting new group contains a first column consisting of all pathways from the column of pathways we started from. Each pathway now resides in its own row. Its second column shows, for each pathway, the one or more genes from our original group that are in that pathway.

One thing to note is that all of the properties and transforms we've done so far have been based on the first column, but they don't have to be. They can start from any column containing objects. Let's go back to our original gene group using the browser's back navigation and create a new transform column consisting of the protein products of each gene. You can select another column by clicking in the header, which highlights the selected column. Now the transforms and properties apply to that column so we can see the properties of proteins, including its experimentally obtained molecular weight. Let's add a column for that using the properties menu, and now we have molecular weight of the protein product of the gene and we can do operations on that column when we select it. We'll sort them from highest to lowest by clicking the sort arrow pointing downward.

The web groups system contains a large selection of transformations. We encourage you to explore them all. Please keep in mind that the list of transforms available, which shows up in the menu here, depends on what type of object you've selected. When a column of genes is selected, these transforms are available. If we select a different column, containing different types of objects, such as pathways, different transformations will be available. We no longer need these columns, so let's delete them using the minus button.

Let's now create a new group consisting of the single gene trpR by selecting its row and going to Groups->New->Group from checked rows. We can transform this group to the set of all genes regulated by trpR using the transformation menu, and then to the set of all pathways in which those genes' products occur, and then to the set of all metabolites containing those pathways. We'll create a new group containing that non-redundant set of metabolites by clicking "+." We can display the chemical structures of those metabolites.   [Use this example to illustrate the use of "+" in a couple of places]

Various regulation-related transforms are also available. Starting with trpR again, we can transform it to all DNA sites to which this transcription factor binds, and we can obtain the sequence of each binding site as shown here.