

Working with vCONTACT2 Output in Cytoscape

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Note: Assumes you have already installed Cytoscape. You can download it here:
<https://cytoscape.org/>

1. In Cytoscape, import your network (.ntw) file by clicking **File > Import > Network from file**.
2. In the window that pops up, click the “Advanced Options” button at the bottom.
3. Check the box next to “Space” to indicate that your network file is delimited by spaces, then “OK”.
4. Click the top of the first column and select the green circle icon. For the second column, select the red target icon. The third you can leave as the purple notepad icon. Click OK and your network will begin to import.
5. A window will appear asking if you want to create a view for large networks now (and warning it may take a while). Click “OK” to view your network diagram. This could take several minutes depending on the size of the network.
6. Select **Edit > Remove Duplicate Edges** and, in the window that pops up, check the box next to “Ignore edge direction”. Click “OK”. Click **Edit > Remove Self Loops** (I usually don’t have any of these but it’s good to check). Click “OK”.
7. Once your view has been created, load in your “genome_by_genome_overview.csv” file by selecting **File > Import > Table from file**. Note: if you have not already, you will need to add a column indicating the source of the sequences (i.e. “user” for your sequences and “database” for those from the reference database). Below is some awk code that can help you do that. You will need to change “USER_SEQUENCE” to whatever your sequences begin with (e.g. mine all begin with “EDGE”).

```
awk -F"," 'BEGIN { OFS = "," } NR==1{$(NF+1)="source"; print; next} {if ($2 ~ /^USER_SEQUENCE/) $(NF+1)="user"; else $(NF+1)="database"; print $0;}' genome_by_genome_overview.csv > genome_by_genome_overview.new.csv
```

8. In the window that pops up, select “To select networks only” from the dropdown menu for “Where to Import Table Data”. Select your network from the “Network List” that appears. Next to “Import Data as” select “Node Table Columns”. Finally, click the top of the “Genome” column in your data table and select the key icon. It should turn the whole column bold. Now hit “OK”.
9. Under the “Style” tab, select “Fill Color”. Next to “Column”, select “source” from the dropdown menu. Next to “Mapping Type”, select “Discrete Mapping”. You can pick

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whichever two contrasting colors you like for “user” and “database” sequences. This will differentiate the two on your network diagram.