

Network2Canvas v1.0 - User Manual

Create Your Own Interactive Canvases

Written by Christopher M. Tan and Avi Ma'ayan

Updated on 03/04/2013

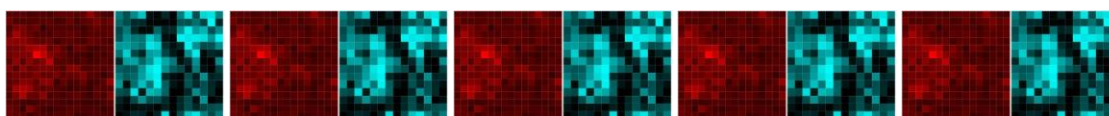
Table of Contents

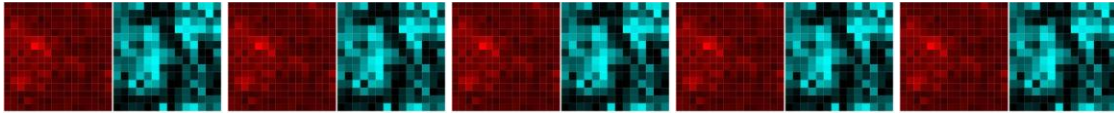
1. Abstract
2. Installation and Requirements
3. Workflow of Network2Canvas
4. How to Run the Annealer?
5. Creating Adjacency Matrices from GMT files and Networks
 - a. Converting a GMT File to a Mean Adjacency Matrix
 - b. Converting a Network to a Mean Adjacency Matrix

Abstract

Networks are central in computational systems biology research, but visualizing large networks can be a challenge. For networks larger than ~100 nodes and ~200 links, ball-and-stick diagrams fail to convey much information. To address this, we developed Network2Canvas (N2C), a web application that provides an alternative way to view networks. N2C visualizes network nodes by placing them on a square toroidal grid. These nodes are then clustered together on the grid using simulated annealing to maximize local connections. For visualizing the canvas, a node's brightness is made proportional to its local fitness; the brighter a node is, the stronger its connections to its neighbors. The grid is interactive, implemented in HTML5 and the Java Script library D3.

We applied N2C to create canvases for 25 gene-gene functional association networks connecting human and mouse genes and 6 drug-drug networks connecting FDA approved drugs based on their shared properties. N2C also has functions to perform enrichment analysis which can create unique metasignatures for the input gene list. Given a list of genes or drugs, N2C highlights enriched terms on the grid as well as computes the degree of clustering for these enriched nodes. In summary, N2C provides a new flexible method to visualize large networks and to perform and visualize enrichment analysis on functional drug and gene networks. N2C is freely available at <http://www.maayanlab.net/N2C>.

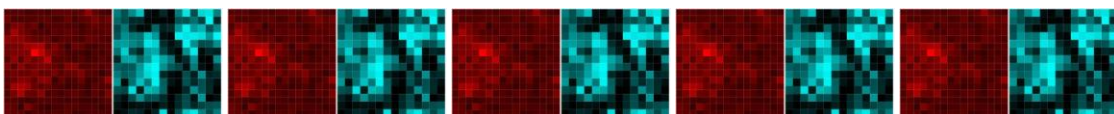


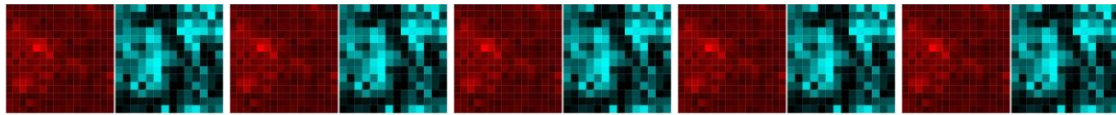


Installation and Requirements

Network2Canvas provides the ability for users to create their own canvases from networks and gene set libraries. These are Python scripts that generate the SVG, JavaScript and HTML5 pages. These scripts require Python 2.7 or higher to run. The scripts do not have any other dependencies. The latest version of Python can be found at <http://www.python.org>.

For optimal performance of the Python scripts, installing PyPy is highly recommended. The latest version of PyPy can be downloaded at <http://www.pypy.org>. To use PyPy from the command line, replace “python” with “pypy” after adding PyPy to the path.





The Workflow of Network2Canvas

Input: Network in a tabular format, GMT File, or a Mean Adjacency Matrix

Output: JSON file containing the Canvas

HTML File containing a canvas constructed from the input.

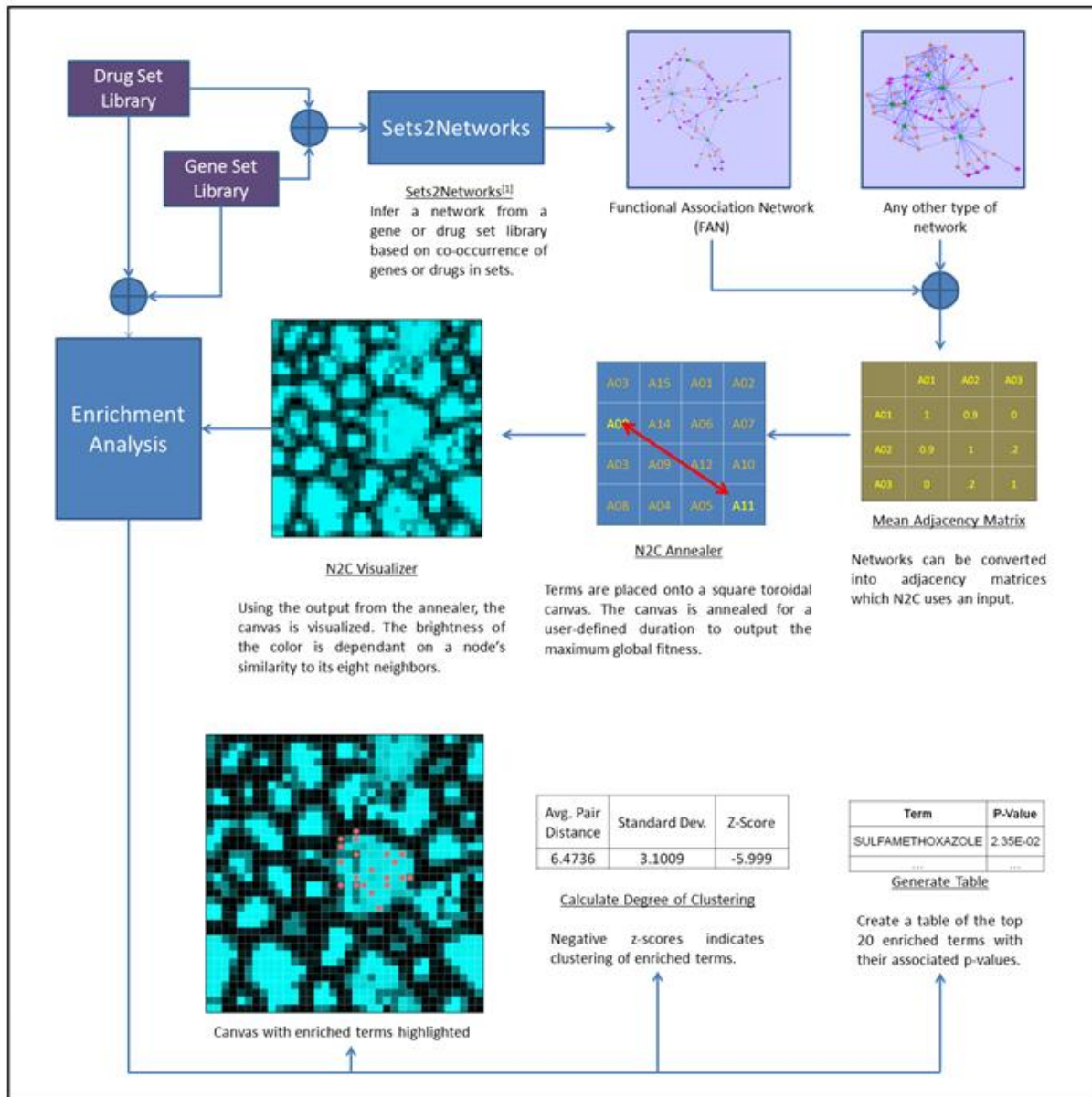
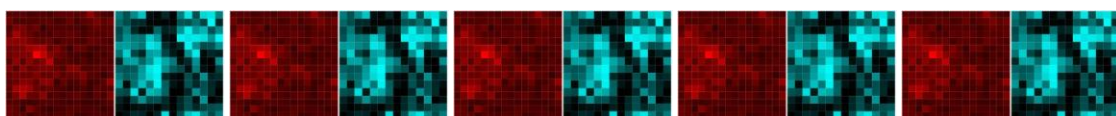
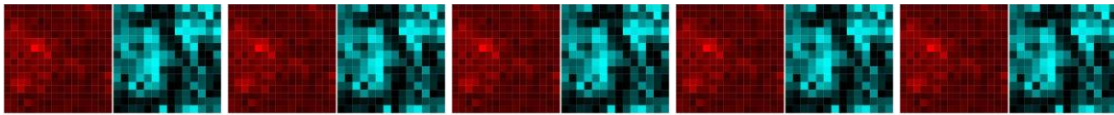


Figure 1: The workflow of Network2Canvas. Mean adjacency matrices can be created from an interaction list representing a network or a functional association network derived from a Gene Set Library. The mean adjacency matrix is used as input for the Annealer which outputs a JSON file representing the created canvas and an HTML file that contains the Visualizer. The visualizer shows the created canvas as a 2D grid and can be used to run additional analysis using gene lists. It also provides a way to modify and download the canvas image.





How to Run the Annealer

The Network2Canvas Annealer can be run from either the command line or the Python's IDLE. The program inputs should be placed inside the Input folder. The outputs will appear in the Output and HTML Files folder. The Annealer Network2Canvas script only accepts tab-delimited mean adjacency matrices and GMT files.

--

The Annealer Network2Canvas script takes in two command line arguments: the location of the input matrix and the time for annealing in seconds. The longer the time, the closer the canvas becomes to its ideal global fitness.

An optional argument can be added to the two arguments: this is the location of the GMT File that would be needed for performing enrichment analyses. The addition of this argument enables the gene or drug list enrichment analyses functionality to be added to the output HTML Network2Canvas Visualizer page.

--

Running the Network2Canvas Annealer from the Command Line

The Network2Canvas Annealer can be run from the command line with the following text:

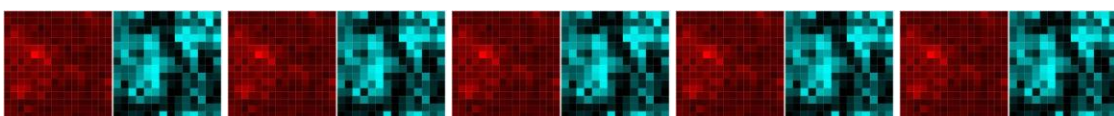
```
>> python Network2Canvas.py matrix_location time_to_anneal gmt_location(optional)
```

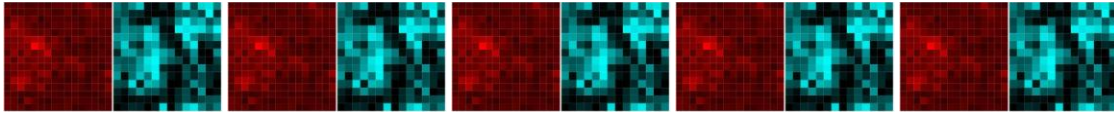
```
C:\ Command Prompt
Microsoft Windows XP [Version 5.1.2600]
(C) Copyright 1985-2001 Microsoft Corp.

C:\Documents and Settings\Administrator>cd my documents\finished scripts\
C:\Documents and Settings\Administrator\My Documents\Finished Scripts>cd network2canvas
C:\Documents and Settings\Administrator\My Documents\Finished Scripts\Network2Canvas> python Network2Canvas.py Input/AERS.txt 20000 Input/AERS_GMT_filt.txt
```

Figure 2: Running N2C from the Command Line. Note that the "Input/AERS_GMT_filt.txt" part is optional.

The file Network2Canvas web-site containing all the needed files will be found in the HTML output folder once the script is complete.





Running Network2Canvas from Python IDLE

Open the Network2Canvas Annealer script using the IDLE Editor. Select Run from the Run dropdown (or press F5). The Python Shell should pop up, outputting an error. Afterwards add the following:

```
> import Network2Canvas
> args = ["", matrix_location, time_to_anneal, gmt_location(optional)]
> Network2Canvas.main(args)
```

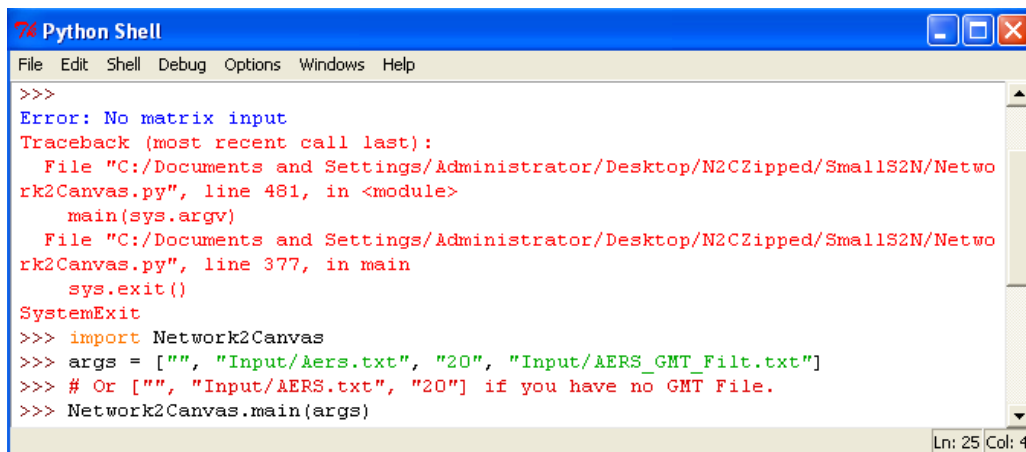
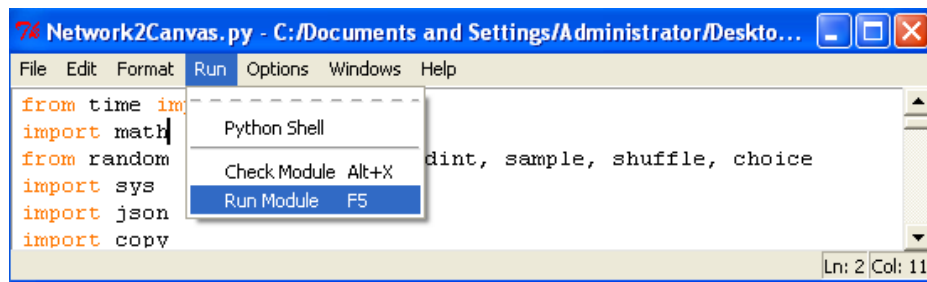
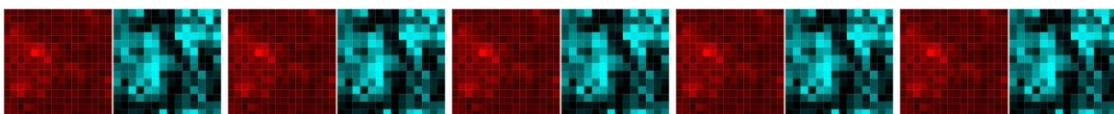
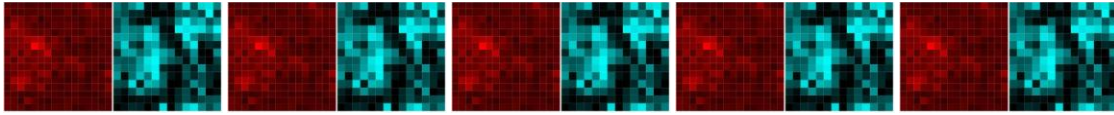


Figure 3: Running Network2Canvas from the IDLE GUI. After loading the Network2Canvas file, select Run Module. Afterwards, you can input the aforementioned lines containing the command line arguments into the shell to create a canvas.





Creating Adjacency Matrices from GMT files and Networks

Converting a GMT File into a Mean Adjacency Matrix

The Network2Canvas package includes the script “Sets2Networks.py” which converts GMT Files into Functional Association Networks. These networks are represented as mean adjacency matrices, making them suitable for use as input to the Network2Canvas Annealer script. Please consult the Sets2Networks documentation for help on using this script: <http://maayanlab.net/S2N/S2N-man-chris.pdf>

Converting a Network into a Mean Adjacency Matrix

Provided with the Network2Canvas package is the script “List2Matrix.py” which converts a tab-delimited interaction list into a mean adjacency matrix.

The format of the interaction list input file for this script should be:

source target value

In unweighted networks, the value is always 1 for every source-target pair. In weighted networks such as the functional association networks we implemented, this value will be between 0 and 1.

The interaction list should be located in the Input folder of where the List2Matrix.py script resides. The output file will be located in the Output folder the List2Matrix.py will create. The script, like the frNetwork2Canvas Annealer script, can be run from the command prompt or from the Python IDLE GUI.

--

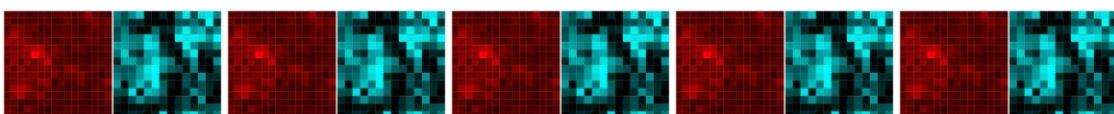
From Command Prompt:

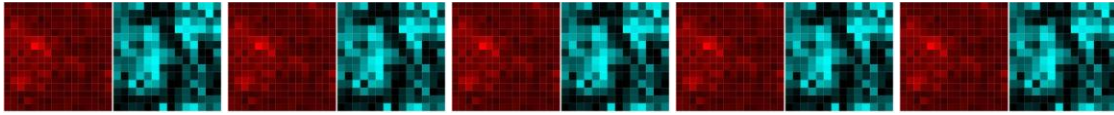
```
> python List2Matrix.py location_of_interaction_list
```

From IDLE GUI:

Open the List2Matrix script from IDLE. Select Run. Afterwards, input the following commands.

```
> import List2Matrix
> List2Matrix.main(["", location_of_interaction_list])
```





The Output

JSON File:

The JavaScript Object Notation (JSON) file represents the canvas and can be found in the Output folder after running Network2Canvas. It shares the same name as the input matrix file except with “.json” as the file extension. This file holds the object representing the canvas: two arrays of same length called *names* and *weights*. Each item in the array appears in the order of their placement within the canvas. The canvas width is determined by the square root of an array’s length.

The *names* array contains the names of the nodes, while the *weights* array contains the brightness scores for each node (which ranges from 0 to 8).

HTML File/Visualizer:

The Visualizer can be found in the HTML Files after running Network2Canvas. The HTML page has the same name as the input file except with the “.html” extension. The Visualizer page comes embedded with the JSON object representing the canvas.

If Network2Canvas was run with a GMT File, gene list enrichment analysis will be enabled for the webpage.

Instructions on how to use the Network2Canvas Visualizer can be found at <http://www.maayanlab.net/N2C/res/N2C-Web-Interface-User-Manual.pdf>.

