

Example demonstrating how to run the APCluster plugin on the original data provided by the authors of AP, includes an example of storing the clustering results in text file

Go to the Affinity Propagation homepage

http://www.psi.toronto.edu/affinitypropagation/

Diagram of conjugate... Knuth-Morris-Pratt Al... XML in PHP 5 - What's... Stop TB Partnership - ... WHO | Pursue high-q... Extensively drug-resi... Multi-drug-resistant L...

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AFFINITY PROPAGATION

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[Clustering by Passing Messages Between Data Points](#), *Science* **315**, 972–976. [\[PDF\]](#) [\[BibTeX\]](#)

Interested in a **commercial license** for the extended software toolkit?
Send email to email to [Brendan Frey](#)

Data sets and software are provided at the bottom of this page

[Click here to analyze data using the affinity propagation web application](#)

NEW: [Affinity Propagation FAQ](#)

How would you identify a small number of face images that together accurately represent a data set

Figure: <http://www.psi.toronto.edu/affinitypropagation/>

Find the section with Data Sets and download the similarities, for example “clustering two-dimensional data points”

median of the other similarities. The MATLAB code executes 100 iterations of affinity propagation. After execution, the combined evidence $r(i,k)+a(i,k)$ is stored in the $N \times N$ matrix E , the number of exemplars is stored in π , the data instance indices of the exemplars are stored in the K -vector τ , and the exemplar indices of the data instances are stored in the N -vector i_{dx} . (Note, instance i is assigned to the data instance with index $i_{dx}(i)$.)

Data Sets

CLUSTERING TWO-DIMENSIONAL DATA POINTS

The similarity between every pair of 2D data points was set to the negative squared distance between the points. To prevent degenerate solutions, where affinity propagation tries to place two points in one cluster, but both data points are equally good as cluster centers, Gaussian noise with $\sigma=10^{-12}$ was added to the similarities, before affinity propagation was applied.

- [Text files containing 2-D data points, similarities, and preferences \(median of S\)](#)
- [MATLAB file containing data, similarities and preferences](#)

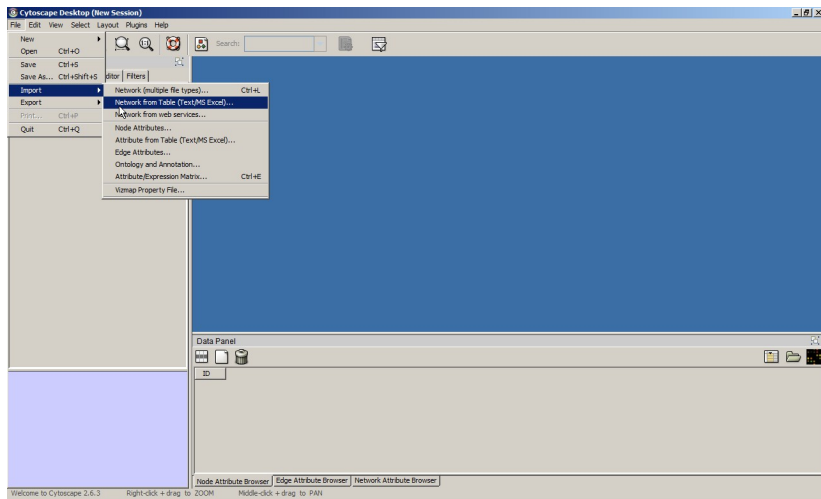
CLUSTERING IMAGES DERIVED FROM OLIVETTI FACE DATABASE

Each 64×64 face image from the first 100 images in the Olivetti database was smoothed using a Gaussian kernel with $\sigma=0.5$ and then rotated by -10° , 0° and 10° and scaled by a factor of 0.9, 1.0 and 1.1 (using nearest-neighbor interpolation), to produce a total of 900 images. To avoid including the background behind each face, a central window of size 50×50 pixels was extracted. Finally, the pixels in each 50×50 image were normalized to have mean 0 and variance 0.1. The similarity between two images was set to the negative sum of squared pixel differences.

- [Image showing all the data instances](#)
- [Text files containing similarities \(5MB\) and preferences](#)
- [MATLAB file containing similarities based on squared error \(19MB\)](#)

FINDING GENES AND EXONS USING PUTATIVE EXON EXPRESSION DATA

Run Cytoscape with the "APCluster" in the plugins directory and open the interface for importing a network



Choose the "ToyProblemSimilarities.txt" network

Cytoscape Desktop (New Session)

File Edit View Select Layout Plugins Help

Control Panel

Network | VisMapper™ | Editor | Filters |

Network Nodes Edge

Import Network and Edge Attributes from Table

Import Network from Table

Data Sources

Import File: file://C:/Users/misaki/Desktop/ToyProblemSimilarities.txt [Select File(s)]

Interaction Definition

Source Interaction: Select Source node col... Interaction Type: Default Interaction Target Interaction: Select Target node col...

⚠ Columns in BLUE will be loaded as EDGE ATTRIBUTES.

Advanced

Show Text File Import Options

Preview

Text File Left Click: Enable/Disable Column, Right Click: Edit Column

ToyProblemSimilarities.txt

Column 1	Column 2	Column 3	Column 4	Column 5
001		002		-1.860905
001		003		-4.065932
001		004		-9.292907
001		005		-3.581147
001		006		-3.093119
001		007		-27.966812
001		008		-32.147129
001		009		-44.921228
001		010		-47.966678

Import Cancel

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

Node Attribute Browser | Edge Attribute Browser | Network Attribute Browser

Select appropriate columns as in the picture below and import data

Import Network from Table

Data Sources

Input File: file:///C:/Users/insiek/Desktop/ToyProblemSimilarities.txt

Interaction Definition

Source Interaction: Column 1 Interaction Type: Column 5 Target Interaction: Column 3

Columns in BLUE will be loaded as EDGE ATTRIBUTES.

Advanced

Show Text File Import Options

Preview

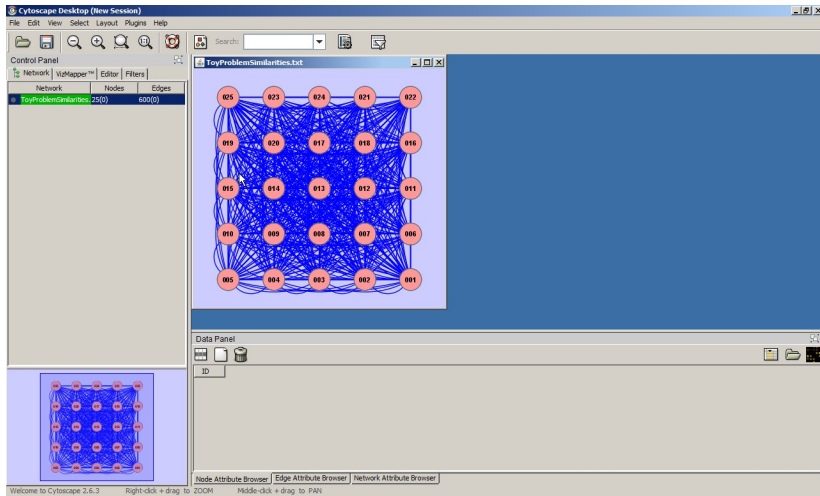
Text File: ToyProblemSimilarities.txt

Column 1	Column 2	Column 3	Column 4	Column 5
001	002	-1.860905		-1.860905
001	003	-4.065932		-4.065932
001	004	-9.292907		-9.292907
001	005	-3.581147		-3.581147
001	006	-3.093119		-3.093119
001	007	-27.966812		-27.966812
001	008	-32.147129		-32.147129
001	009	-44.921228		-44.921228
001	010	-47.966678		-47.966678

Node Attribute Browser | Edge Attribute Browser | Network Attribute Browser

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

The network that you should obtain



Activate the "APCluster" plugin from the "plugins" menu

The screenshot displays the Cytoscape Desktop interface with a network graph loaded from a file named "ToyProblemSimilarities.txt". The graph consists of 25 nodes arranged in a 5x5 grid, labeled from 001 to 025. The nodes are interconnected by a dense network of blue edges. The "Plugins" menu is open, showing the "APCluster" option selected. The "Data Panel" at the bottom is currently empty, with an "ID" field visible. The interface includes a menu bar (File, Edit, View, Select, Layout, Plugins, Help), a toolbar, and a control panel on the left. A small thumbnail of the network graph is visible in the bottom-left corner.

File Edit View Select Layout Plugins Help

Control Panel

Network | VizMapper™ | Editor

Network: ToyProblemSimilarities: 25(0)

Node

- APCluster
- MCOSE
- Cluster

Search:

ToyProblemSimilarities.txt

Data Panel

ID

Node Attribute Browser | Edge Attribute Browser | Network Attribute Browser

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

Go to the "APCluster" plugin tab

The screenshot shows the Cytoscape Desktop interface with the APCluster plugin selected. The main window displays a network graph with 25 nodes (001-025) and many edges. The left sidebar shows the Control Panel with various settings for the APCluster plugin, including parameters like Edge weight attribute, Number of iterations, Stop criterion, Preference, Lambda, Add noise, and Log transform edge weights. The bottom of the window shows the Data Panel and several attribute browser tabs.

Control Panel

Parameters

Edge weight attribute: DEFAULT

Number of iterations: 500

Stop criterion: 50

Preference: 0.500

Lambda: 0.5

Add noise:

Log transform edge weights:

Output attributes

Cluster ID: cluster_id

Center ID: center_id

Graph mode

Undirected edges Directed edges

Advanced options Start

Highlight centers

Network Preferences Lambda Clusters

Delete row Details

ToyProblemSimilarities.txt

Data Panel

ID

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

Reload the list of appropriate attributes, and select "interaction"

The screenshot displays the Cytoscape Desktop interface with a new session. The main window shows a network graph titled "ToyProblemSimilarities.txt" with 25 nodes (001-025) and numerous blue edges. The Control Panel on the left is active, showing parameters for the network. The "Number of iterations" field is set to "interaction" and is highlighted by a mouse cursor. Other parameters include "Edge weight attribute" (DEFAULT), "Stop criterion" (50), "Preference" (0.500), and "Lambda" (0.5). The "Output attributes" section shows "Cluster ID" and "Center ID" both set to "cluster_id". The "Graph mode" is set to "Undirected edges". The "Data Panel" at the bottom is empty, and the "Node Attribute Browser", "Edge Attribute Browser", and "Network Attribute Browser" are visible at the bottom of the window.

Cytoscape Desktop (New Session)

File Edit View Select Layout Plugins Help

Control Panel

Network | vizMapper™ | Editor | Filters | APCluster

Parameters

Edge weight attribute: DEFAULT

Number of iterations: interaction

Stop criterion: 50

Preference: 0.500

Lambda: 0.5

Add noise:

Log transform edge weights:

Output attributes

Cluster ID: cluster_id

Center ID: center_id

Graph mode

Undirected edges Directed edges

Advanced options Start

Highlight centers

Network Preferences Lambda Clusters

Delete row Details

ToyProblemSimilarities.txt

Data Panel

ID

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

Choose the "Directed edges" option

The screenshot displays the Cytoscape Desktop interface with a network graph loaded from a file named "ToyProblemSimilarities.txt". The graph consists of 25 nodes arranged in a 5x5 grid, labeled from 001 to 025. The nodes are connected by a dense network of blue edges, which are highlighted as directed edges. The interface includes a menu bar (File, Edit, View, Select, Layout, Plugins, Help), a toolbar, and a Control Panel on the left. The Control Panel shows parameters for the network, such as "Edge weight attribute" set to "interaction", "Number of iterations" set to 500, and "Stop criterion" set to 50. The "Graph mode" section is set to "Directed edges". The Data Panel at the bottom right is empty, and the status bar at the bottom indicates the current zoom and pan settings.

Cytoscape Desktop (New Session)

File Edit View Select Layout Plugins Help

Control Panel

Network | VisMapper™ | Editor | Filters | APCluster

Parameters

Edge weight attribute: interaction

Number of iterations: 500

Stop criterion: 50

Preference: -16.159

Lambda: 0.5

Add noise:

Log transform edge weights:

Output attributes

Cluster ID: cluster_id

Center ID: center_id

Graph mode

Undirected edges Directed edges

Advanced options Start

Highlight centers

Network Preferences Lambda Clusters

Delete row Details

ToyProblemSimilarities.txt

Data Panel

ID

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

Click "Start" button to run the algorithm

The screenshot displays the Cytoscape Desktop interface. The main window shows a network graph with 20 nodes arranged in a 5x4 grid, labeled 001 through 025. The nodes are connected by a dense network of blue edges. The 'Start' button in the 'Advanced options' section of the Control Panel is highlighted with a mouse cursor. The Control Panel includes various settings for the network, such as 'Edge weight attribute' (interaction), 'Number of iterations' (500), 'Stop criterion' (50), 'Preference' (-16.159), and 'Lambda' (0.5). The 'Output attributes' section shows 'Cluster ID' and 'Center ID' set to 'cluster_id' and 'center_id' respectively. The 'Graph mode' is set to 'Undirected edges'. The 'Data Panel' at the bottom is empty. The status bar at the bottom of the window reads: 'Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN'.

The algorithm will converge.

The screenshot displays the Cytoscape Desktop interface. The main window shows a network graph with 20 nodes (IDs 005 to 025) and numerous edges. Node 020 is highlighted in yellow. A dialog box titled "Clustering completed" is open, displaying the following information:

- Description: Per
- Status: Ce
- Progress: [Progress bar]
- Algorithm converged after: 54 iterations

The dialog box includes "Close", "Cancel", and "OK" buttons. The background graph is titled "ToyProblemSimilarities.txt".

The Control Panel on the left shows the following settings:

- Edge weight attribute: interaction
- Number of iterations: 500
- Stop criterion: 50
- Preference: -16,159
- Lambda: 0,5
- Add noise:
- Log transform edge weights:
- Output attributes: Cluster ID: cluster_id, Center ID: center_id
- Graph mode: Undirected edges, Directed edges
- Advanced options: Start
- Highlight centers: center_id
- Network: ToyProble..., Preferences: -16,159, Lambda: 0,5, Clusters: 3

The Data Panel at the bottom shows a table with the following data:

ID
007
020
003

At the bottom of the window, there are tabs for "Node Attribute Browser", "Edge Attribute Browser", and "Network Attribute Browser". The status bar at the very bottom reads: "Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN".

You should obtain this layout

The screenshot displays the Cytoscape Desktop interface for a new session. The main window shows a network visualization of 'ToyProblemSimilarities.txt' with nodes arranged in a grid and connected by a dense web of blue edges. The control panel on the left includes the following settings:

- Parameters:
 - Edge weight attribute: interaction
 - Number of iterations: 500
 - Stop criterion: 50
 - Preference: -16, 159
 - Lambda: 0.5
 - Add noise:
 - Log transform edge weights:
- Output attributes:
 - Cluster ID: cluster_id
 - Center ID: center_id
- Graph mode: Undirected edges, Directed edges
- Buttons: Advanced options, Start
- Highlight centers: center_id

The Data Panel at the bottom shows a table with the following data:

Network	Preferences	Lambda	Clusters
ToyProble...	-16, 159	0, 5	3

Below the table are buttons for 'Delete row' and 'Details'. The status bar at the bottom indicates 'Welcome to Cytoscape 2.6.3' and provides instructions for zooming and panning.

Show "cluster_id" and "center_id" attributes in Data panel

The screenshot displays the Cytoscape Desktop interface. The main window shows a network graph with yellow nodes and red edges. The Control Panel on the left is configured with the following settings:

- Edge weight attribute: interaction
- Number of iterations: 500
- Stop criterion: 50
- Preference: -16,159
- Lambda: 0.5
- Add noise:
- Log transform edge weights:
- Output attributes: cluster_id, center_id
- Graph mode: Undirected edges, Directed edges
- Advanced options: Start
- Highlight centers: center_id

The Data Panel at the bottom shows a table with the following columns: Network, Preferences, Lambda, and Clusters. The table contains one row for the network 'ToyProble...'. The Clusters column shows the value '0,5'.

Network	Preferences	Lambda	Clusters
ToyProble...	-16,159	0,5	3

The Data Panel also shows a list of attributes with checkboxes: canonicalName, center_id, and cluster_id. The center_id and cluster_id attributes are checked.

At the bottom of the window, there is a status bar with the text: "Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN".

Select all nodes and choose the option "Export → Entire Table" in Data panel

The screenshot shows the Cytoscape Desktop interface. The main window displays a network graph with green nodes and red edges. The Control Panel on the left contains various settings for network visualization. The Data Panel at the bottom shows a table with columns for ID, center_id, and cluster_id. A context menu is open over the table, with the 'Export...' option selected, and a sub-menu showing 'Selected Cells' and 'Entire Table'.

Control Panel

Parameters

- Edge weight attribute: interaction
- Number of iterations: 500
- Stop criterion: 50
- Preference: -16.159
- Lambda: 0.5
- Add noise:
- Log transform edge weights:

Output attributes

- Cluster ID: cluster_id
- Center ID: center_id

Graph mode

- Undirected edges
- Directed edges

Advanced options **Start**

Highlight centers: center_id

Network	Preferences	Lambda	Clusters
ToyProble...	-16,159	0,5	3

Data Panel

ID	center_id	cluster_id
001	003	0
002	003	0
003	0	
004	0	
005	0	
006	0	
007	0	
008	0	
009	0	

Export... → Selected Cells, Entire Table

Welcome to Cytoscape 2.6.3 Right-click + drag to ZOOM Middle-click + drag to PAN

Save your clustering in text format

```
clustering.txt
1 ID center_id cluster_id
2 013 003 0
3 012 007 1
4 008 007 1
5 011 003 0
6 022 003 0
7 003 003 0
8 009 007 1
9 025 007 1
10 007 007 1
11 021 020 2
12 005 003 0
13 018 020 2
14 024 020 2
15 014 007 1
16 015 007 1
17 004 003 0
18 020 020 2
19 010 007 1
20 016 020 2
21 023 020 2
22 019 020 2
23 001 003 0
24 017 020 2
25 002 003 0
26 006 003 0
27
```