

Module IV - Basic Analysis

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June 29, 2010

Agenda for Module IV

Loading data from multiple sources

- ▶ Local network data files
- ▶ Building directly from the Internet

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Brief review of Python dictionaries

- ▶ **Why is the dict so useful?**
- ▶ **How NetworkX utilizes it?**

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- ▶ Why is the dict so useful?
- ▶ How NetworkX utilizes it?

Running basic centralities

- ▶ Degree, Closeness, Betweenness Eigenvector
- ▶ Calculating degree distribution
- ▶ Plotting statistics using matplotlib
- ▶ Calculating cliques, clustering and transitivity

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Outputting data into multiple formats

- ▶ Writing network data
- ▶ Saving network analysis statistics

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Outputting data into multiple formats

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Basic visualization

- ▶ Review of NetworkX's plotting algorithms
- ▶ Adding analysis to visualization

As we have seen, one of the main advantages of working with NetworkX is that it can read many different network formats

- ▶ For those that are unfamiliar with working at the command-line, however, the process can be confusing

NX syntax for loading a file

```
>>> G = nx.read_format("path/to/file.txt", ...options...)
```


Net variable

↑

NX function, file directory path



Graph type, nodes type, etc.

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Loading the Hartford drug users network

Starting NetworkX and loading data

```
»> hartford=nx.read_edgelist("../data/hartford-drug.txt", create_using=nx.DiGraph(), nodetype=int)
»> nx.info(hartford)
```

Name:

Type: Di Graph

Number of nodes: 212

Number of edges: 337

Average in degree: 1.5896

Average out degree: 1.5896

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- ▶ Specified path to Hartford drug users file

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- ▶ Used the `read_edgelist` function to load EL file
- ▶ Specified path to Hartford drug users file
- ▶ Used the `create_using` option to force NX to create as a directed graph

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- ▶ Used the `info` function to check that it all worked

Loading the Hartford drug users network

Starting NetworkX and loading data

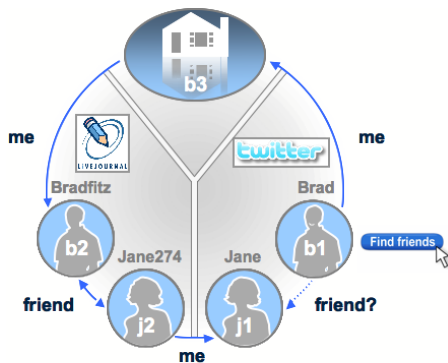
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What did we just do?

- ▶ Used the `read_edgelist` function to load EL file
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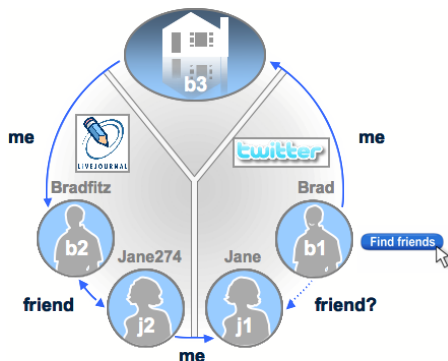
Some formats may have more or less options, always check the documentations!

Building the social network among LiveJournal users



Perhaps the most powerful aspect of NetworkX is its ability to work in Python to generate networks from live-streaming data

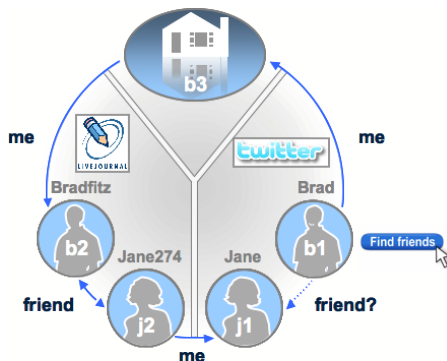
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- In Python, use NetworkX, cjson and a other standard scientific libraries to parse Google's SocialGraph data

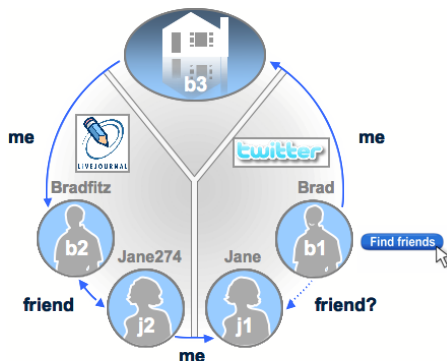
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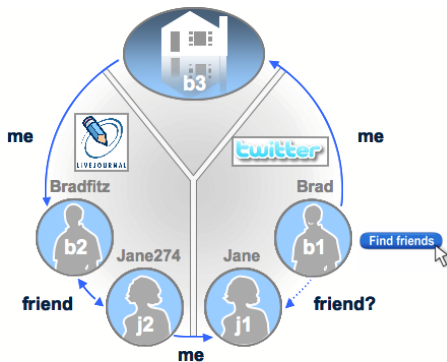
- ▶ In Python, use NetworkX, cjson and a other standard scientific libraries to parse Google's SocialGraph data
- ▶ Using a "seed" user, we will build out a network

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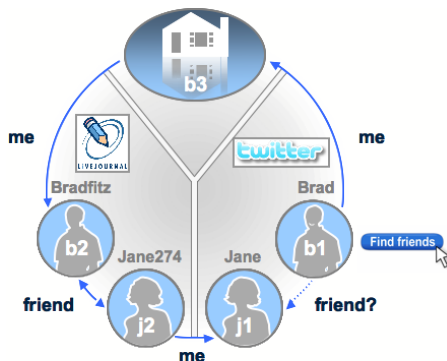
- ▶ In Python, use NetworkX, cjson and a other standard scientific libraries to parse Google's SocialGraph data
- ▶ Using a “seed” user, we will build out a network
- ▶ Through a process called “k-snowball searching”
 $\text{seed} \rightarrow \text{friend} \rightarrow \dots \rightarrow \text{friend}_k$



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- ▶ In Python, use NetworkX, BeautifulSoup and a other standard scientific libraries to parse Google's SocialGraph data
- ▶ Using a “seed” user, we will build out a network
- ▶ Through a process called “k-snowball searching”
seed \rightarrow friend $\rightarrow \dots \rightarrow$ friend_k
 - ▶ Seed: imichaeldotorg.livejournal.com
 - ▶ k = 3

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- ▶ In Python, use NetworkX, `cj son` and a other standard scientific libraries to parse Google's SocialGraph data
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 $\text{seed} \rightarrow \text{friend} \rightarrow \dots \rightarrow \text{friend}_k$
 - ▶ Seed: `imichaeldotorg.livejournal.com`
 - ▶ $k = 3$
- ▶ **Note the low value of k**

The code, part 1

Loading the libraries and scraping egonet

```
from json import *
from urllib import *
from time import *
from scipy import array, unique
...
if __name__ == "__main__":
    seed="imichael.dotor@gmail.com"
    seed_url="http://"+seed+".livejournal.com"
    # 3.1 Scrape, parse and build seed's ego net
    sg=get_sg(seed_url)
    net, newnodes=create_ego_net(sg)
    nx.write_pajek(net, ".../data/"+seed+"_ego.net")
    nx.info(net)
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def get_sg(seed_url):
    sgapi_url="http://socialgraph.apis.google.com/lookup?q="+seed_url+"&edo=1&edi=1&fme=1&pretty=0"
    try:
        furl=urlopen(sgapi_url)
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    except IOError:
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Name:	['http://imichaeldotorg.livejournal.com/']
Type:	Di Graph
Number of nodes:	5
Number of edges:	5
Average in degree:	1.0
Average out degree:	1.0

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def get_sg(seed_url):
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Build egonet and snowball

Creating the egonet

```
def create_egonet(s):
    try:
        raw=decode(s)
        G=nx.DiGraph()
        pendants=[]
        n=raw['nodes']
        nk=n.keys()
        G.name=str(nk)
        pendants=[]
        for a in range(0,len(nk)):
            for b in range(0,len(nk)):
                if a!=b:
                    G.add_edge(nk[a],nk[b])
        for k in nk:
            ego=n[k]
            ego_out=ego['nodes-referenced']
            for o in ego_out:
                G.add_edge(k,o)
                pendants.append(o)
            ego_in=ego['nodes-referenced-by']
            for i in ego_in:
                G.add_edge(i,k)
                pendants.append(i)
        pendants=array(pendants, dtype=str)
        pendants.flatten()
        pendants=unique(pendants)
        return G, pendants
    except DecodeError:
        ...
    except KeyError:
```

Rolling the snowball

```
def snowball_round(G, seeds, myspace=False):
    t0=time()
    if myspace:
        seeds=get_myspace_url(seeds)
    sb_data=[]
    for s in range(0, len(seeds)):
        s_sg=get_sg(seeds[s])
        new_ego, pen=create_egonet(s_sg)
        for p in pen:
            sb_data.append(p)
    if s<1:
        sb_net=nx.compose(G, new_ego)
    else:
        sb_net=nx.compose(new_ego, sb_net)
    del new_ego
    if s==round(len(seeds)*0.2):
        sb_net.name='20% complete'
        nx.info(sb_net)
        print 'AT: ' +strftime('%m/%d/%Y, %H:%M:%S', gmtime())
        print "
    ...
    # More time keeping, probably a MUCH better way to do this
    sb_data=array(sb_data)
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Build the whole network

Step	Nodes	Edges	Mean Degree	Density
Seed	5	5	2.0	0.25
k = 2	75	115	3.0	0.02
k = 3	4,938	8,659	3.5	$3.6(10^{-4})$

Build the whole network

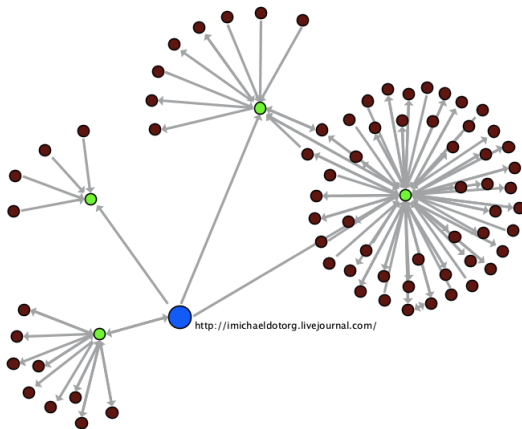
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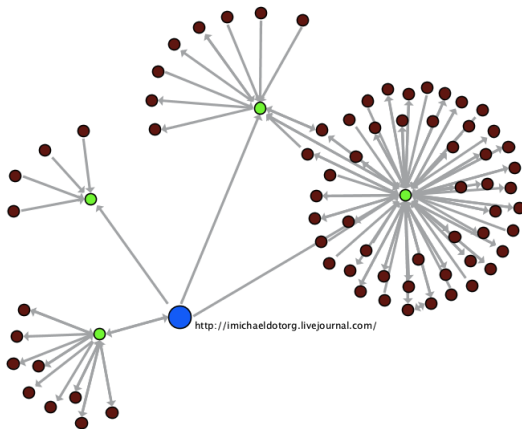
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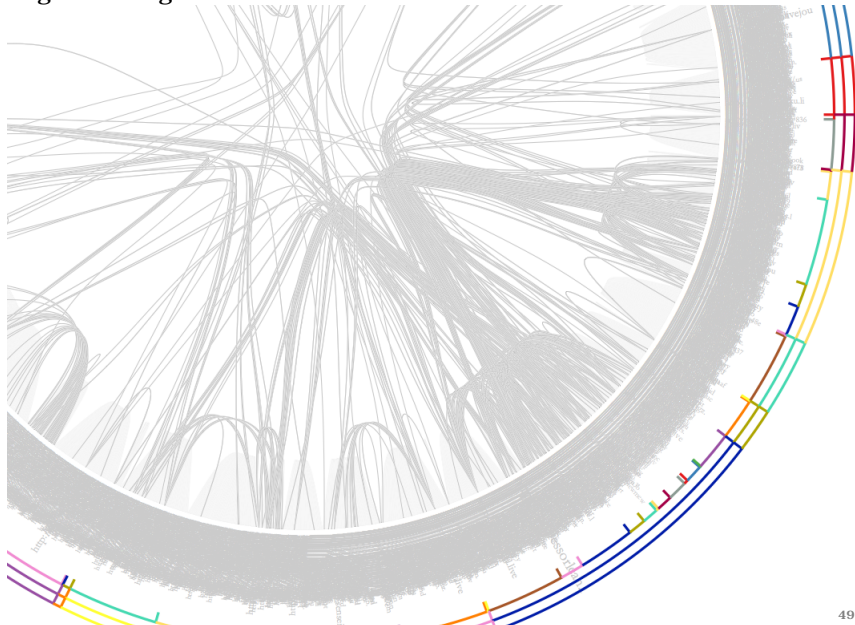
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- ▶ Large jump after first snowball
- ▶ Massive structural leap at k = 3



The full network

To get a feeling for the size of the full network...



The `dict` type is a data structure that represents a `key`→`value` mapping

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Working with the `dict` type

Keys and values can be of any data type

```
»> fruit_dict = {"apple": 1, "orange": [0.23, 0.11], "banana": True }
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The `dict` type is a data structure that represents a key→value mapping

Working with the `dict` type

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# Keys and values can be of any data type
>>> fruit_dict={"apple": 1, "orange": [0.23, 0.11], "banana": True }

# Can retrieve the keys and values as Python lists (vector)
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- ▶ This is particularly useful when performing analysis on networks, where node labels are natural keys

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Now, try creating a `dict` of your own

From the documentation...

networkx.closeness centrality

```
closeness centrality(G, v=None, weighted_edges=False)
```

Compute closeness centrality for nodes.

Closeness centrality at a node is 1/average distance to all other nodes.

Parameters: **G** : graph

A networkx graph

v : node, optional

Return only the value for node v.

weighted_edges : bool, optional

Consider the edge weights in determining the shortest paths. If False, all edge weights are considered equal.

Returns: **nodes** : dictionary

Dictionary of nodes with closeness centrality as the value.

NetworkX's metric's make extensive use of the dict type

- In this case the key→value mapping is of the form: {node-label : metric}

Let's look at an example:

```
>>> in_cen=nx.in_degree_centrality(hartford)
>>> in_cen
{1: 0.014218009478672987, 2: 0.018957345971563982, ...
...
90: 0.0047393364928909956, 293: 0.0}
```

We can see that node #90 has in-degree centrality 0.0047

- But we can do so much more!

For our first analysis in NetworkX, we will do some basic network manipulation, then run multiple measures to find highest centrality nodes

- First, we will need to convert to an undirected network, and extract the main component

```
# Many of the centrality metrics require undirected graphs, so we will symmetrize
>> hartford-ud=hartford.to-undirected()
# The network also has many small components, but for
# this analysis we are interested in the largest
>> hartford-mc=hartford-main=nx.connected-component-subgraphs(hartford-ud)[0]
```

Next, we will calculate multiple measures

```
# Betweenness centrality
>> bet-cen=nx.betweenness-centrality(hartford-mc)
# Closeness centrality
>> clo-cen=nx.closeness-centrality(hartford-mc)
# Eigenvector centrality
>> ei-g-cen=nx.eigenvector-centrality(hartford-mc)
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# Closeness centrality
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For our first analysis in NetworkX, we will do some basic network manipulation, then run multiple measures to find highest centrality nodes

- First, we will need to convert to an undirected network, and extract the main component

```
# Many of the centrality metrics require undirected graphs, so we will symmetrize
>> hartford-ud=hartford.to-undirected()
# The network also has many small components, but for
# this analysis we are interested in the largest
>> hartford-mc=hartford-main=nx.connected-component-subgraphs(hartford-ud)[0]
```

Next, we will calculate multiple measures

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Finding most central actors

To find the most central actors we will use Python's list comprehension technique to do basic data manipulation on our centrality dictionaries

```
def highest-centrality(cent-dict):  
    """Returns node key with largest value from  
    NX centrality dict"""  
    # Create ordered tuple of centrality data  
    cent-items=cent-dict.items()  
    # List comprehension!  
    cent-items=[(b, a) for (a, b) in cent-items]  
    # Sort in descending order  
    cent-items.sort()  
    cent-items.reverse()  
    return cent-items[0][1]
```

Now, just ask for the answer

Finding Most central actors

```
>>> print("Actor "+str(highest-centrality(bet-cen))+  
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Actor 82 has the highest Betweenness centrality
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List comprehension

- ▶ Given a dict: `d={1: 0.15, 2: 0.67}`
- ▶ `d.items()` → `[(1, 0.15), (2, 0.67)]`
- ▶ `d=[(b, a) for (a, b) in d]` →
`[(0.15, 1), (0.67, 2)]`

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Here, we use list comprehension in order to use Python's built-in sort and reverse list functions

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>> print("Actor "+str(highest-centrality(bet-ken))+ " has the highest Betweenness centrality")  
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One of the most popular network level statistical description of a network is its degree distribution

- ▶ In NetworkX this is a simply one-line operation

Get list of degree rank frequency

```
# Create a Barabasi - Albert network
>>> ba-net=barabasi-albert-graph(1000, 2)
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>>> dh=degree-histogram(ba-net)
```

Calculating degree distribution

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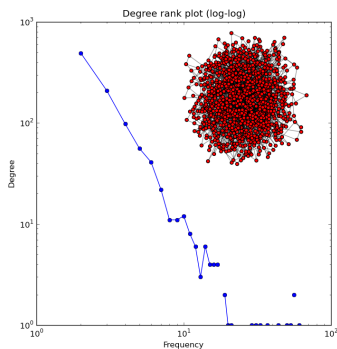
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- ▶ As we will see next, we can use `matplotlib` to take this data and create publication ready plots

- ▶ Ex. from <http://networkx.lanl.gov/examples/drawing/degree-histogram.html>



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- ▶ For each node find the fraction of possible triangles that exist, $c_v = \frac{2T(v)}{\deg(v)(\deg(v)-1)}$, where $T(v)$ is the number of triangles through node v .

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We will use clustering coefficients to identify community structure in the Hartford drug network

Toy community detection example (not a good one)

Calculating clustering coefficients

```
# Calculate clustering coefficients of each node (return as dict)
clus=clustering(hartford-mc, with-labels=True)
# Get counts of nodes membership for each clustering coefficient, and clean up
unique-clus=list(unique(clus.values()))
clus-counts=zip(map(lambda c: clus.values().count(c), unique-clus), unique-clus)
clus-counts.sort()
clus-counts.reverse()
# Create a subgraph from nodes with most frequent clustering coefficient
mode-clus-sg=subgraph(hartford-mc, [(a) for (a,b) in clus.items() if b==clus-counts[0][1]])
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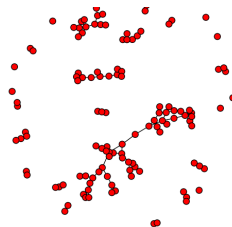
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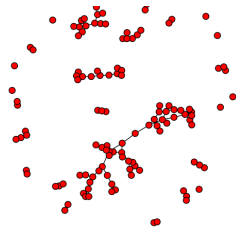


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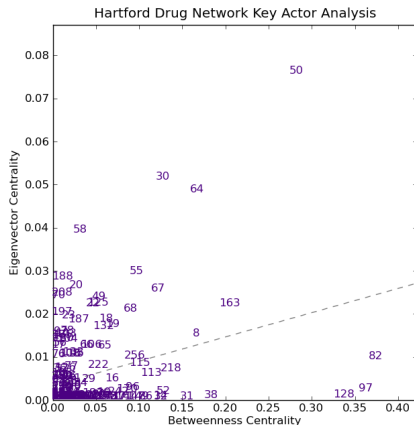
Later, we'll learn how to create a network visualization like the one above

Recall Python's scientific computing trinity: NumPy, SciPy and matplotlib

- ▶ **While NumPy and SciPy do most of the behind the scenes work, you will interact with matplotlib frequently for when doing network analysis**

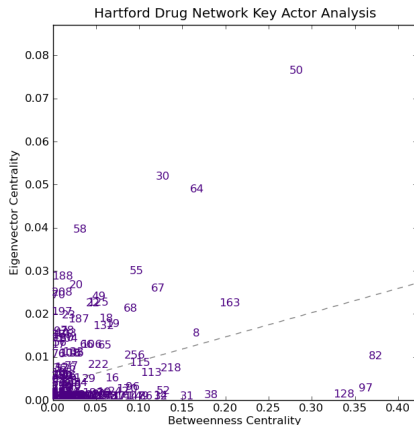
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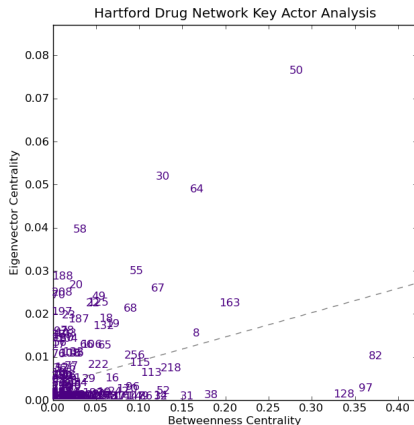
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We will need to create a function that takes two centrality dict and generates this plot

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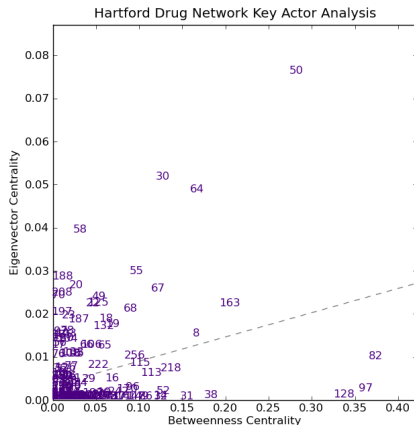


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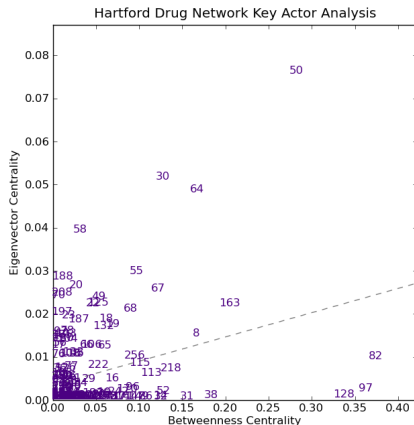


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1. Create a matplotlib figure
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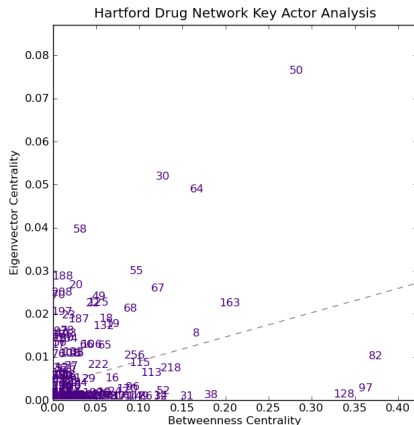


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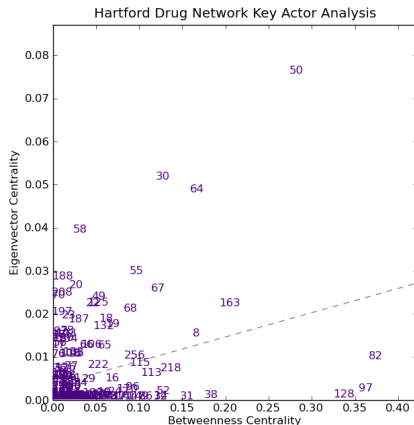


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We will need to create a function that takes two centrality dict and generates this plot

1. Create a matplotlib figure
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3. Add a "best fit" line
4. Add axis and title labels
5. Save figure as a PNG file

The centrality-scatter function, part one

```
def centrality_scatter(met_dict1, met_dict2, path="", ylab="", xlab="", title="", reg=False):
    # Create figure and drawing axis
    fig = P.figure(figsize=(7, 7))
    ax1 = fig.add_subplot(111)
    # Create items so actors can be sorted properly
    met_items1 = met_dict1.items()
    met_items2 = met_dict2.items()
    met_items1.sort()
    met_items2.sort()
    # Grab data
    xdata = [(b) for (a, b) in met_items1]
    ydata = [(b) for (a, b) in met_items2]
    # Add each actor to the plot by ID
    for p in xrange(len(met_items1)):
        ax1.text(x=xdata[p], y=ydata[p], s=str(met_items1[p][0]), color="indigo")
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- Create a canvas to draw on

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- ▶ manipulate and store centrality data

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- ▶ Create a canvas to draw on
- ▶ manipulate and store centrality data
- ▶ Add points to plot as node labels

The centrality-scatter function, part one

```
def centrality_scatter(met_dict1, met_dict2, path="", ylab="", xlab="", title="", reg=False):
    ...
    # If adding a best fit line, we will use NumPy to calculate the points.
    if reg:
        # Function returns y-intercept and slope. So, we create a function to
        # draw LOBF from this data
        slope, yint = polyfit(xdata, ydata, 1)
        xline = P.xticks()[0]
        yline = map(lambda x: slope*x + yint, xline)
        # Add line
        ax1.plot(xline, yline, ls='-', color='grey')
    # Set new x- and y-axis limits to data
    P.xlim((0.0, max(xdata) + (.15 * max(xdata)))) # Give a little buffer
    P.ylim((0.0, max(ydata) + (.15 * max(ydata))))
    # Add labels
    ax1.set_title(title)
    ax1.set_xlabel(xlab)
    ax1.set_ylabel(ylabel)
    # Save figure
    P.savefig(path, dpi=100)
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- Add a best fit line

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    ax1.set_title(title)
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    ax1.set_ylabel(ylabel)
    # Save figure
    P.savefig(path, dpi=100)
```

- ▶ Add a best fit line
- ▶ Resize figure to fit data

The centrality-scatter function, part one

```
def centrality_scatter(met_dict1, met_dict2, path="", ylab="", xlab="", title="", reg=False):
    ...
    # If adding a best fit line, we will use NumPy to calculate the points.
    if reg:
        # Function returns y-intercept and slope. So, we create a function to
        # draw LOBF from this data
        slope, yint = polyfit(xdata, ydata, 1)
        xline = P.xticks()[0]
        yline = map(lambda x: slope*x+yint, xline)
        # Add line
        ax1.plot(xline, yline, ls='-', color='grey')
    # Set new x- and y-axis limits to data
    P.xlim((0.0, max(xdata)+(.15*max(xdata)))) # Give a little buffer
    P.ylim((0.0, max(ydata)+(.15*max(ydata))))
    # Add labels
    ax1.set_title(title)
    ax1.set_xlabel(xlab)
    ax1.set_ylabel(ylabel)
    # Save figure
    P.savefig(path, dpi=100)
```

- ▶ Add a best fit line
- ▶ Resize figure to fit data
- ▶ Add labels, and save the figure as a PNG file

As powerful as NetworkX and the complementing scientific computing packages in Python are, it may often be useful or necessary to output your data for additional analysis

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Next, we will review how to save data in different formats and export metrics to a CSV file using the Hartford drug net data

The syntax for exporting network data follows exactly the syntax for loading it

NX syntax for writing a network file

```
>>> nx.write_format(G, "path/to/file.txt", ...options...)
      ↑           ↑           ↑
    NX function, net variable  File to be written  Nodes/edge data, etc.
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Saving network data in different formats

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NX syntax for writing a network file

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```

 ↑ ↑ ↑

 NX function, net variable File to be written Nodes/edge data, etc.

Let's try!

- ▶ Output the Hartford drug net data as an adjacency list
- ▶ Add metric data to each node of the network
- ▶ Output new network in Pajek format with node attributes

As shown, this is a simple one line operation

Output Hartford drug net data as an adjacency list

```
nx.write_adjlist(hartford_mc, "../data/hartford-mc-adj.txt")
```

Next, we will add the Eigenvector centrality of each node to the graph object

Adding node attributes

```
def add_metric(G, met_dict):  
    """Adds metric data to G from a dictionary keyed by node labels"""  
    if(G.nodes().sort()==met_dict.keys().sort()):  
        for i in met_dict.keys():  
            G.add_node(i, metric=met_dict[i])  
        return G  
    else:  
        raise ValueError("Node labels do not match")
```

As shown, this is a simple one line operation

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```

- ▶ Quick error checking
- ▶ Add node attribute as “metric”

Python has powerful built-in tools for reading and writing standard data formats

- ▶ One of the most useful, and frequently used, is the CSV library and the `Dic tWri ter`

```
import csv
...
def csv_exporter(data_dict, path):
    """Takes a dict of centralities keyed by column headers and exports
    data as a CSV file"""
    # Create column header list
    col_headers=["Actor"]
    col_headers.extend(data_dict.keys())
    # Create CSV writer and write column headers
    writer=csv.DictWriter(open(path, "w"), fieldnames=col_headers)
    writer.writerow(dict((h, h) for h in col_headers))
    # Write each row of data
    for j in data_dict[col_headers[1]].keys():
        # Create a new dict for each row
        row=dict.fromkeys(col_headers)
        row["Actor"]=j
        for k in data_dict.keys():
            row[k]=data_dict[k][j]
        writer.writerow(row)
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```

We can now open the CSV file in our favorite spreadsheet program

- ▶ Perform traditional data exploration
- ▶ Load into other analytics platforms for additional analysis (e.g., R)
- ▶ Store for latter use

	A	B	C	D
1	Actor	Closeness	Betweenness	Eigenvector
2	1	0.12467532	0.0072576	0.00025176
3	2	0.12475634	0.01767427	0.00025964
4	3	0.12565445	0.05687441	0.00023185
5	4	0.10223642	0.03108639	1.44E-05
6	5	0.1443609	0	0.00313152
7	6	0.09943035	0.01041667	1.49E-07
8	7	0.11340815	0.04362093	6.78E-05
9	8	0.20512821	0.16354003	0.01471888
10	9	0.11267606	0.00741624	0.0001101
11	10	0.13983977	0.05258239	0.00095456
12	11	0.1703638	0.01250999	0.0032333
13	13	0.13892909	0	1.79E-05
14	14	0.17219731	0.11848775	0.00029737
15	15	0.13521127	0.00079897	2.11E-05
16	16	0.15907208	0.06203647	0.00432838

What makes a good network visualization technique

Development of visualization techniques and algorithms has become somewhat of a cottage industry

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- ▶ Maximize “visibility” of network
- ▶ Scale up to very large graphs
- ▶ Display nodal- (centrality) of network-level (community structure) information

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NetworkX was designed as a data manipulation and analysis tool, and therefore is not meant as a visualization platform

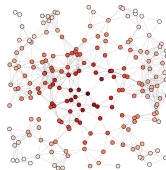
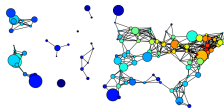
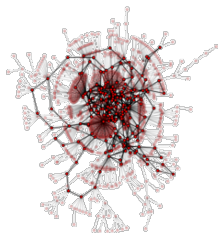
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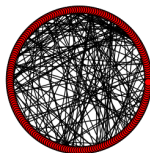
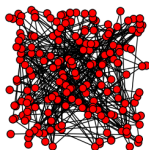
NetworkX was designed as a data manipulation and analysis tool, and therefore is not meant as a visualization platform

- ▶ **It is, however, still capable of making very nice visualization**



The most basic visualization techniques are the random and circular layouts

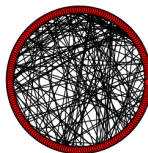
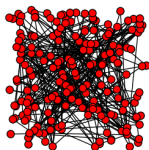
- ▶ The random layout places nodes in...random positions
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```
# Use subplots to draw random and circular layouts
# of drug net side-by-side
fig1=P.figure(figsize=(9, 4))
fig1.add_subplot(121)
nx.draw_random(hartford-mc, with_labels=False, node_size=60)
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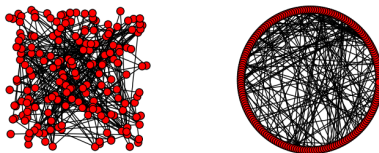
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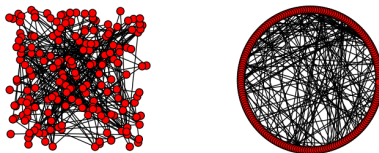
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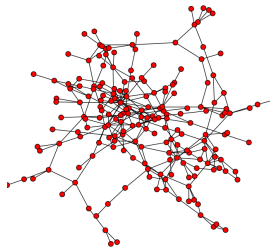


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More commonly used visualization techniques include the spring and spectral layouts

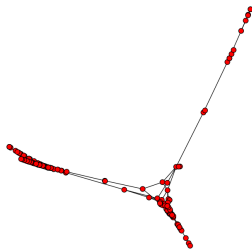
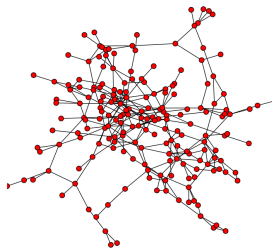
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- ▶ The spring layout is a version of the Fruchterman-Reingold force-directed algorithm, which attempts to minimize overlapping edges
- ▶ The spectral layout finds node position using the eigenvectors of the graph Laplacian, which is useful for quickly visualizing structural clustering



The shell layout draws nodes as concentric circles

- ▶ Two dimensional extension of the circle layout
- ▶ We may have some reason to isolate certain nodes

25th percentile Eigenvector centrality actors

```
P.figure(figsize=(8, 8))
# Find actors in 25th percentile
max_eig=max([(b) for (a, b) in eig_cen.items()])
s1=[(a) for (a, b) in eig_cen.items() if b>=.25*max_eig]
s2=hartford_mc.nodes()
# setdiff1d is a very useful NumPy function!
s2=list(setdiff1d(s2, s1))
shell_s=[s1, s2]
# Calculate position and draw
shell_pos=shell_layout(hartford_mc, shell_s)
draw_networkx(hartford_mc, shell_pos, with_labels=False, node_size=60)
P.savefig("../images/networks/shell.png")
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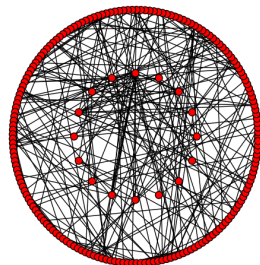
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max_eig=max([(b) for (a, b) in eig_cen.items()])
s1=[(a) for (a, b) in eig_cen.items() if b>=.25*max_eig]
s2=hartford_mc.nodes()
# setdiff1d is a very useful NumPy function!
s2=list(setdiff1d(s2, s1))
shells=[s1, s2]
# Calculate position and draw
shell_pos=shell_layout(hartford_mc, shells)
draw_networkx(hartford_mc, shell_pos, with_labels=False, node_size=60)
P.savefig("../images/networks/shell.png")
```

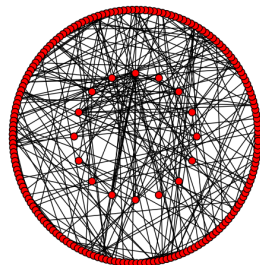


The shell layout draws nodes as concentric circles

- ▶ Two dimensional extension of the circle layout
- ▶ We may have some reason to isolate certain nodes

25th percentile Eigenvector centrality actors

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Beyond layout, we may also want to add analytical data to our visualization

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In our final exercise, we will add the following analysis to the Hartford drug network

- ▶ **Node size by Eigenvector centrality**
- ▶ **Intensity of node color by betweenness centrality**
- ▶ **Edge thickness by edge betweenness**

The code to add analysis to visualization

More list comprehension and matplotlib colormaps

```
# Adding analysis to visualization
P.figure(figsize=(15, 15))
P.subplot(111, axisbg="lightgrey")
spring_pos=nx.spring_layout(hartford_mc, iterations=1000)
# Use betweenness centrality for node color intensity
bet_color=bet_cen.items()
bet_color.sort()
bet_color=[(b) for (a, b) in bet_color]
# Use Eigenvector centrality to set node size
eig_size=eig_cen.items()
eig_size.sort()
eig_size=[((b)*2000)+20 for (a, b) in eig_size]
# Use matplotlib's colormap for node intensity
draw_networkx(hartford_mc, spring_pos, node_color=bet_color, ...
    ... cmap=P.cm.Greens, node_size=eig_size, with_labels=False)
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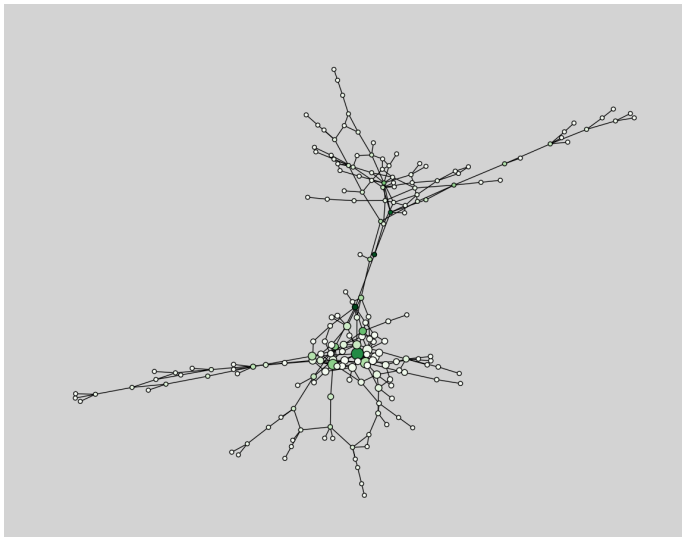
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Final visualization



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Questions?