Module IV - Basic Analysis

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

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- Writing network data
- Saving network analysis statistics

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

Loading a network file

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

$$\underset{\text{Net variable}}{\underset{\uparrow}{>>> G}} \quad = \quad \underset{\text{NX function, file directory path}}{\underset{\uparrow}{\text{nx.read\_format(“path/to/file.txt”,}}} \qquad \underset{\text{Graph type, nodes type, etc.}}{\underset{\uparrow}{\textit{...options...})}}$$

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Let's try!

- We will load the edge list of Hartford drug users network
- Specify that the network be a directed graph, and the nodes be integers
- Use `nx.info()` to check that data has been loaded correctly

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:                   DiGraph
Number of nodes:        212
Number of edges:        337
Average in degree:      1.5896
Average out degree:     1.5896
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What did we just do?

- Used the `read_edgelist` function to load EL file

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What did we just do?

- Used the `read_edgelist` function to load EL file
- Specified path to Hartford drug users file

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What did we just do?

- 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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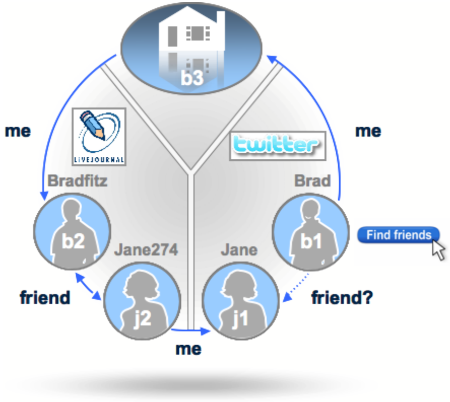
Some formats may have more or less options, **always check the documentations!**

Building the social network among LiveJournal users



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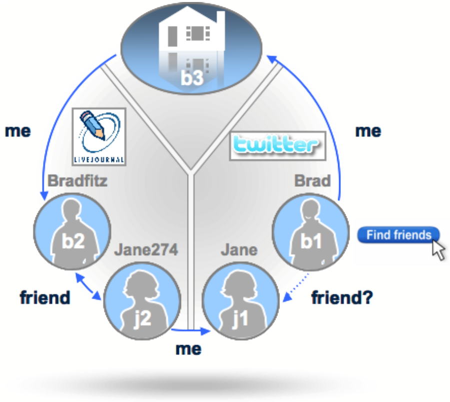

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- In Python, use `NetworkX`, `cjson` and a other standard scientific libraries to parse Google's SocialGraph data

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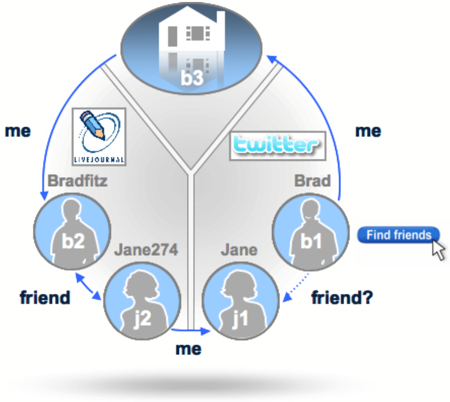

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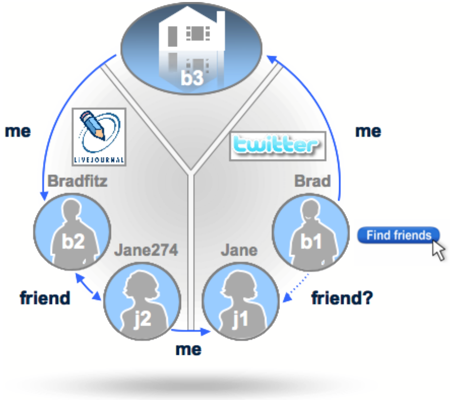

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- In Python, use `NetworkX`, `cjson` and a other standard scientific libraries to parse Google's SocialGraph data
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- Through a process called "k-snowball searching" $seed \longrightarrow friend \longrightarrow \cdots \longrightarrow friend_k$

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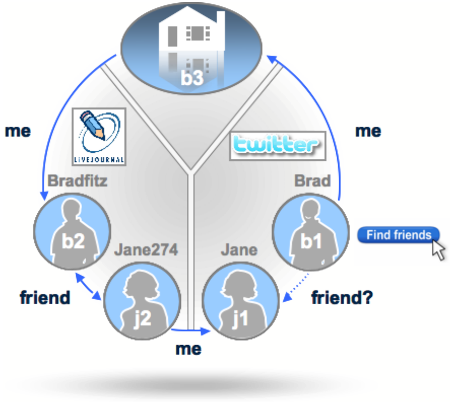

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  - Seed: imichaeldotorg.livejournal.com
  - $k = 3$

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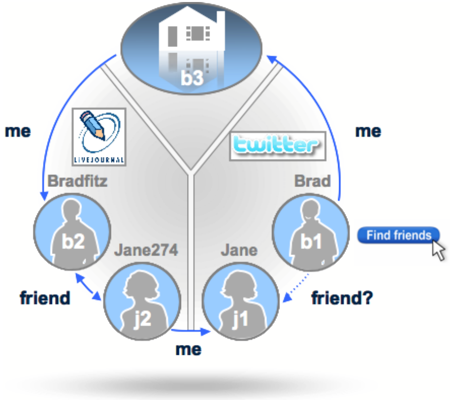

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- Through a process called "k-snowball searching" $seed \longrightarrow friend \longrightarrow \cdots \longrightarrow friend_k$
  - Seed: imichaeldotorg.livejournal.com
  - $k = 3$
- Note the low value of k

The code, part 1

Loading the libraries and scraping egonet

```
from cjson import *
from urllib import *
from time import *
from scipy import array,unique
...
if __name__ == "__main__":
    seed="imichaeldotorg"
    seed_url="http://"+seed+".livejournal.com"
    # 3.1 Scrape, parse and build seed's ego net
    sg=get_sg(seed_url)
    net,newnodes=create_egonet(sg)
    nx.write_pajek(net,"../../data/"+seed+"_ego.net")
    nx.info(net)
```

```
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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```
Name:                  ['http://imichaeldotorg.livejournal.com/']
Type:                  DiGraph
Number of nodes:       5
Number of edges:       5
Average in degree:     1.0
Average out degree:    1.0
```

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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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Step	Nodes	Edges	Mean Degree	Density
Seed	5	5	2.0	0.25
$k = 2$	75	115	3.0	0.02
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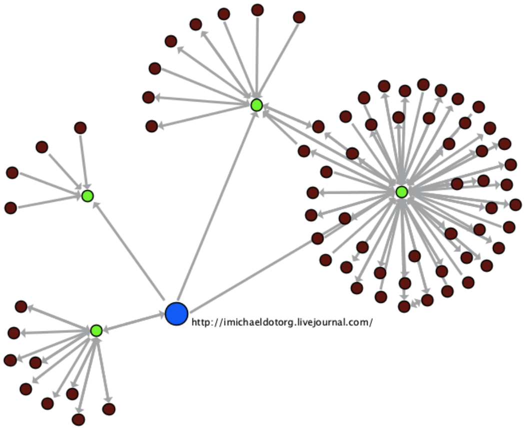

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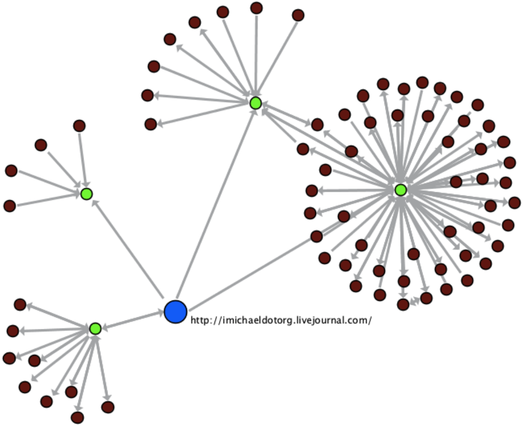
- Massive structural leap at $k = 3$



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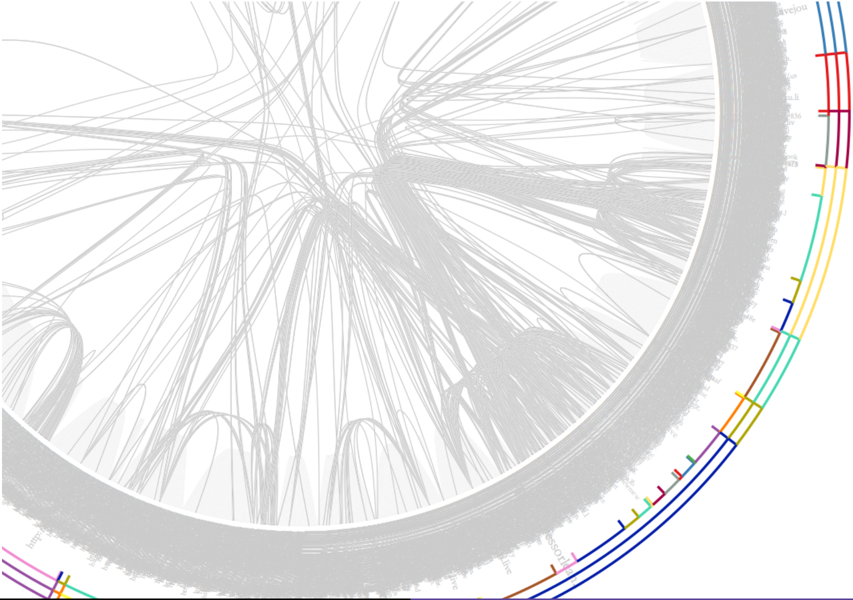
To get a feeling for the size of the full network...



Python Dictionaries

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Working with the dict type

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Now, try creating a `dict` of your own

Using dictionaries for network analysis

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!

Running multiple measures

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
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# Eigenvector centrality
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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))+" has the highest Betweenness centrality")
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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Calculating degree distribution

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

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# Create a Barabasi-Albert network
>>> ba_net=barabasi_albert_graph(1000,2)
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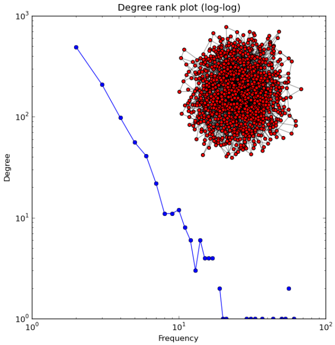
- As we will see next, we can use matplotlib to take this data and create publication ready plots
- Ex. from http://networkx.lanl.gov/examples/drawing/degree_histogram.html



Calculating basic community structure

Often in network analysis we are interested in estimating the cohesiveness of a network, or the communities that exists within the structure

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- Maximal cliques are the largest complete subgraph containing a given point. There are several algorithms for finding cliques, including Bron Kerbosch (1973), Tomita, Tanaka and Takahashi (2006), Cazals and Karande (2008)

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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()
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# 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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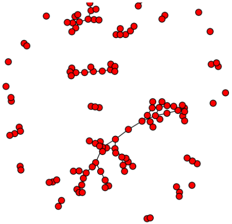

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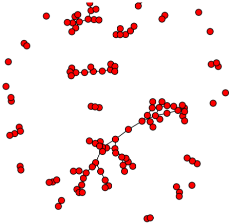

Later, we'll learn how to create a network visualization like the one above

Introduction to `matplotlib`

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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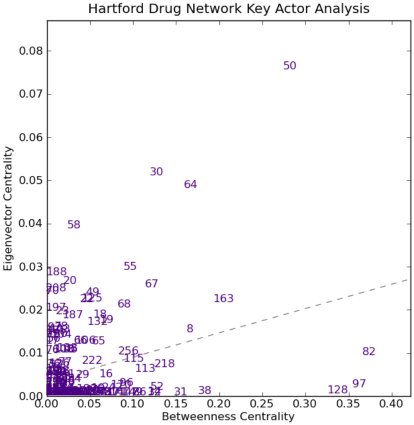

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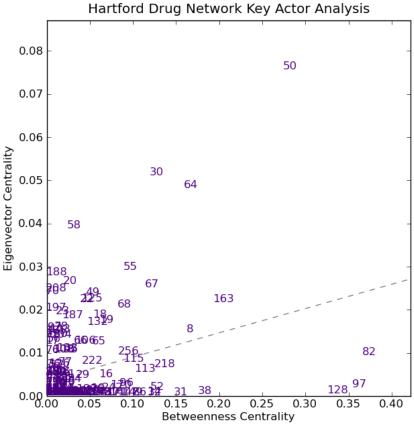

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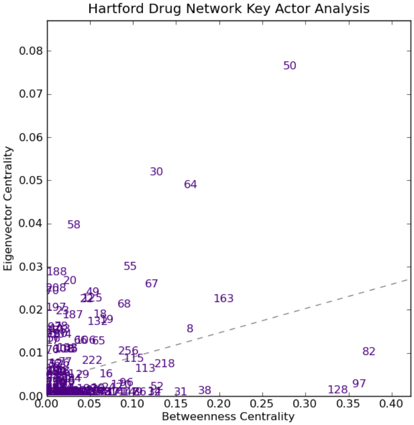

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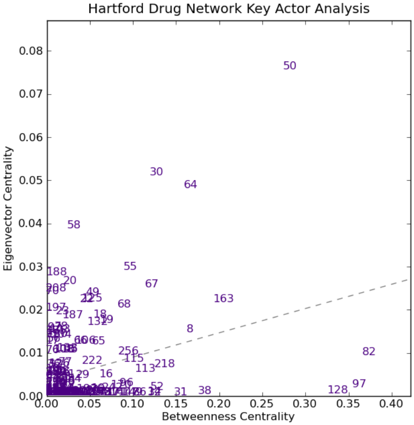

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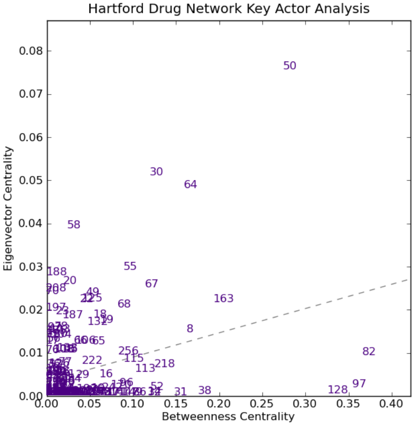

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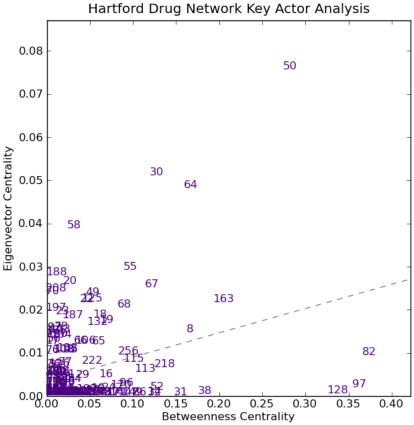

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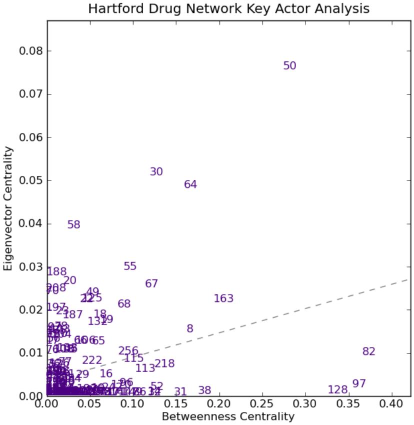

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3. Add a "best fit" line
4. Add axis and title labels
5. Save figure as a PNG file

Creating a key actor plot in matplotlib

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]
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    # Add each actor to the plot by ID
    for p in xrange(len(met_items1)):
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- Create a canvas to draw on
- manipulate and store centrality data
- Add points to plot as node labels

Creating a key actor plot in matplotlib

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(ylab)
    # Save figure
    P.savefig(path,dpi=100)
```

Creating a key actor plot in matplotlib

The centrality_scatter function, part one

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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(ylab)
    # Save figure
    P.savefig(path,dpi=100)
```

- Add a best fit line

Creating a key actor plot in matplotlib

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- 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

Exporting network data and analytics

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3. Depending on your needs you may prefer one, the other or both

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

Saving network data in different formats

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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- "path/to/file.txt", ↑ File to be written
- *...options...*) ↑ 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

Saving network data and adding 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")
```

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

Using the Python CSV library

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 DictWriter

```
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
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```

The results of CSV export

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	Betweeness	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

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

What makes a good network visualization technique

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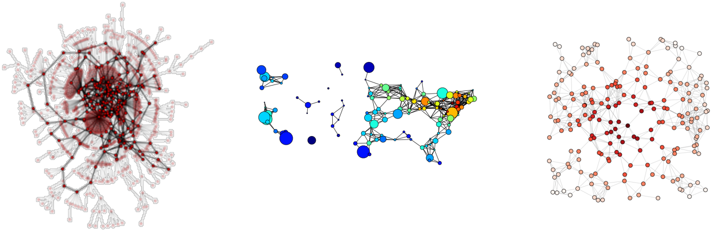
`NetworkX` was designed as a data manipulation and analysis tool, and therefore is not meant as a visualization platform

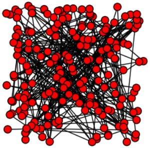
- It is, however, still capable of making very nice visualization

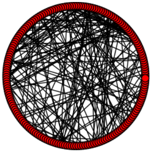


Visualization algorithms in NetworkX - Random & Circle

The most basic visualization techniques are the random and circular layouts

- The random layout places nodes in...random positions
- The circular layout places nodes in...a circle





```
# 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)
fig1.add_subplot(122)
nx.draw_circular(hartford_mc,with_labels=False,node_size=60)
P.savefig("../../images/networks/rand_circ.png")
```

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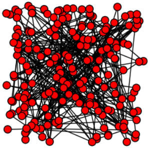

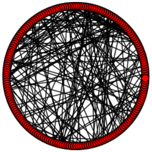

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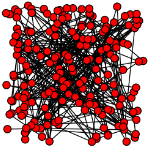

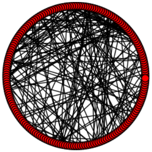

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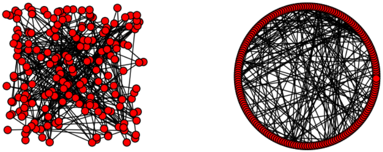

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Visualization algorithms in NetworkX - Spring & Spectral

More commonly used visualization techniques include the spring and spectral layouts

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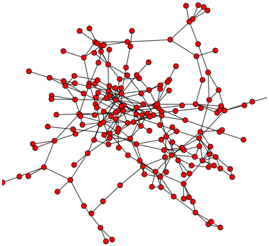
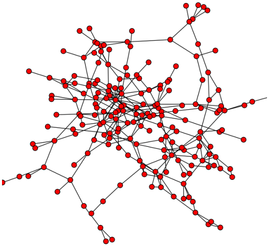
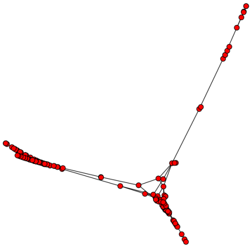


More commonly used visualization techniques include the spring and spectral layouts

- 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





Visualization algorithms in NetworkX - Shell

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))
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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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))
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")
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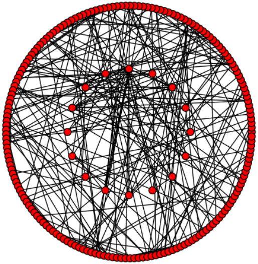

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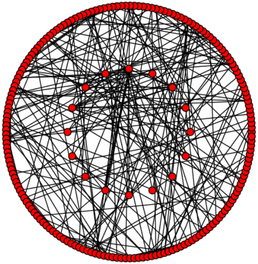

Beyond layout, we may also want to add analytical data to our visualization

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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 betweeneess 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,...
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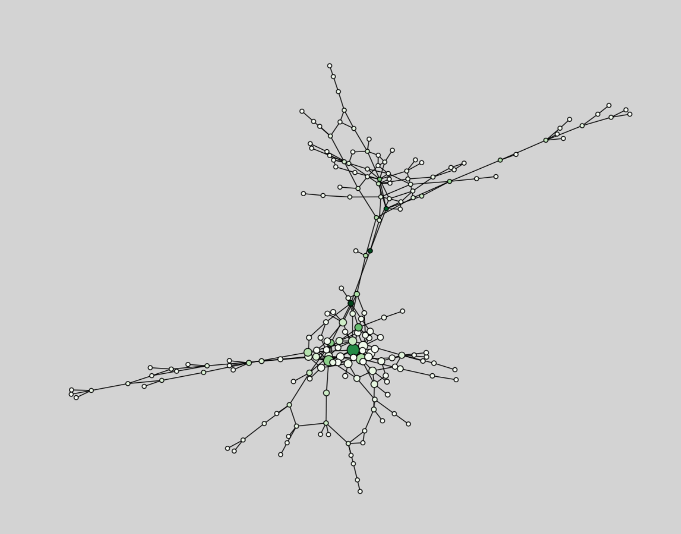
Final visualization



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Questions?