Scientific Computation

Spring, **2019**

Lecture 6

- "Naive" approach:
 - Loop through S one character at a time
 - Check for matches with P one character at a time (breaking this check after first mismatch
 - What is the cost?
 - Worst-case, O(MN) operations
 - (How) can we do better?
 - Binary search?
 - N log₂N to sort
 - Then log₂(N) for each search
 - But this requires storing N length-M strings/arrays
 - Hash table? Faster, but still with wasteful memory usage

- A (partial) solution:
 - Use a rolling hash function
 - Compute hash for pattern, P
 - Then apply function sequentially to each length-M substring in S
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 - And memory usage will also be O(M+N)

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- What is a rolling hash function?
 - First, genetic sequences can be rewritten in base 4
 - A=0, C=1, G=2, T=3
 - A simplistic function convert sequence from base 4 to base
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 - Example: S = GCTAT = 21303 $H(S) = 2*4^4 + 1*4^3 + 3*4^2 + 0*4^1 + 3$
 - Or more generally, evaluate a M-1th-order polynomial for each length-M substring of S

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 - This doesn't really help O(M) operations for all (N-M) substrings
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- Need to think about computing hash of consecutive sub-strings
- Let S_i be the ith length-M sub-string in S
- And H(S_i) is computed as before:

$$H(S_i) = S_{i,1} 4^{M-1} + S_{i,2} 4^{M-2} + ... + S_{i,M-1} 4 + S_{i,M}$$

Then:

$$H(S_{i+1}) = H(S_i)^*4 - S_{i,1}4^M + S_{i+1,M}$$

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- So, 4 rather than ~2M operations per hash evaluation (except i=1)
- Still have one potential problem when M is large, fast arithmetic can be a problem (this is programming language dependent)
 - Particularly important for problems in base-26 rather than base-4)
- Can alleviate this problem with modulo operator...

We have:

$$H(S_i) = S_{i,1} 4^{M-1} + S_{i,2} 4^{M-2} + ... + S_{i,M-1} 4 + S_{i,M}$$

$$H(S_{i+1}) = H(S_i)^* 4 - S_{i,1} 4^M + S_{i+1,M}$$

- **Define** $h(S_i) = H(S_i) \mod q$ with q a large prime number
- Use rules from modular arithmetic to simplify calculation of h:

$$h(S_i+1) = (h(S_i)^*4 - S_{i,1}(4^M \mod q) + S_{i+1,M}) \mod q$$

How does this look in Python?

We have:

$$H(S_i) = S_{i,1} 4^{M-1} + S_{i,2} 4^{M-2} + ... + S_{i,M-1} 4 + S_{i,M}$$

$$H(S_{i+1}) = H(S_i)^* 4 - S_{i,1} 4^M + S_{i+1,M}$$

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```
h(S<sub>i</sub>+1) = (h(S<sub>i</sub>)*4 - S<sub>i,1</sub> (4<sup>M</sup> mod q) + S<sub>i+1,M</sub>) mod q

bm = (4**m) % q

for ind in range(1,n-m+1):

    #Update fingerprint
    hi = (4*hi - int(S[ind-1])*bm + int(S[ind-1+m])) % q

if hi==hp: #If fingerprints match, check if strings match
    if match(S[ind:ind+m],P): imatch.append(ind)
```

Notes:

- hp is the hash for the pattern and has been pre-computed
- As has hi for ind=0
- Function match uses a naïve search to check if substrings S and P match
- Worst-case cost for Rabin-Karp is O(NM) (why?)
- Benefits from R-K will be seen when there are many "near-misses", i.e. many substrings 1st x letters match the pattern with x close to but less than m

- Rabin-Karp is one of several algorithms that have been developed for string matching
- It isn't "too" old introduced in 1987
- There are many applications outside of bioinformatics
 - Plagiarism detection
 - "Find" function in software applications

Complex networks

Today:

- Basics of network science
- Using networkx package in python

Networks

Examples of significant networks include:

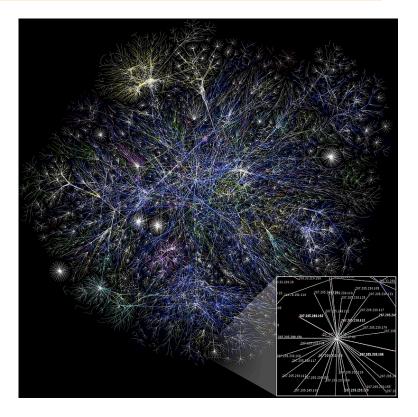
Social networks

World-wide web

Internet

Air transportation network

Cellular network

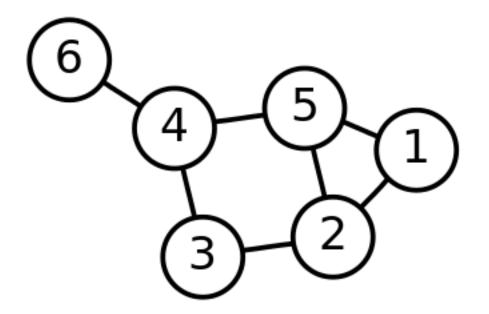


https://en.wikipedia.org/wiki/Complex_network

The science of networks is an important, rapidly growing field

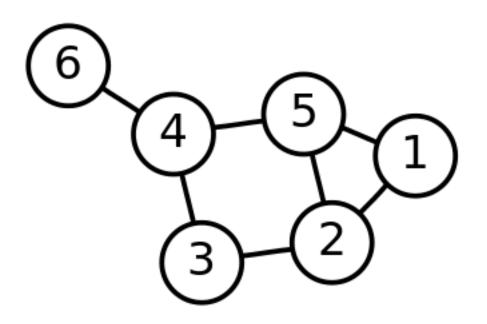
- A network has N nodes and L links between nodes
- Each node has a label, e.g. 1, 2, ..., N
- Then a link between node i and j can be represented simply as (i, j)

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Example: 6 nodes, 7 links Node one has two edges: (1,2) and (1,5)

The graph can be represented by the *adjacency matrix*, A A_{ij}=1 if there is link between nodes i and j

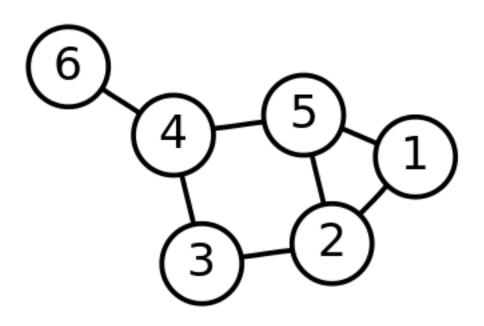


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The graph can be represented by the *adjacency matrix*, A A_{ij}=1 if there is link between nodes i and j

$$\begin{pmatrix} 0 & 1 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \end{pmatrix}$$

A is symmetric.



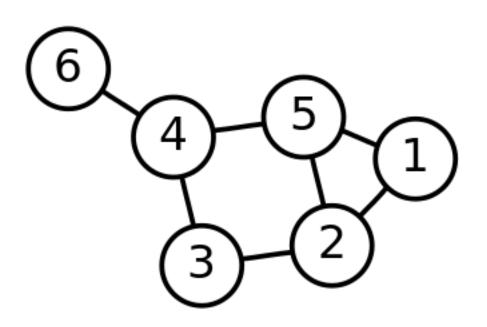
Can also represent connected portions of graph with edge list:

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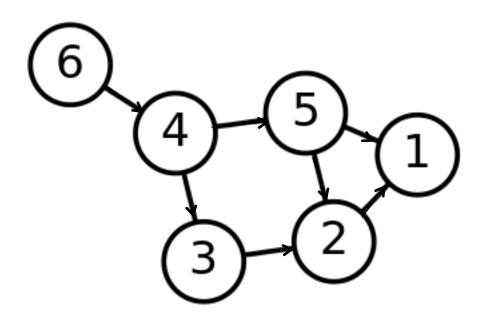


The degree of a node is the the total number of links connected to it:

$$q_1 = 2, q_5 = 3, ...$$

The degree distribution, P(q) is particularly important. P(q) is the fraction of nodes in the graph with degree = q

$$P(1) = 1/6, P(2) = 2/6, P(3) = 3/6$$



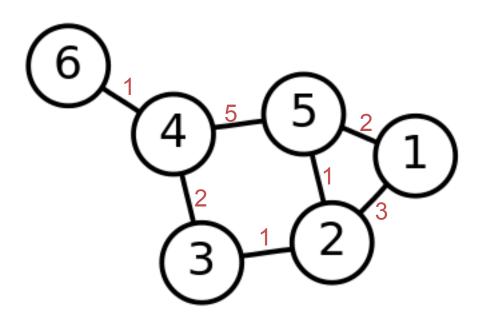
Networks can also be directed

Then

A_{ii}=1 if there is a link to i from j

$$\left(\begin{array}{ccccccc}
0 & 1 & 0 & 0 & 1 & 0 \\
0 & 0 & 1 & 0 & 1 & 0 \\
0 & 0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0
\end{array}\right)$$

A is *not* symmetric.



Networks can be weighted (e.g. transportation networks)

$$\left(\begin{array}{ccccccccc}
0 & 3 & 0 & 0 & 2 & 0 \\
3 & 0 & 1 & 0 & 1 & 0 \\
0 & 1 & 0 & 2 & 0 & 0 \\
0 & 0 & 2 & 0 & 5 & 1 \\
2 & 1 & 0 & 5 & 0 & 0 \\
0 & 0 & 0 & 1 & 0 & 0
\end{array}\right)$$

- A is symmetric if network is undirected
- Network can be both directed and weighted

Network	Nodes	Links	Directed / Undirected	N	L	(K)
Internet	Routers	Internet connections	Undirected	192,244	609,066	6.34
www	Webpages	Links	Directed	325,729	1,497,134	4.60
Power Grid	Power plants, transformers	Cables	Undirected	4,941	6,594	2.67
Mobile-Phone Calls	Subscribers	Calls	Directed	36,595	91,826	2.51
Email	Email addresses	Emails	Directed	57,194	103,731	1.81
Science Collaboration	Scientists	Co-authorships	Undirected	23,133	93,437	8.08
Actor Network	Actors	Co-acting	Undirected	702,388	29,397,908	83.71
Citation Network	Papers	Citations	Directed	449,673	4,689,479	10.43
E. Coli Metabolism	Metabolites	Chemical reactions	Directed	1,039	5,802	5.58
Protein Interactions	Proteins	Binding interactions	Undirected	2,018	2,930	2.90

Table 2.1

Canonical Network Maps

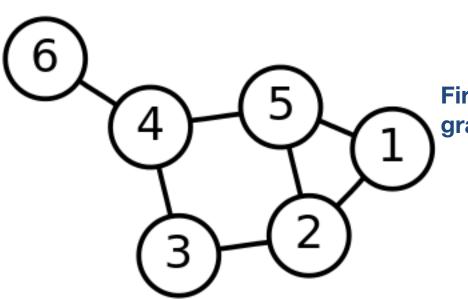
The basic characteristics of ten networks used throughout this book to illustrate the tools of network science. The table lists the nature of their nodes and links, indicating if links are directed or undirected, the number of nodes (N) and links (L), and the average degree for each network. For directed networks the average degree shown is the average in– or out–degrees $\langle k \rangle = \langle k_{in} \rangle = \langle k_{out} \rangle$ (see Equation (2.5)).

Generally interested in large complex networks

Analysis can be complicated and expensive (classical example: computing shortest path between nodes)

Networkx package provides a suite of tools for working with complex networks

More generally: avoid writing own code whenever possible!
Many powerful highly-efficient libraries are available



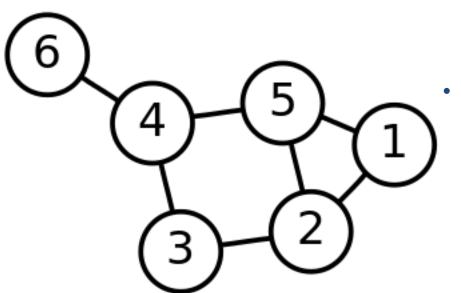
 Let's work with this network in networkx

First, import the module, and initialize a

graph:

In [55]: import networkx as nx

In [56]: G = nx.Graph()



- Let's work with this network in networkx
- First, import the module, and initialize a graph:

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ln [56]: G = nx.Graph()

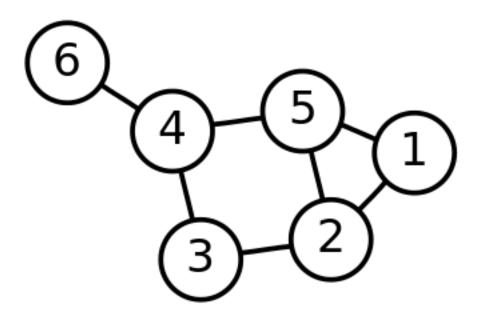
 There are numerous methods for building a graph

In [57]: G.add_edge(1,2)

In [58]: G.edges()
Out[58]: [(1, 2)]

In [59]: G.nodes()

Out[59]: [1, 2]



Can add several edges (or nodes) at once:

```
In [65]: e = [(1,5),(2,5),(2,3),(3,4),(4,5),(4,6)]
```

In [66]: G.add_edges_from(e)

In [67]: G.edges()

Out[67]: [(1, 2), (1, 5), (2, 3), (2, 5), (5, 4), (3, 4), (4, 6)]

In [68]: G.nodes()

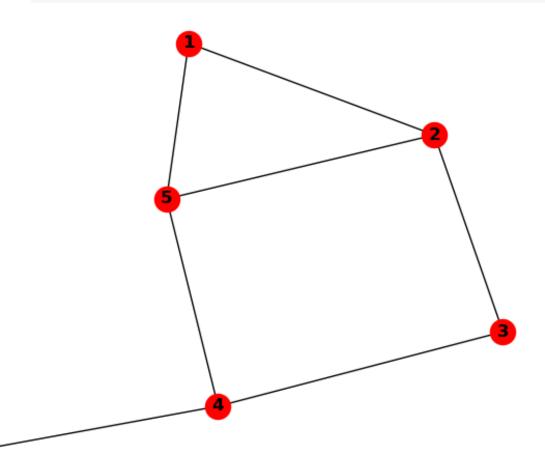
Out[68]: [1, 2, 5, 3, 4, 6]

Use nx.draw to visualize the network:

In [69]: figure()

Out[69]: <matplotlib.figure.Figure at 0x1515e3fef0>

In [70]: nx.draw(G, with_labels=True, font_weight='bold')



Can now analyze our graph:

```
In [74]: A = nx.adjacency_matrix(G)
In [75]: type(A)
Out[75]: scipy.sparse.csr.csr_matrix
In [76]: A.todense()
Out[76]:
matrix([[0, 1, 1, 0, 0, 0],
[1, 0, 1, 1, 0, 0],
[1, 1, 0, 0, 1, 0],
[0, 1, 0, 0, 1, 0],
[0, 0, 1, 1, 0, 1],
[0, 0, 0, 0, 1, 0]], dtype=int64)
```

Can now analyze our graph:

```
In [78]: G.adjacency_list()
Out[78]: [[2, 5], [1, 3, 5], [1, 4, 2], [2, 4], [3, 5, 6], [4]]

In [79]: G.nodes()
Out[79]: [1, 2, 5, 3, 4, 6]
```

- Adjacency list representation is much more efficient for sparse networks!
- Most complex networks are sparse

Can now analyze our graph:

```
In [83]: nx.degree histogram?
Signature: nx.degree_histogram(G)
Docstring:
Return a list of the frequency of each degree value.
Returns
hist: list
A list of frequencies of degrees.
The degree values are the index in the list.
In [84]: h = nx.degree histogram(G)
In [85]: h
Out[85]: [0, 1, 2, 3]
```

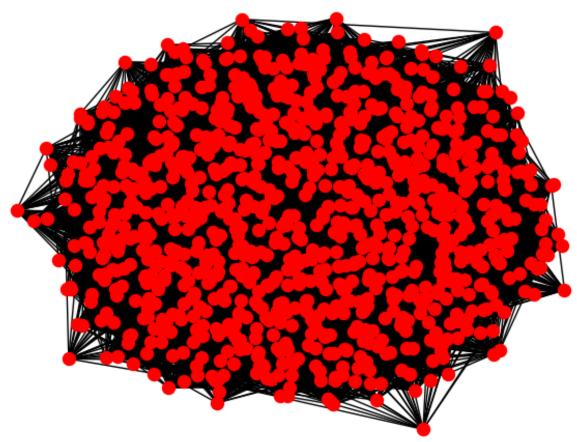
Graph has one degree-1 node, two degree-2 nodes, and three degree-3 nodes

Degree distribution is more interesting for large networks:

Erods-Renyi network
N nodes, a link is
placed between a pair
of nodes with
probability p:

In [119]: $Grandom = nx.gnp_random_graph(1000,0.05)$

In [120]: nx.draw(Grandom,node_shape='.')



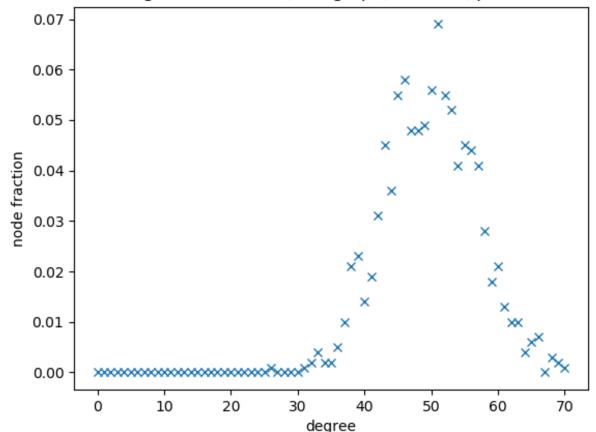
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Degree distribution follows the binomial distribution

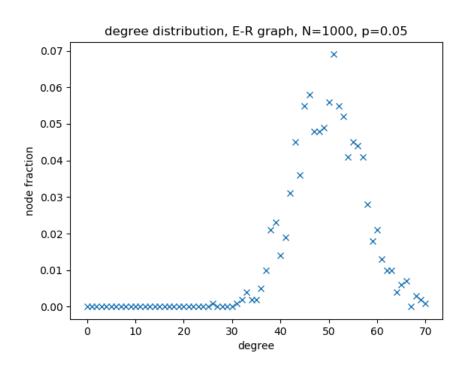
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degree distribution, E-R graph, N=1000, p=0.05



Degree distribution follows a binomial distribution:



- Should compute degree distributions for several graphs (with fixed N,P) and average
- Generally, when there is randomness in the problem, statistics are the quantities of interest (mean, variance, etc...)
- For large degree, distribution decays away exponentially – most real complex networks have large-degree hubs

- Two other important quantities are the clustering coefficient and shortest path
- Clustering coefficient for node i with degree q_i:
 C_i = # of links between neighbors/(q_i/2*(q_i-1))

```
In [16]: nx.clustering(G,500)
Out[16]: 0.044096728307254626
```

In [17]: nx.clustering(G,100)

Out[17]: 0.064646464646465

In [18]: nx.clustering(G,0)

Out[18]: 0.04645760743321719

For $G_{N,P}$ graph, expect $C_i = P$

- Two other important quantities are the clustering coefficient and shortest path
- Shortest path: find route between two nodes traversing fewest number of links

In [20]: nx.shortest_path(G,source=0,target=500)

Out[**20**]: [0, 233, 15, 500]

- Two other important quantities are the clustering coefficient and shortest path
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```
In [20]: nx.shortest_path(G,source=0,target=500)
Out[20]: [0, 233, 15, 500]
```

→ Very important in study algorithms (lectures 7+8)

Notes: GNP graph is not a good model for large complex networks

- Degree distribution should include large-degree nodes, power-law decay for large q
- Clustering coefficient should be large and the average degree should be small
- Will consider a more-realistic model in this week's lab

Networkx: getting started

- Read the online tutorial: https://networkx.github.io/documentation/stable/tutorial.html
- Browse through the online reference section: https://networkx.github.io/documentation/stable/reference/index.html
- Try out one or two graph generators
- Use networkx 2.x (I'm using 2.2)

Python notes

Main differences between arrays and lists:

Lists are *flexible*: heterogeneous data, can grow or shrink, numerical calculations can be slow/cumbersome

Arrays: calculations are generally faster, but elements must be homogeneous, difficult to adjust size