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Reading from data files: email, powergrid, protein

```
In [1]: import numpy as np;

meta = np.loadtxt('../networks/metabolic.edgelist.txt').astype(np.int64)
power = np.loadtxt('../networks/powergrid.edgelist.txt').astype(np.int64)
protein = np.loadtxt('../networks/protein.edgelist.txt').astype(np.int64)
```

Get adjacency matrices. No self-loop, multi-edge; undirected graphs used

DISCLAIMER: I followed the instructions word-by-word, and for some questions I went with my own interpretations while keeping original route for comparison purposes

```
In [2]: def build_matrix(x):
        a = np.zeros((np.amax(x)+1, np.amax(x)+1))
        for i in range(len(x)):
            a[x[i][0]][x[i][1]] = 1
        # undirected
        for i in range(len(a)):
            for j in range(len(a)):
                if i == j:
                    a[i][i] = 0
                elif a[i][j] != a[j][i]:
                    a[i][j] = 1
                    a[j][i] = 1
        return a
```

```
In [3]: a_meta = build_matrix(meta)
        a_power = build_matrix(power)
        a_protein = build_matrix(protein)
```

```
In [4]: def build_matrix_no_simp(x):
        a = np.zeros((np.amax(x)+1, np.amax(x)+1))
        for i in range(len(x)):
            a[x[i][0]][x[i][1]] = 1
        return a
```

```
In [5]: a_meta_original = build_matrix_no_simp(meta)
        a_power_original = build_matrix_no_simp(power)
        a_protein_original = build_matrix_no_simp(protein)
```

Question 1

a) degree distribution

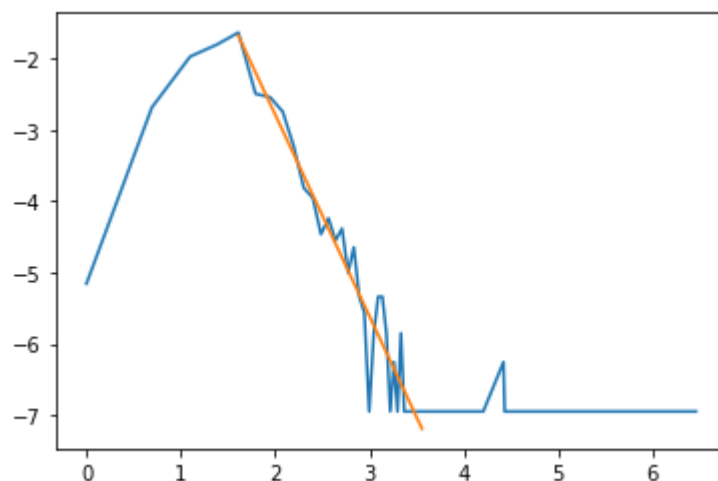
```
In [6]: import matplotlib.pyplot as plt
```

```
In [7]: def get_degree(a, m, begin, end):
    my_list = np.sort(np.sum(a, axis = 1)).tolist()
    freq = {}
    k = []
    v = []
    for items in my_list:
        freq[items] = my_list.count(items)
    for key, value in freq.items():
        k.append(key)
        v.append(value)
    v[:] = [x / sum(v) for x in v]
    x = np.log(k)
    y = np.log(v)
    fit = np.polyfit(x[begin:end], y[begin:end], m)
    print("Coefficients 'a' and 'b' for the linear equation y = ax +
b: ", fit)
    print("Degree distribution")
    x2 = x[begin:end]
    y2 = fit[0] * x2 + fit[1]
    plt.plot(x, y)
    plt.plot(x2, y2)
    plt.show()
```

Simplified graph

```
In [8]: get_degree(a_meta, 1, 4, 31)
```

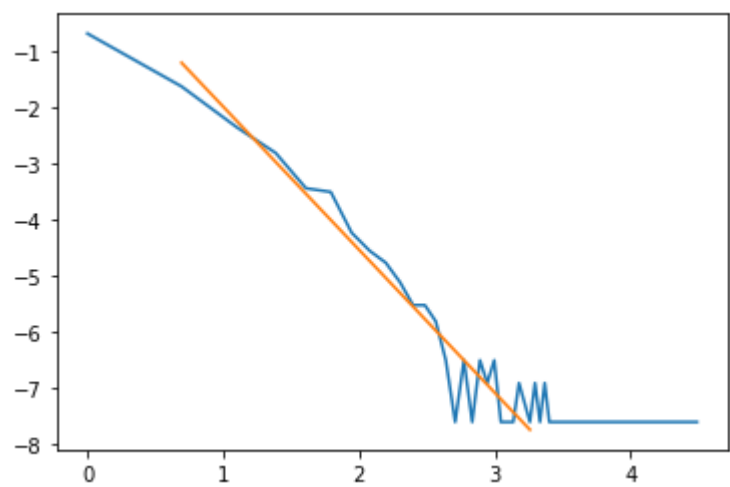
Coefficients 'a' and 'b' for the linear equation $y = ax + b$: [-2.83183691 2.88065408]
Degree distribution



```
In [9]: get_degree(a_protein,1, 2, 25)
```

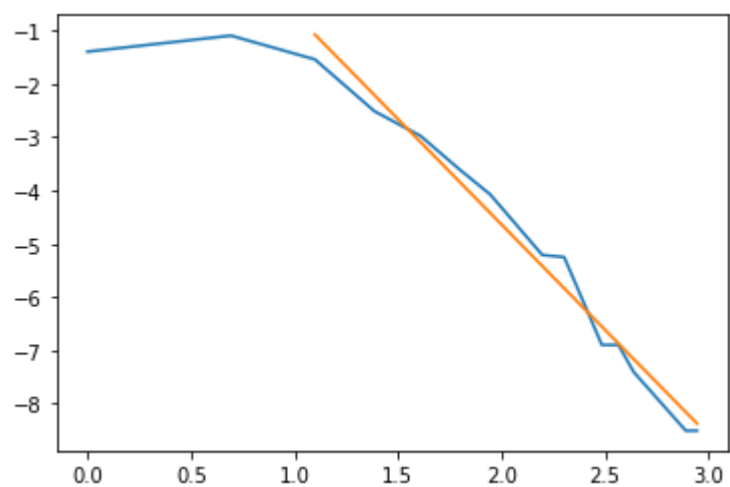
Coefficients 'a' and 'b' for the linear equation $y = ax + b$: [-2.54545078 0.54654605]
Degree distribution

/home/andybai/anaconda3/lib/python3.7/site-packages/ipykernel_launcher.py:12: RuntimeWarning: divide by zero encountered in log
if sys.path[0] == '':



```
In [10]: get_degree(a_power, 1,2,16)
```

Coefficients 'a' and 'b' for the linear equation $y = ax + b$: [-3.9535314 3.27040433]
Degree distribution

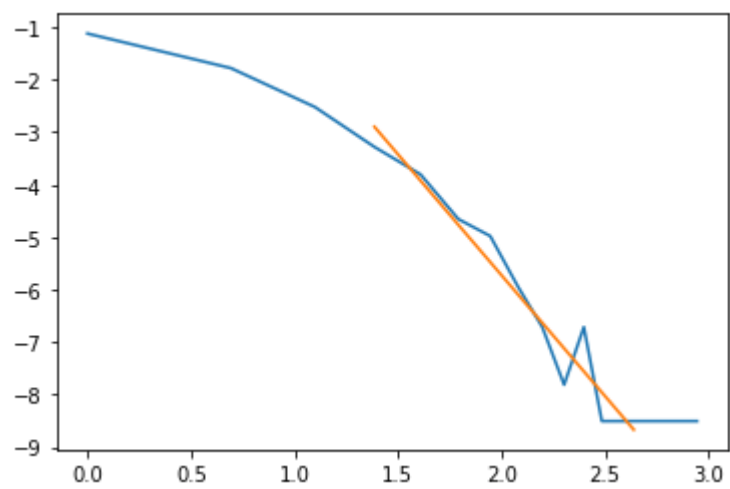


Original graph

```
In [11]: get_degree(a_power_original, 1, 4, 15)
```

Coefficients 'a' and 'b' for the linear equation $y = ax + b$: [-4.60809169 3.49206023]
Degree distribution

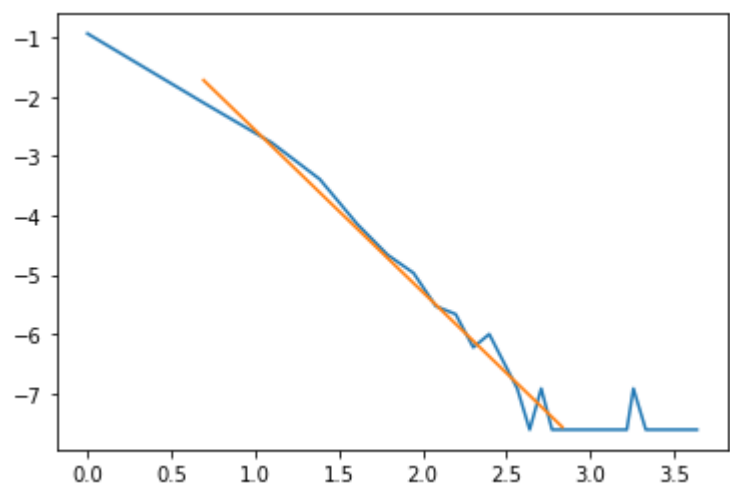
/home/andybai/anaconda3/lib/python3.7/site-packages/ipykernel_launcher.py:12: RuntimeWarning: divide by zero encountered in log
if sys.path[0] == '':



```
In [12]: get_degree(a_protein_original, 1, 2, 17)
```

Coefficients 'a' and 'b' for the linear equation $y = ax + b$: [-2.72861611 0.1674617]
Degree distribution

/home/andybai/anaconda3/lib/python3.7/site-packages/ipykernel_launcher.py:12: RuntimeWarning: divide by zero encountered in log
if sys.path[0] == '':

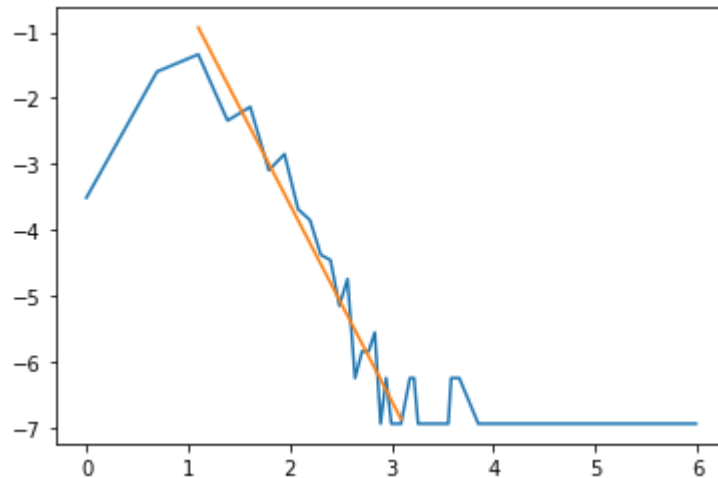


```
In [13]: get_degree(a_meta_original, 1, 3, 23)
```

```
/home/andybai/anaconda3/lib/python3.7/site-packages/ipykernel_launcher.py:12: RuntimeWarning: divide by zero encountered in log
  if sys.path[0] == '':
```

```
Coefficients 'a' and 'b' for the linear equation y = ax + b: [-2.984
36132  2.34978742]
```

Degree distribution



b) clustering coefficient distribution

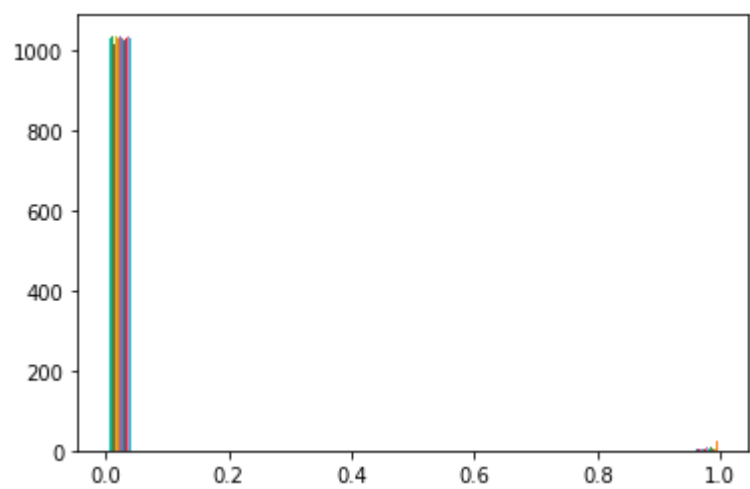
```
In [14]: def clustering_coeff(a):
    c_local = []
    a2 = a * a
    a3 = a2 * a
    a3_diag = np.diag(a3)
    trace = np.trace(a3)
    denom = np.sum(a2) - np.trace(a2)
    print("Total number triangles: ", trace/6)
    print("Global: ", trace/denom)
    degree = np.multiply(np.sum(a, axis = 0), np.sum(a, axis = 0) - 1
)
    degree2 = np.multiply(np.sum(a, axis = 1), np.sum(a, axis = 1) -
1)
    for i in range(len(degree)):
        if degree[i] == 0:
            c_local.append(0)
        else:
            c_local.append(a3_diag[i]/degree[i])
    print("Clustering coefficient, first 10: ", c_local[0:10])
    print("Max clustering coefficient: ", max(c_local))
    print("Min clustering coefficient: ", min(c_local))
    plt.hist(a, bins='auto')
    plt.show()
```

We can see that since the matrices are so sparse, the diagonal of A^3 is a vector of zeros. This means the clustering coefficients are zeros.

Simplified graphs

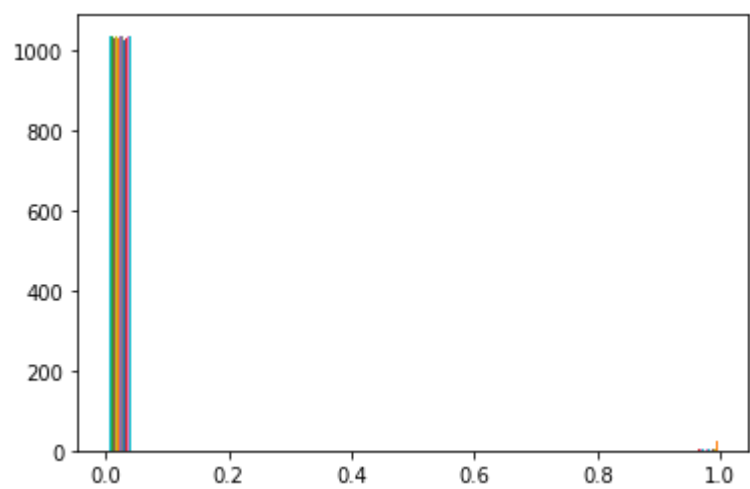
```
In [15]: clustering_coeff(a_meta)
```

Total number triangles: 0.0
Global: 0.0
Clustering coefficient, first 10: [0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
Max clustering coefficient: 0.0
Min clustering coefficient: 0.0



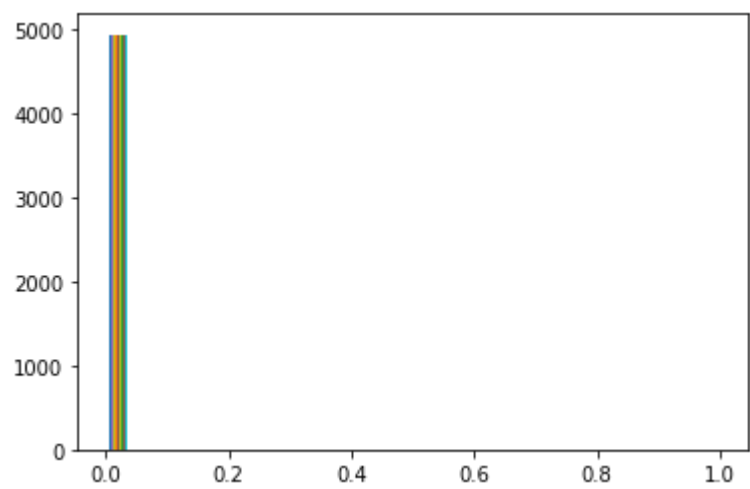
```
In [16]: clustering_coeff(a_meta_original)
```

Total number triangles: 0.0
Global: 0.0
Clustering coefficient, first 10: [0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
Max clustering coefficient: 0.0
Min clustering coefficient: 0.0



```
In [17]: clustering_coeff(a_power)
```

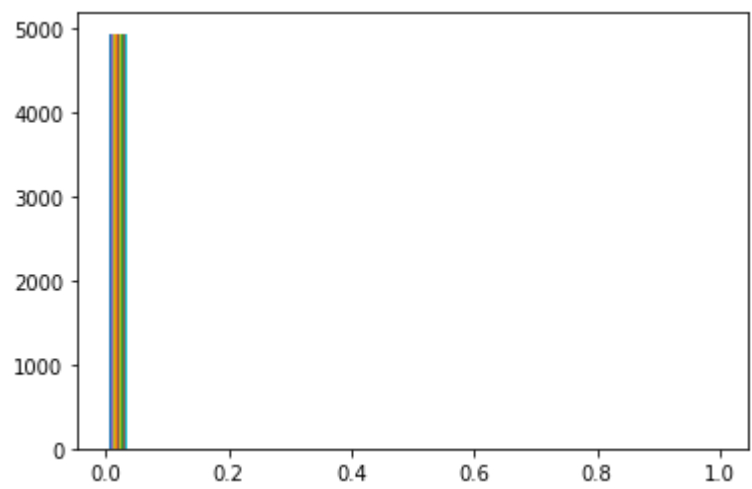
Total number triangles: 0.0
Global: 0.0
Clustering coefficient, first 10: [0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
Max clustering coefficient: 0.0
Min clustering coefficient: 0.0



Original graphs

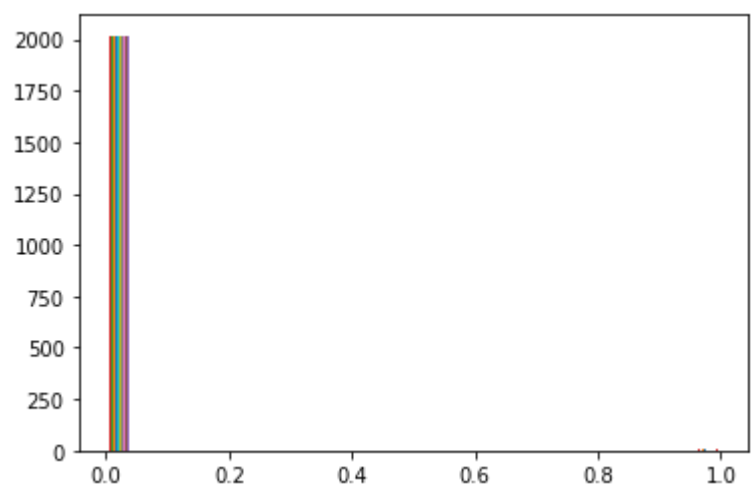
```
In [18]: clustering_coeff(a_power_original)
```

Total number triangles: 0.0
Global: 0.0
Clustering coefficient, first 10: [0, 0, 0, 0, 0, 0, 0, 0, 0.0, 0]
Max clustering coefficient: 0
Min clustering coefficient: 0



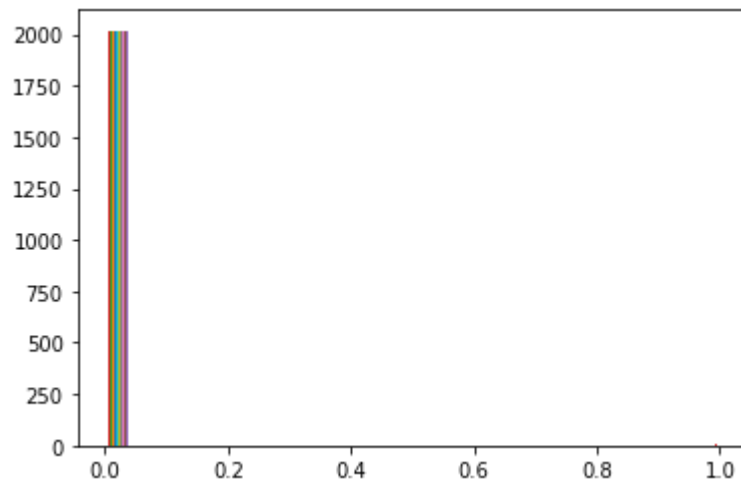
```
In [19]: clustering_coeff(a_protein)
```

Total number triangles: 0.0
Global: 0.0
Clustering coefficient, first 10: [0, 0, 0, 0, 0, 0, 0, 0, 0.0, 0]
Max clustering coefficient: 0
Min clustering coefficient: 0



```
In [20]: clustering_coeff(a_protein_original)
```

```
Total number triangles: 37.5  
Global: 0.08317929759704251  
Clustering coefficient, first 10: [0, 0, 0, 0, 0, 0, 0, 0, 0, 0]  
Max clustering coefficient: 0.5  
Min clustering coefficient: 0
```



For c) and d) I only did for the simplified graphs

c) shortest paths distribution

```
In [21]: from scipy.sparse import csr_matrix  
from scipy.sparse.csgraph import shortest_path  
from scipy.sparse.csgraph import breadth_first_order  
from scipy.sparse.csgraph import depth_first_order
```

```
In [22]: names = ['metabolism', 'powergrid', 'protein']  
simplified = [a_meta, a_power, a_protein]  
original = [a_meta_original, a_power_original, a_protein_original]
```

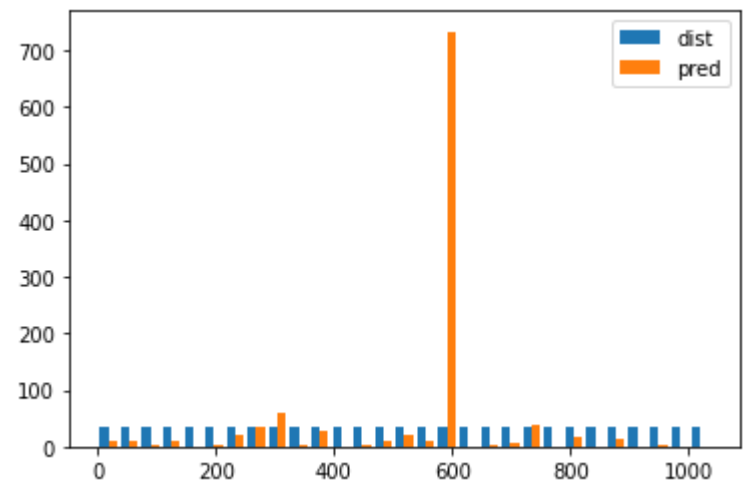


```
In [23]: for i in range(len(names)):
graph = simplified[i]
graph = csr_matrix(graph)
dist_matrix = breadth_first_order(csgraph=graph, i_start=0)[0]
predecessors = breadth_first_order(csgraph=graph, i_start=0)[1]
predecessors[0] = breadth_first_order(csgraph=graph, i_start=1)[1]
]
]

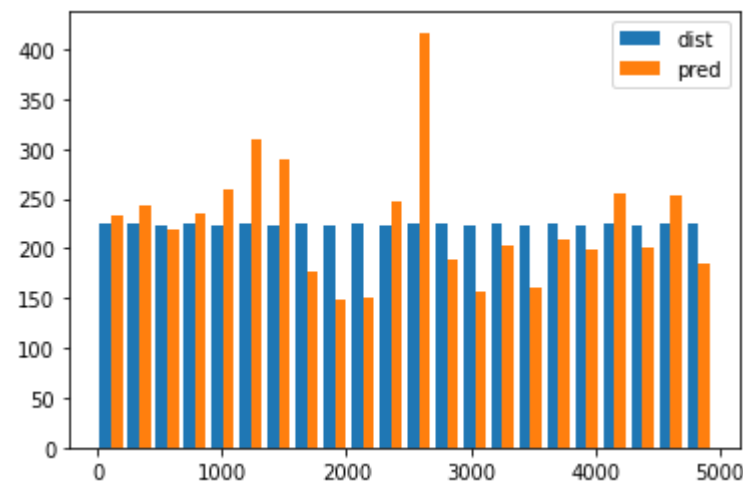
for j in range(len(predecessors)):
    if predecessors[j] == -9999:
        predecessors[j] = breadth_first_order(csgraph=graph, i_start=j+1)[1][j]

    print(names[i])
    print("Distribution vector: ", dist_matrix)
    print("Predecessors: ", predecessors)
    print("Histograms for shortest path distributions and predecessor
s\n")
    plt.hist([dist_matrix, predecessors], bins = 'auto', label=['dist', 'pred'])
    plt.legend(loc='upper right')
    plt.show()
    print("-----")
# dist_matrix, predecessors = shortest_path(csgraph=graph, directed=False, indices=0, return_predecessors=True)
```

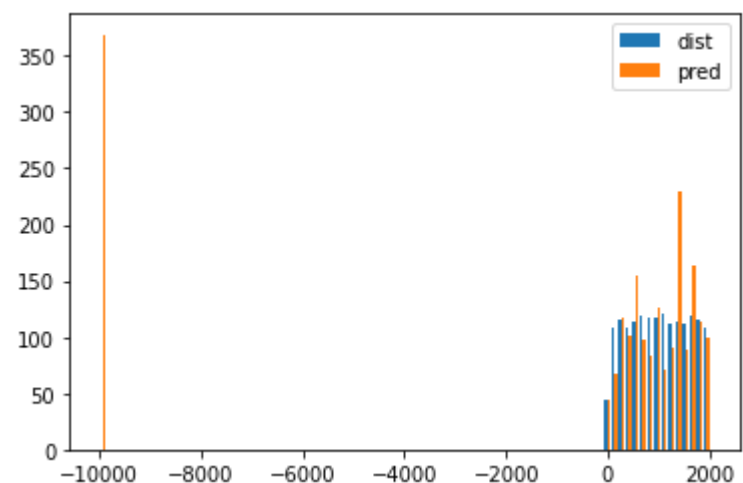
metabolism
Distribution vector: [0 496 499 ... 238 443 447]
Predecessors: [589 589 589 ... 589 589 589]
Histograms for shortest path distributions and predecessors



powergrid
Distribution vector: [0 386 395 ... 4397 4350 4379]
Predecessors: [395 3586 3583 ... 4929 4933 819]
Histograms for shortest path distributions and predecessors



protein
Distribution vector: [0 1050 362 ... 470 1003 116]
Predecessors: [1050 229 229 ... 806 1982 1637]
Histograms for shortest path distributions and predecessors



d) number of connected components

```
In [24]: from scipy.sparse.csgraph import connected_components
```

```
In [25]: for i in range(len(names)):
graph = original[i]
graph = csr_matrix(graph)
dist_matrix = connected_components(csgraph=graph, directed=False,
return_labels=True)[0]
predecessors = connected_components(csgraph=graph, directed=False
, return_labels=True)[1]
print(names[i])
print('Number of connected components: ', dist_matrix)
print('Labels: ', predecessors)
print('Fraction: ', len(np.unique(predecessors))/len(original[i]))
print("-----")
```

```
metabolism
Number of connected components: 1
Labels: [0 0 0 ... 0 0 0]
Fraction: 0.0009624639076034649
-----
powergrid
Number of connected components: 1
Labels: [0 0 0 ... 0 0 0]
Fraction: 0.00020238818053025704
-----
protein
Number of connected components: 185
Labels: [0 0 0 ... 0 0 0]
Fraction: 0.09167492566897918
-----
```

e) eigenvalue distribution

Since we are working with undirected graphs, degree matrix is a diagonal matrix and we can take 'short cuts' to get the Laplacian matrix ($L = D - A$):

1) Take negative of $A[i][j]$ where $i \neq j$. 2) Direct subtract element wise on the diagonal

```
In [26]: from scipy.sparse.linalg import eigs
```

```
In [27]: def eigenvalues(a):
l = np.zeros(np.shape(a))
d_i = np.sum(a, axis = 0)
for i in range(len(a)):
    for j in range(len(a)):
        if i == j:
            l[i][j] = d_i[i] - a[i][j]
        else:
            l[i][j] = -a[i][j]
vals, vecs = eigs(l, k = 100)
print("First 100 eigenvalues: \n", vals.real)
print("Spectral Gap, smallest non-zero eigenvalue for the first 1
00: ", np.amin(vals.real))
```

```
In [28]: eigenvalues(a_meta)
```

```
First 100 eigenvalues:
[639.00369299 461.00769966 300.01858498 253.03355538 244.01125795
140.024371    113.19322153 105.95092568 99.97549584 85.83296667
83.00698054 84.35134135 67.88033483 61.01881756 54.4144073
52.3472176 47.95808529 40.31997677 38.7925341 35.82868185
31.06574579 30.1137395 29.37276965 29.06534315 28.70100681
28.23300288 27.37510699 27.15566935 26.49210695 25.4748767
24.97782724 24.67568235 24.51124427 24.42283077 24.05954869
23.92242291 23.81433488 23.27668833 22.53730101 22.35876669
22.02287877 21.89057527 21.54350782 21.41948332 21.06071878
20.85035686 20.48591237 20.37364865 20.05239133 19.71905362
19.608905    19.00706007 18.93839974 18.73162569 18.48919392
18.46049692 18.26619604 18.08695384 17.98476779 17.92699474
17.83812291 17.69688457 17.51475483 17.46135429 17.30464392
17.22318967 17.15326895 17.18294348 16.8673785 16.81628718
16.74250819 16.49427838 16.45235344 16.42623394 16.27832818
16.2299508 16.11084694 15.79375843 15.67896154 15.61101152
15.56413221 15.48135261 15.3387175 15.22892272 15.05822925
14.86714526 14.7748687 14.61991023 14.58092543 14.55238427
14.35936387 14.34952075 14.30414186 14.31058637 14.31449423
14.07539236 14.03005824 13.97556635 13.86454182 13.82734751]
Spectral Gap, smallest non-zero eigenvalue for the first 100: 13.827
347512074564
```

```
In [29]: eigenvalues(a_power)
```

```
First 100 eigenvalues:
[20.10961638 19.12040004 15.53449922 15.09944316 15.06742763 14.3628
3872
14.44031338 14.43826971 14.12174676 14.09434772 13.99260146 13.36898
903
13.24934523 13.21895354 13.10166182 13.10060907 12.67055292 12.62922
198
12.47916386 12.40992733 12.38069949 12.36199878 12.33621813 12.17672
119
12.19248363 12.19921282 12.07821727 11.76714754 11.69925684 11.60144
844
11.53268182 11.43900231 11.42075779 11.41498983 11.35582107 11.31966
786
11.2957789 11.29861273 11.20695083 11.18674019 11.17710596 11.17250
185
11.16586853 11.14390006 11.13337106 11.09830284 11.06712566 11.04864
904
10.92360037 10.8631632 10.72548644 10.62953864 10.60360614 10.55202
785
10.5228627 10.45082532 10.42190636 10.40841961 10.40272777 10.38225
706
10.35592678 10.33699412 10.33356385 10.31260832 10.27222366 10.23724
402
10.22183286 10.22740566 10.18366836 10.16249509 10.1238946 10.08133
988
10.03432053 10.02076735 10.01885597 9.96275101 9.9386608 9.87901
416
9.84340905 9.82809191 9.80005708 9.64848183 9.64702091 9.61098
323
9.59156298 9.57337319 9.57335967 9.50198503 9.47834303 9.46844
359
9.3938688 9.36367353 9.34897219 9.35738015 9.33863969 9.30894
845
9.29124456 9.24129441 9.22578292 9.21702997]
Spectral Gap, smallest non-zero eigenvalue for the first 100: 9.2170
29967092815
```

```
In [30]: eigenvalues(a_protein)
```

```
First 100 eigenvalues:
[90.17842632 82.0563165 80.93315955 51.06632128 45.00888074 43.2449
1536
38.19367812 31.14190255 30.10368216 30.11833778 29.63420717 27.99609
746
27.73614027 27.05324546 24.97313848 24.81667957 24.28050261 22.22313
349
21.39642026 21.02771712 21.01576766 20.27860418 19.79652388 19.46455
393
19.04617627 18.64419499 18.14425632 17.27041702 17.11152025 16.61834
26
15.39546503 15.403596 15.19677793 15.16923845 15.07889447 14.49197
983
14.08251916 13.96831376 13.69029899 13.52937671 13.4864022 13.44390
849
13.34491274 13.33742644 13.16347371 13.10420386 12.99193218 12.92063
607
12.70616086 12.58772502 12.50077552 12.31368265 12.02925772 11.85780
264
11.57302397 11.4255173 11.35220868 11.31698276 11.29967868 11.26114
023
11.08161508 11.0742745 11.04384324 10.91230838 10.880104 10.86185
407
10.76025888 10.65170897 10.57400815 10.41047904 10.34391436 10.13549
587
10.08501948 10.05817254 10.02190807 9.96648631 9.87541734 9.82967
164
9.72664359 9.67526016 9.52688111 9.51528889 9.4921126 9.40560
267
9.38481847 9.3407356 9.28653602 9.24283566 9.19056186 9.08151
602
9.06431483 8.98815457 8.85298914 8.85850807 8.78647354 8.72078
121
8.7106943 8.64308939 8.57481549 8.55710394]
Spectral Gap, smallest non-zero eigenvalue for the first 100: 8.5571
03935335212
```

f) degree correlations

```
In [31]: from scipy.stats.stats import pearsonr
```

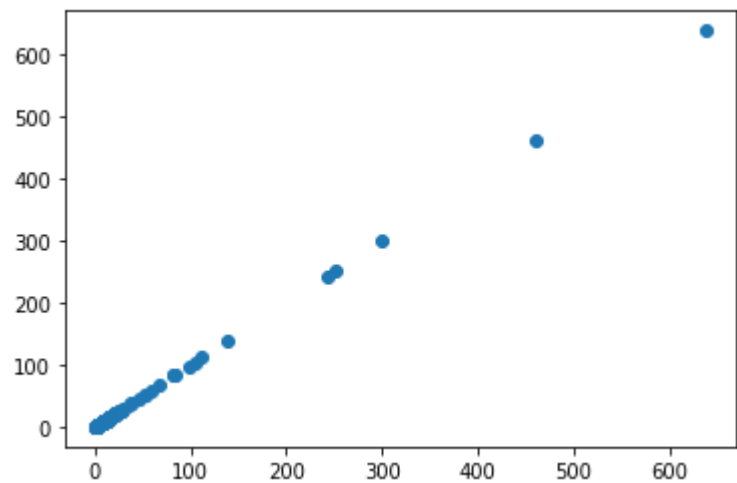
If we keep the simplification stated above, the correlation would be 1. We can investigate how things look like without it.

```
In [32]: def scatter(a):
          d_i = np.sum(a, axis = 0)
          d_j = np.sum(a, axis = 1)
          plt.scatter(d_i, d_j)
          print("Pearson Correlation Coefficient: ", pearsonr(d_i,d_j)[0])
```

Simplified graphs

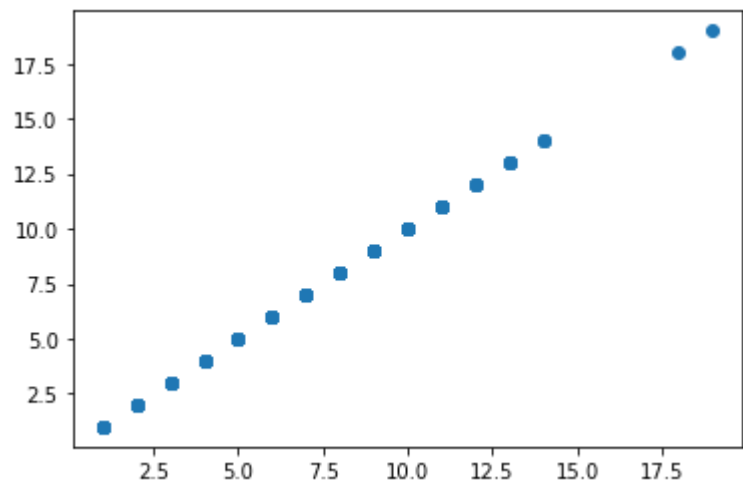
```
In [33]: scatter(a_meta)
```

Pearson Correlation Coefficient: 1.0



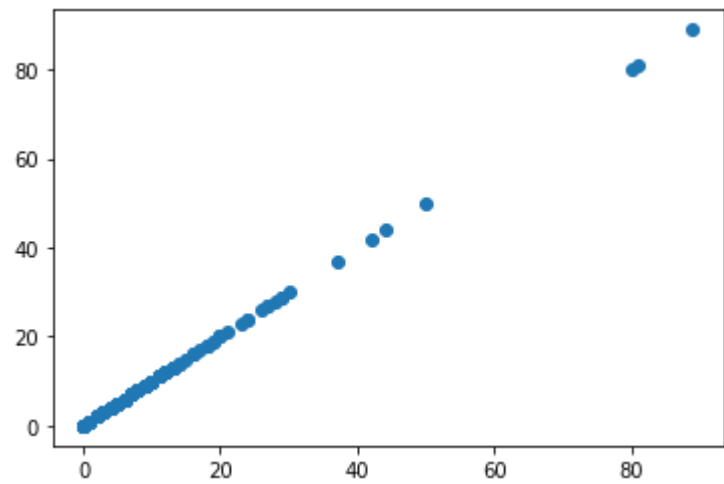
```
In [34]: scatter(a_power)
```

Pearson Correlation Coefficient: 1.0



```
In [35]: scatter(a_protein)
```

Pearson Correlation Coefficient: 0.9999999999999999

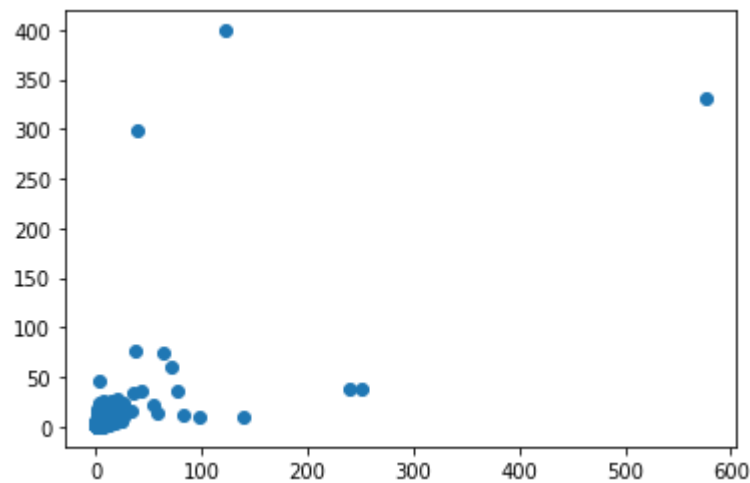


But it would be interesting to see what things are for the original graphs

Original graphs

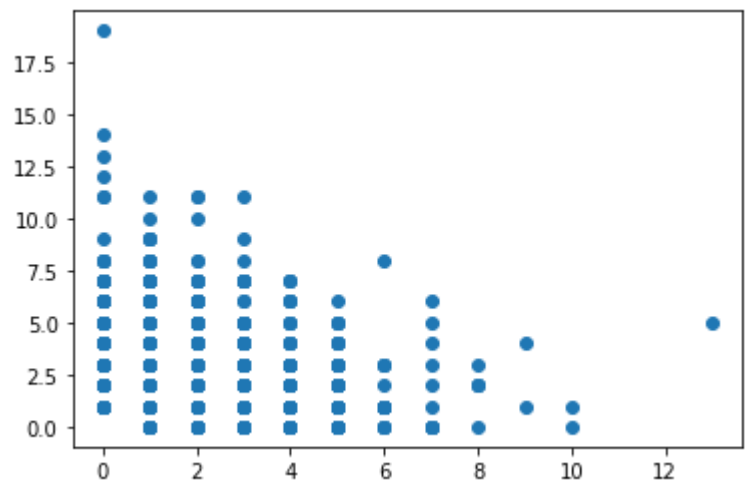
```
In [36]: scatter(a_meta_original)
```

Pearson Correlation Coefficient: 0.6332477523312626



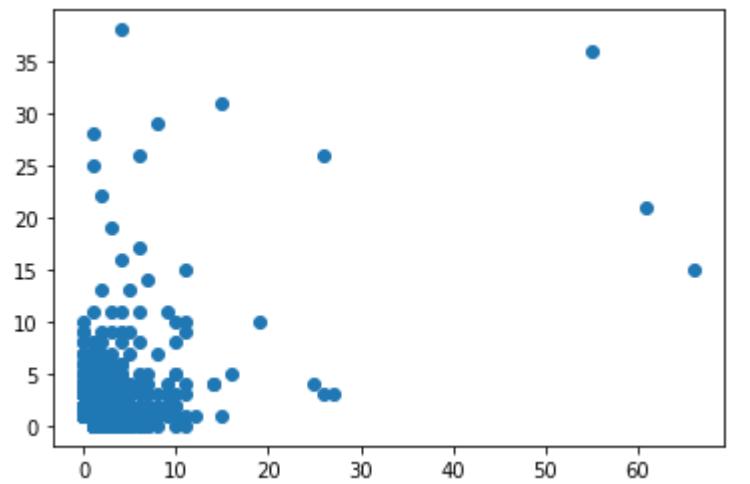
```
In [37]: scatter(a_power_original)
```

Pearson Correlation Coefficient: -0.1770073443062277



```
In [38]: scatter(a_protein_original)
```

Pearson Correlation Coefficient: 0.4064423366631729



As we can see, they are clearly not correlated as before. The reason being that an undirected, self-loop free and single-edged graph is essentially a two-direction simple graph. This would make them to have benign behaviours.

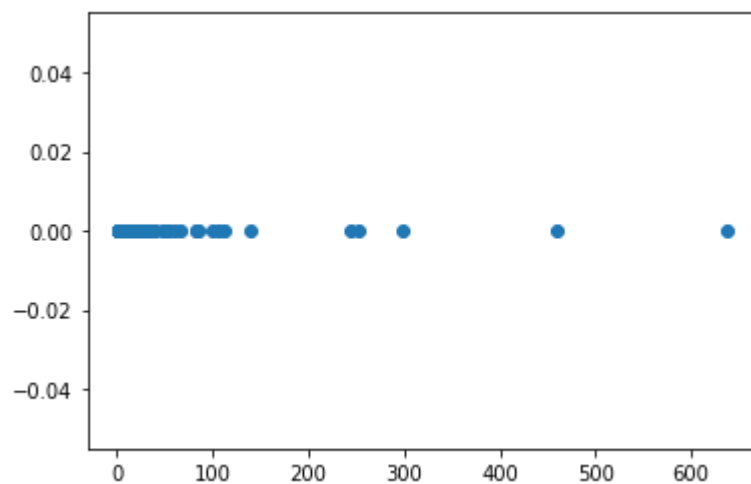
g) degree-clustering coefficient relation

```
In [39]: def d_c(a):
          c_local = []
          a2 = a * a
          a3 = a2 * a
          a3_diag = np.diag(a3)
          degree = np.multiply(np.sum(a, axis = 0), np.sum(a, axis = 0) - 1
          )
          degree2 = np.multiply(np.sum(a, axis = 1), np.sum(a, axis = 1) -
          1)
          for i in range(len(degree)):
              if degree[i] == 0:
                  c_local.append(0)
              else:
                  c_local.append(a3_diag[i]/degree[i])
          d_i = np.sum(a, axis = 0)
          plt.scatter(d_i,c_local)
```

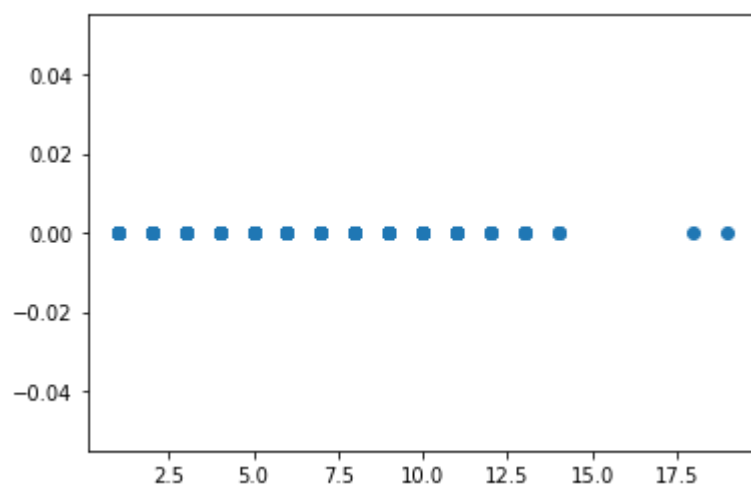
From previous questions, we know that since the clusering coefficients are essentially zero, there would not be any 'definable' correlation.

Simplified graphs

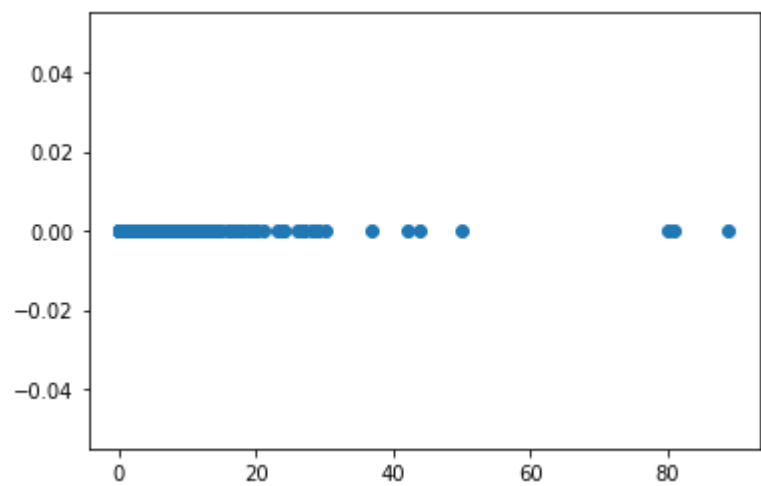
```
In [40]: d_c(a_meta) # metabolism
```



```
In [41]: d_c(a_power)
```

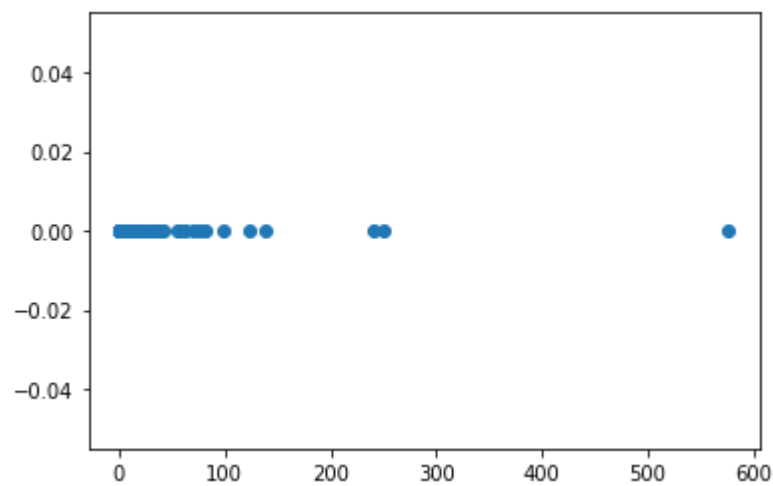



```
In [42]: d_c(a_protein)
```

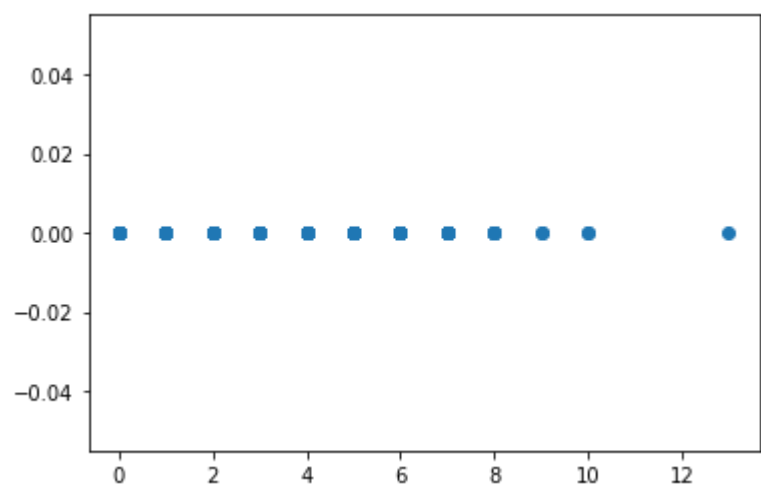


Original graphs

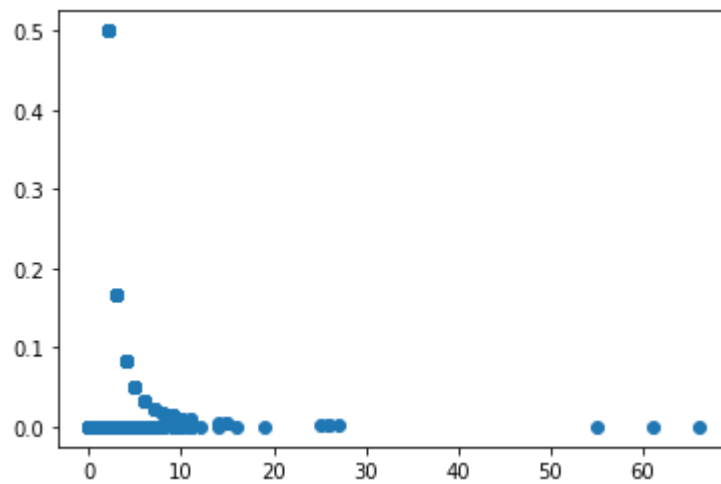
```
In [43]: d_c(a_meta_original)
```



```
In [44]: d_c(a_power_original)
```



```
In [45]: d_c(a_protein_original)
```



Question 2

Building Adjacency matrix with $n \times n$ shape: n^2 for filling in the entries, then for simplification, n^n access for modification. Therefore $O(n^2)$

a) Get sum: n operations, initializations: 1 operation, traverse through all sums to build key-value pairs: n operations. Therefore $O(n^2)$

b) Matrix multiplications: $O(n^3)$, but could use some more advanced as here it is naive. All other operations are similar to the previous questions and are of $O(n)$ or $O(n^2)$. Taking the worst, $O(n^3)$

c) Since it is BFS/DFS based approach, we visit each node and the complexity is $O(n + m)$ where m is the number of edges in the graph. In an undirected graph, the worst case, $m = n(n-1)/2$

d) Similar to c) the complexity is $O(n + m)$ where m is the number of edges in the graph. In an undirected graph, the worst case, $m = n(n-1)/2$

e) To get Laplacian, we need $O(n^2)$ for $n \times n$ matrices. Then for eigenvalue the best implementation is $O(n^{2.376})$. Taking the worst, $O(n^{2.376})$

f) $O(n)$ summations

g) $O(n)$ for summation to get degree, $O(n^3)$ in the clustering coefficient calculations. Taking the worst, $O(n^3)$

Part 2

Reading from data files: email, powergrid, protein

```
In [1]: import numpy as np;

meta = np.loadtxt('../networks/metabolic.edgelist.txt').astype(np.int
64)
power = np.loadtxt('../networks/powergrid.edgelist.txt').astype(np.in
t64)
protein = np.loadtxt('../networks/protein.edgelist.txt').astype(np.in
t64)
```

If we take the raw text data for graphs

```
In [2]: # Get sizes of the three networks
# meta
print("Graph 1, edge/node: ", len(meta), np.amax(meta))
# power
print("Graph 2, edge/node: ", len(power), np.amax(power))
# protein
print("Graph 3, edge/node: ", len(protein), np.amax(protein))
```

```
Graph 1, edge/node:  5802 1038
Graph 2, edge/node:  6594 4940
Graph 3, edge/node:  2930 2017
```

With all simplifications, the number of edges, taken as undirected (2 directions), are:

```
In [3]: def build_matrix(x):
a = np.zeros((np.amax(x)+1, np.amax(x)+1))
for i in range(len(x)):
    a[x[i][0]][x[i][1]] = 1
# undirected
for i in range(len(a)):
    for j in range(len(a)):
        if i == j:
            a[i][i] = 0
        elif a[i][j] != a[j][i]:
            a[i][j] = 1
            a[j][i] = 1
    return a

a_meta = build_matrix(meta)
a_power = build_matrix(power)
a_protein = build_matrix(protein)
print("Edges for Graphs 1-3: ", np.sum(a_meta)/2, np.sum(a_power)/2,
np.sum(a_protein)/2)
print("Edges for Graphs 1-3, undirected: ", np.sum(a_meta), np.sum(a_
power), np.sum(a_protein))
```

```
Edges for Graphs 1-3:  4741.0 6594.0 2705.0
Edges for Graphs 1-3, undirected:  9482.0 13188.0 5410.0
```

We will pass these values to the model

File failed to load: file:///home/andybai/Desktop/COMP-596-Network-Science/a1/Q3_files/extensions/MathZoom.js

Question 3

```
In [4]: # AB model implementation
import random

def random_subset_with_weights(weights, m):
    mapped_weights = [
        (random.expovariate(w), i)
        for i, w in enumerate(weights)
    ]
    return { i for _, i in sorted(mapped_weights)[:m] }

def barabasi_albert(n, m):
    # initialize with a complete graph on m vertices
    neighbours = [ set(range(m)) - {i} for i in range(m) ]
    degrees = [ m-1 for i in range(m) ]

    for i in range(m, n):
        # stopping criterion if the number of edges is met
        n_neighbours = random_subset_with_weights(degrees, m)

        # add node with back-edges
        neighbours.append(n_neighbours)
        degrees.append(m)

        # add forward-edges
        for j in n_neighbours:
            neighbours[j].add(i)
            degrees[j] += 1
    return neighbours

def barabasi_albert_capped(n, m, deg_cap):
    # initialize with a complete graph on m vertices
    neighbours = [ set(range(m)) - {i} for i in range(m) ]
    degrees = [ m-1 for i in range(m) ]

    for i in range(m, n):
        # stopping criterion if the number of edges is met
        if sum(degrees) >= deg_cap:
            break;
        else:
            n_neighbours = random_subset_with_weights(degrees, m)

            # add node with back-edges
            neighbours.append(n_neighbours)
            degrees.append(m)

            # add forward-edges
            for j in n_neighbours:
                neighbours[j].add(i)
                degrees[j] += 1

    return neighbours
```

The input is number of nodes - n which dictates the node size of the graph, as well as, m - initial number of nodes to start. For the sake of consistency in this section, we start with 3 nodes and try building the graph counting down nodes while respecting the capacity of edges. However, there are some problems to it and the following is used to only match the number of nodes.

```
In [5]: one = barabasi_albert(1038, 2) # metabolism
two = barabasi_albert(4940, 2) # powergrid
three = barabasi_albert(2017, 2) # protein
```

```
In [7]: a_one = np.zeros((1038, 1038))
        for i in range(len(a_one)):
            for item in list(one[i]):
                a_one[i][item] = 1
```

```
In [8]: a_two = np.zeros((4940, 4940))
        for i in range(len(a_two)):
            for item in list(two[i]):
                a_two[i][item] = 1
```

```
In [9]: a_three = np.zeros((2017, 2017))
        for i in range(len(a_three)):
            for item in list(three[i]):
                a_three[i][item] = 1
```

The following analyses are done with the originally generated graphs

degree distribution

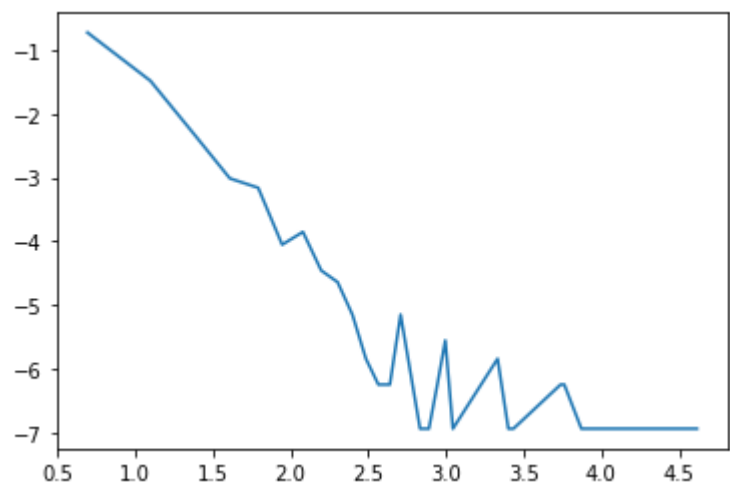
```
In [10]: one_deg = []
        two_deg = []
        three_deg = []
        for i in range(len(one)):
            one_deg.append(len(one[i]))
        for i in range(len(two)):
            two_deg.append(len(two[i]))
        for i in range(len(one)):
            three_deg.append(len(three[i]))
```

```
In [82]: import matplotlib.pyplot as plt

        def get_degree(a):
            my_list = a
            freq = {}
            k = []
            v = []
            for items in my_list:
                freq[items] = my_list.count(items)
            for key, value in freq.items():
                k.append(key)
                v.append(value)
            v[:] = [x / sum(v) for x in v]
            x = np.log(k)
            y = np.log(v)
            fit = np.polyfit(x,y, 1)
            print(fit)
            print("Degree distribution")
            plt.plot(x, y)
            plt.show()
```

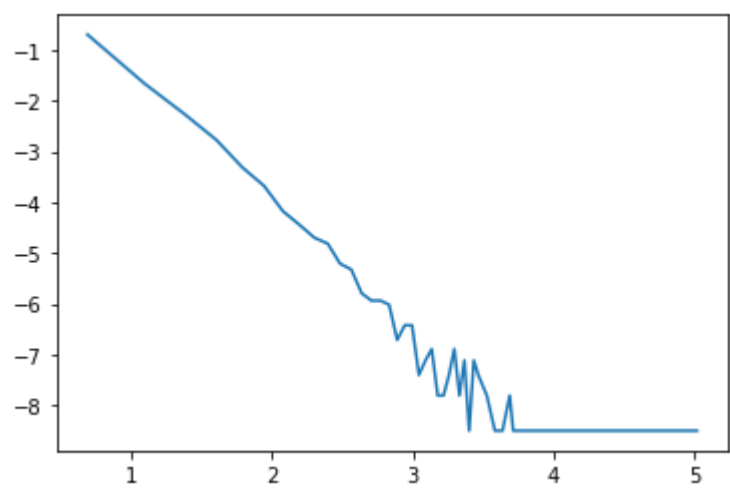
```
In [52]: get_degree(one_deg)
```

`[-1.69337888 -0.67269678]`
Degree distribution



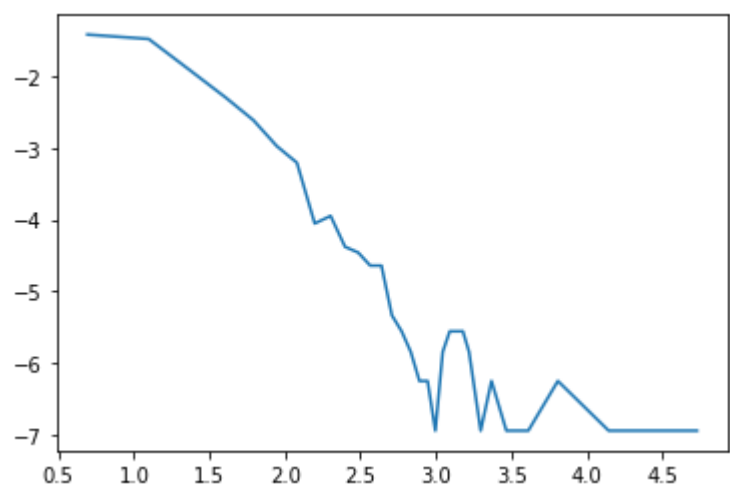
```
In [53]: get_degree(two_deg)
```

`[-1.95573416 -0.43836532]`
Degree distribution



```
In [54]: get_degree(three_deg)
```

`[-1.65273012 -0.37599438]`
Degree distribution



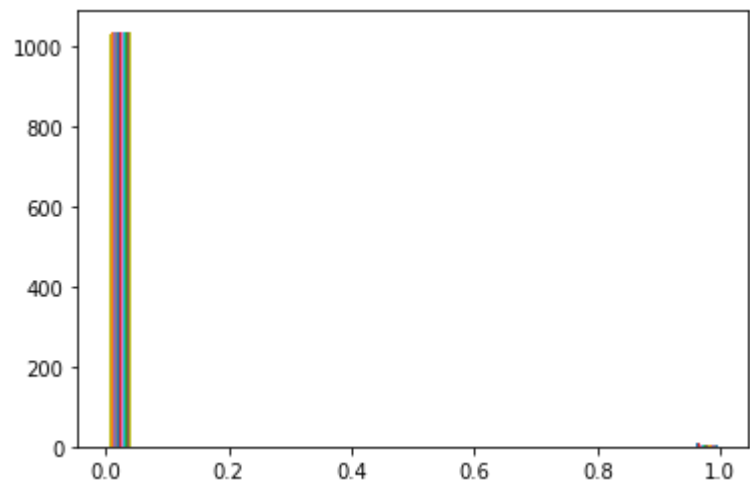
We can fit linear functions very nicely. Here the first number in the list is the slope

clustering coefficient distribution

```
In [15]: def clustering_coeff(a):
c_local = []
a2 = a * a
a3 = a2 * a
a3_diag = np.diag(a3)
trace = np.trace(a3)
denom = np.sum(a2) - np.trace(a2)
print("Total number triangles: ", trace/6)
print("Global: ", trace/denom)
degree = np.multiply(np.sum(a, axis = 0), np.sum(a, axis = 0) - 1
)
degree2 = np.multiply(np.sum(a, axis = 1), np.sum(a, axis = 1) - 1)
for i in range(len(degree)):
    if degree[i] == 0:
        c_local.append(0)
    else:
        c_local.append(a3_diag[i]/degree[i])
print("Clustering coefficient, first 10: ", c_local[0:10])
print("Max clustering coefficient: ", max(c_local))
print("Min clustering coefficient: ", min(c_local))
plt.hist(a, bins='auto')
plt.show()
```

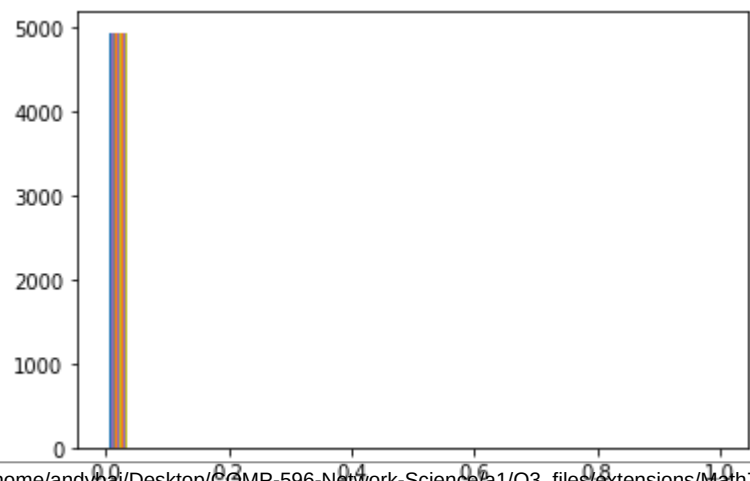
```
In [16]: clustering_coeff(a_one)
```

Total number triangles: 0.0
Global: 0.0
Clustering coefficient, first 10: [0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
Max clustering coefficient: 0.0
Min clustering coefficient: 0.0



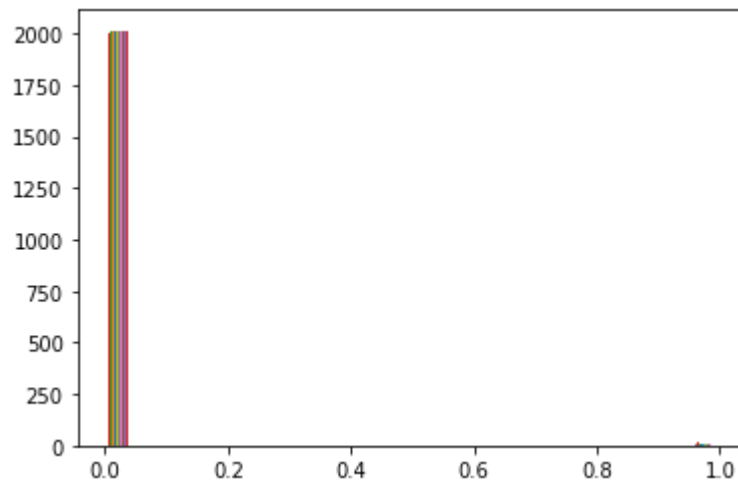
```
In [17]: clustering_coeff(a_two)
```

Total number triangles: 0.0
Global: 0.0
Clustering coefficient, first 10: [0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
Max clustering coefficient: 0.0
Min clustering coefficient: 0.0



```
In [18]: clustering_coeff(a_three)
```

```
Total number triangles: 0.0  
Global: 0.0  
Clustering coefficient, first 10: [0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.  
0, 0.0, 0.0, 0.0]  
Max clustering coefficient: 0.0  
Min clustering coefficient: 0.0
```



Since traces are all zero, the values are all zero.

shortest paths distribution number of connected components

```
In [19]: from scipy.sparse import csr_matrix  
from scipy.sparse.csgraph import shortest_path  
from scipy.sparse.csgraph import breadth_first_order  
from scipy.sparse.csgraph import depth_first_order  
from scipy.sparse.csgraph import connected_components  
  
names = ['One', 'Two', 'Three']  
mats = [a_one, a_two, a_three]
```



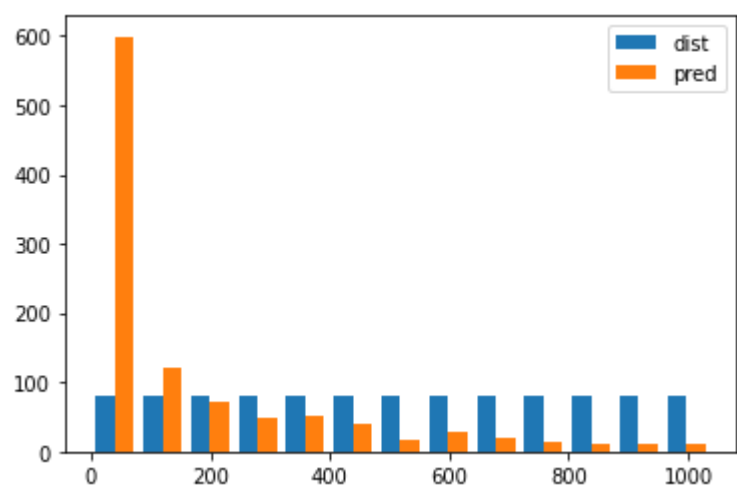
```

In [20]: for i in range(len(names)):
graph = mats[i]
graph = csr_matrix(graph)
dist_matrix = breadth_first_order(csgraph=graph, i_start=0)[0]
predecessors = breadth_first_order(csgraph=graph, i_start=0)[1]
predecessors[0] = breadth_first_order(csgraph=graph, i_start=1)[1]
] [0]
    for j in range(len(predecessors)):
        if predecessors[j] == -9999:
            predecessors[j] = breadth_first_order(csgraph=graph, i_start=j+1)[1][j]

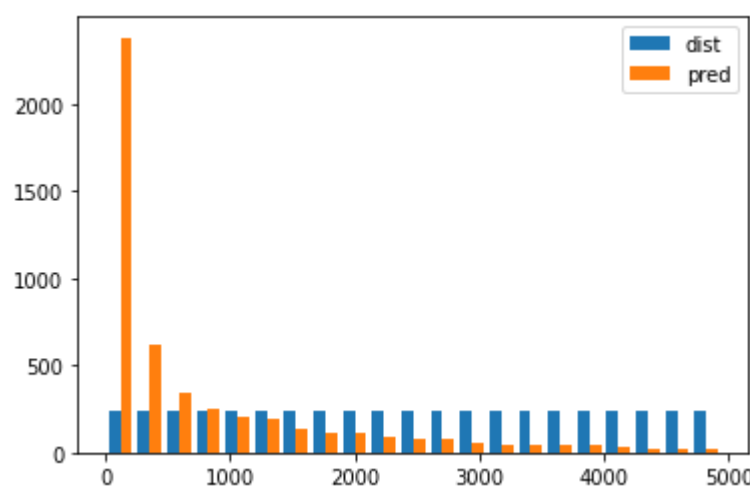
    print(names[i])
    print("Distribution vector: ", dist_matrix)
    print("Predecessors: ", predecessors)
    print("Histograms for shortest path distributions and predecessor
s\n")
    plt.hist([dist_matrix, predecessors], bins = 'auto', label=['dist', 'pred'])
    plt.legend(loc='upper right')
    plt.show()
    print("-----")

```

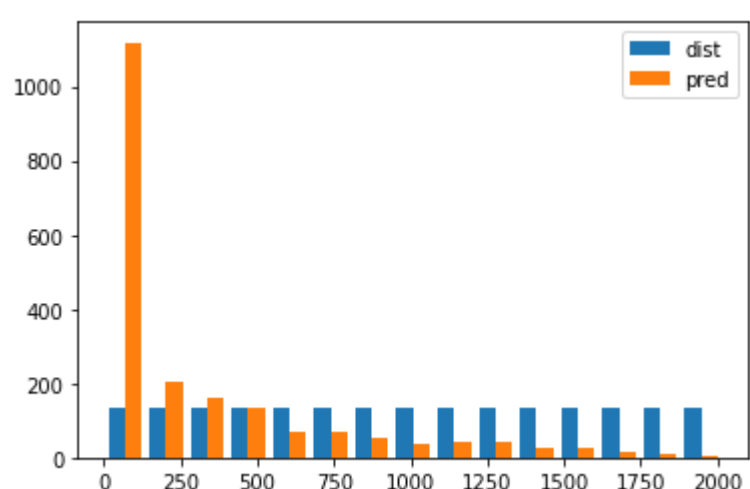
One
Distribution vector: [0 1 2 ... 1007 954 841]
Predecessors: [1 0 0 ... 2 48 24]
Histograms for shortest path distributions and predecessors



Two
Distribution vector: [0 1 2 ... 3156 4067 4236]
Predecessors: [1 0 0 ... 1724 4520 1554]
Histograms for shortest path distributions and predecessors



Three
Distribution vector: [0 1 2 ... 1561 1872 2005]
Predecessors: [1 0 0 ... 63 1059 52]
Histograms for shortest path distributions and predecessors



The predecessor vector values are much more skewed towards lower end while those of distribution matrices are very well spread. Some nodes are much more connected while the rest are much less. It confirms the 'rich get richer' conundrum.

```
In [21]: for i in range(len(names)):
graph = mats[i]
graph = csr_matrix(graph)
dist_matrix = connected_components(csgraph=graph, directed=False,
return_labels=True)[0]
predecessors = connected_components(csgraph=graph, directed=False
, return_labels=True)[1]
print(names[i])
print('Number of connected components: ', dist_matrix)
print('Labels: ', predecessors)
print('Fraction: ', len(np.unique(predecessors))/len(mats[i]))
print("-----")
```

```
One
Number of connected components:  1
Labels:  [0 0 0 ... 0 0 0]
Fraction:  0.0009633911368015414
-----
Two
Number of connected components:  1
Labels:  [0 0 0 ... 0 0 0]
Fraction:  0.00020242914979757084
-----
Three
Number of connected components:  1
Labels:  [0 0 0 ... 0 0 0]
Fraction:  0.0004957858205255329
-----
```

There is only 1 in GCC

eigenvalue distribution

```
In [22]: from scipy.sparse.linalg import eigs

def eigenvalues(a):
    l = np.zeros(np.shape(a))
    d_i = np.sum(a, axis = 0)
    for i in range(len(a)):
        for j in range(len(a)):
            if i == j:
                l[i][j] = d_i[i] - a[i][j]
            else:
                l[i][j] = -a[i][j]
    vals, vecs = eigs(l, k = 100)
    print("First 100 eigenvalues: \n", vals.real)
    print("Spectral Gap, smallest non-zero eigenvalue for the first 1
00: ", np.amin(vals.real))
```

```
In [23]: eigenvalues(a_one)
```

First 100 eigenvalues:
[102.05521777 61.36122693 57.86836162 49.07238684 45.11660979
44.2017448 42.77100739 41.98860484 32.37518507 31.44372381
29.07574337 28.75553207 28.64773623 22.09371301 21.85017486
21.15381948 20.97266458 20.73078091 20.11543885 19.93094085
18.74543295 18.32583458 16.23782461 16.17735616 16.15975529
15.97740865 15.93152314 15.87845801 14.78861499 14.29142139
14.17753208 14.01731904 13.62329072 13.34205331 12.89776933
12.72027018 12.51305684 12.41733904 11.97383259 11.50802843
11.44386277 11.41085756 11.27700435 11.23476915 11.21955105
11.20737659 11.02925909 10.95768719 10.8608926 10.76229435
10.58997014 10.57383329 10.54564365 10.41093942 10.38434219
10.30828258 10.24257019 10.25832344 10.16796867 9.99540648
9.94570396 9.84678326 9.65067775 9.51678307 9.50188927
9.3708234 9.29675108 9.19072595 9.15730719 9.13690726
9.0968882 9.02106231 8.9625121 8.92082499 8.86020021
8.83772555 8.74371865 8.6947344 8.5716959 8.53915842
8.53586607 8.45667118 8.42430757 8.38719557 8.33413545
8.31026274 8.29147675 8.21414261 8.19074608 8.07949163
7.97457743 7.9555335 7.94762125 7.88633205 7.87684497
7.85310645 7.84552926 7.82661684 7.79959204 7.78394185]
Spectral Gap, smallest non-zero eigenvalue for the first 100: 7.7839
41850853903

```
In [24]: eigenvalues(a_two)
```

First 100 eigenvalues:
[152.28741692 147.92502376 137.95699722 122.05861395 89.07973713
76.22864176 71.84359955 71.00529296 70.0362286 65.03296383
61.11357143 56.02195568 53.89368391 53.02920831 49.24851365
43.06236268 42.39751384 41.13256894 41.10722315 38.68984935
37.21677532 35.08509859 35.02194241 33.08393924 32.98897384
32.89206772 32.19880564 32.08665768 31.99771367 32.04058469
31.00196399 30.18459003 30.09593589 30.09083048 30.13667162
29.22604275 29.05378923 28.16856588 27.95756567 28.09334904
28.05730367 28.04925715 27.43900817 27.14154552 27.07965638
27.00411354 25.92878897 25.16919265 24.77828817 24.51500932
24.36252498 24.27119707 24.14756274 23.83009357 23.15105232
23.01959744 22.98044815 22.6888324 22.27742897 22.00699523
21.87664315 21.94352428 21.19670631 21.02120264 20.99733042
20.96968989 20.91093656 20.85150011 20.87926082 20.42491522
20.40515024 20.34628917 20.1666042 20.01277053 20.00660173
19.93953055 19.90445324 19.45923554 19.23160997 19.18905887
19.0586045 18.98915216 18.75577146 18.43584559 18.41877568
18.38516363 18.3343593 18.24946986 18.15704951 18.11939265
18.06937602 17.86050097 17.8213011 17.84478647 17.72502407
17.71713087 17.73564134 17.49527449 17.3594119 17.30931229]
Spectral Gap, smallest non-zero eigenvalue for the first 100: 17.309
31229469935

```
In [25]: eigenvalues(a_three)
```

First 100 eigenvalues:
[114.10412894 94.59764901 92.55919976 75.03194834 64.99770634
63.9496844 46.13136637 45.9760032 38.10158711 33.01392355
31.17547757 29.29316351 28.05900879 26.08968622 26.12946407
25.84256819 25.27550791 25.17478965 25.09005249 24.92999406
23.29704559 23.17492514 23.05350258 22.97229845 22.84187081
22.21456998 21.14009366 21.07714197 20.20649956 19.99417416
19.02266207 18.72642564 18.30250017 18.16157405 18.12070426
17.84884092 17.76038255 17.17022465 16.79418879 16.60380164
16.30358846 16.26203004 16.11891002 15.65152054 15.59395715
15.53660465 15.18760825 15.1411815 15.10241871 15.0657644
14.98621061 14.85731408 14.83266387 14.55003749 14.37939937
14.35540686 14.34210221 14.27190181 14.23431487 14.18066304
14.09955352 14.00523444 13.77977282 13.51324822 13.4893056
13.45613793 13.34609875 13.24722714 13.2171924 13.15518968
13.00944506 12.96105598 12.83764134 12.79915008 12.64770021
12.61136301 12.56849994 12.51586337 12.46767747 12.38658176
12.36479401 12.33493046 12.15296258 12.14191015 12.08001627
11.99325371 11.80925691 11.73656481 11.7092937 11.64238821
11.58413329 11.47871565 11.44802352 11.43473579 11.40350687
11.37074522 11.19817393 11.16706812 11.15228445 11.059209]
Spectral Gap, smallest non-zero eigenvalue for the first 100: 11.059
20900217497

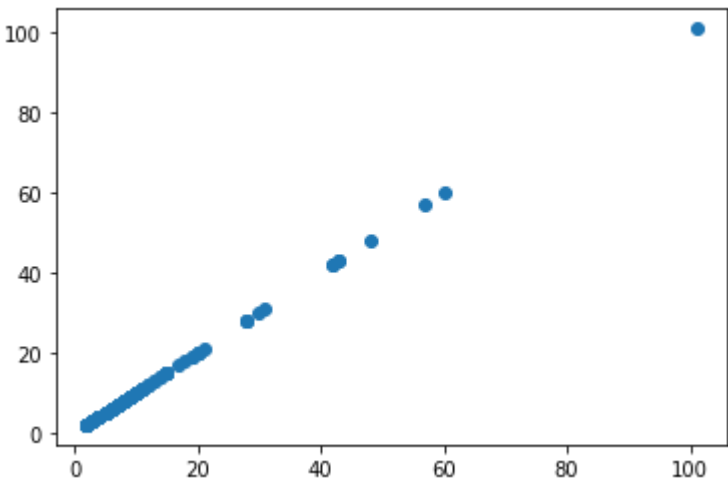
degree correlations

```
In [26]: from scipy.stats.stats import pearsonr

def scatter(a):
    d_i = np.sum(a, axis = 0)
    d_j = np.sum(a, axis = 1)
    plt.scatter(d_i, d_j)
    print("Pearson Correlation Coefficient: ", pearsonr(d_i,d_j)[0])
```

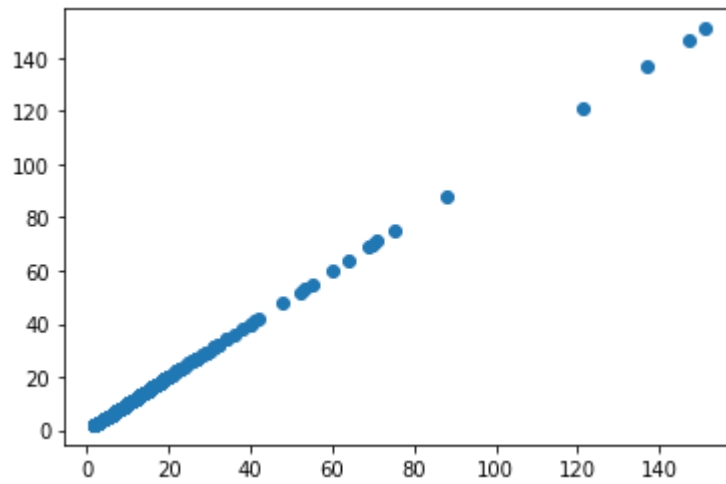
```
In [27]: scatter(a_one)
```

Pearson Correlation Coefficient: 1.0



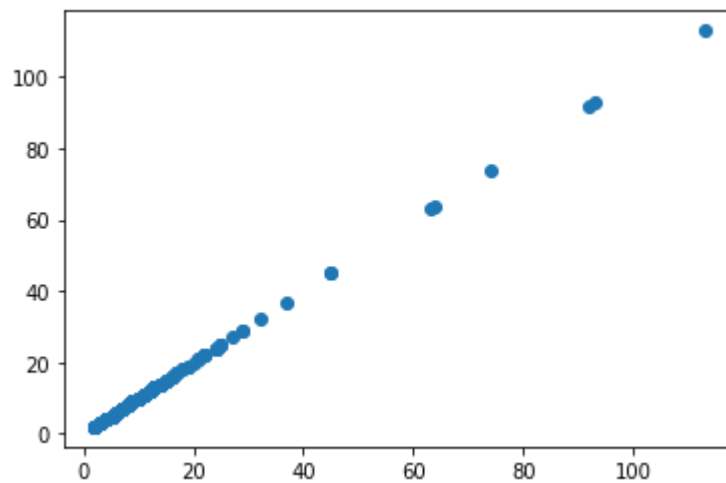
In [28]: `scatter(a_two)`

Pearson Correlation Coefficient: 0.9999999999999956



In [29]: `scatter(a_three)`

Pearson Correlation Coefficient: 0.9999999999999976

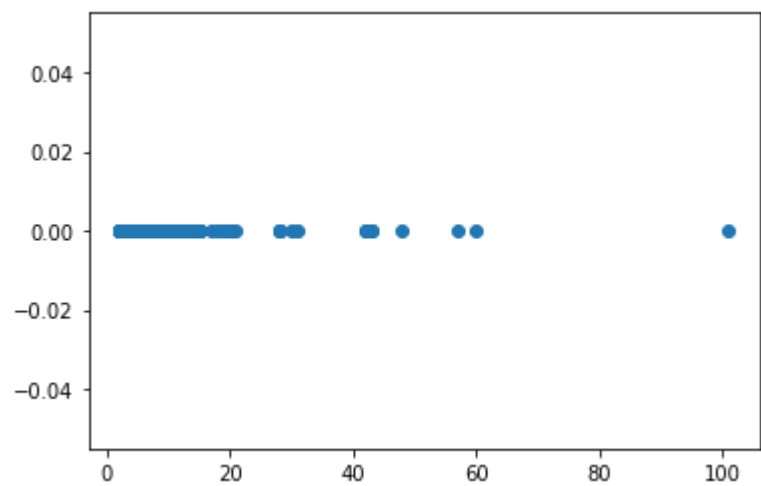


Very high correlation irrespective of number of nodes/edges.

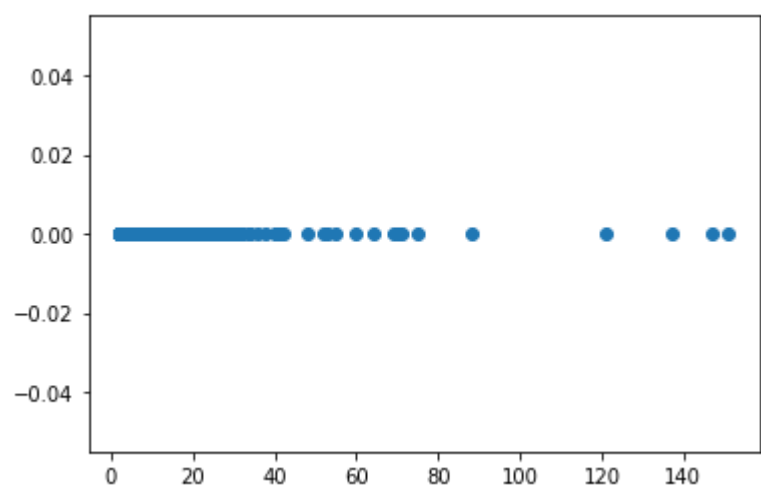
degree-clustering coefficient relation

```
In [30]: def d_c(a):
          c_local = []
          a2 = a * a
          a3 = a2 * a
          a3_diag = np.diag(a3)
          degree = np.multiply(np.sum(a, axis = 0), np.sum(a, axis = 0) - 1)
          degree2 = np.multiply(np.sum(a, axis = 1), np.sum(a, axis = 1) - 1)
          for i in range(len(degree)):
              if degree[i] == 0:
                  c_local.append(0)
              else:
                  c_local.append(a3_diag[i]/degree[i])
          d_i = np.sum(a, axis = 0)
          plt.scatter(d_i,c_local)
```

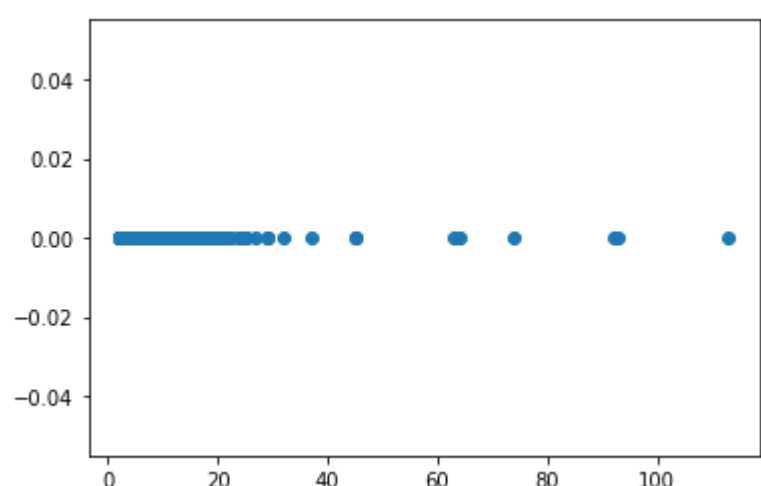
```
In [31]: d_c(a_one)
```



```
In [32]: d_c(a_two)
```



```
In [33]: d_c(a_three)
```



This would be zero since clustering coefficients are zero.

Extension

Try another randomization method for the smallest graph

```
In [74]: def random_subset_with_weights_pareto(weights, m):
mapped_weights = [
    (random.paretovariate(w), i)
    for i, w in enumerate(weights)
]
return { i for _, i in sorted(mapped_weights)[:m] }

def barabasi_albert_one(n, m):
    # initialize with a complete graph on m vertices
    neighbours = [ set(range(m)) - {i} for i in range(m) ]
    degrees = [ m-1 for i in range(m) ]

    for i in range(m, n):
        # stopping criterion if the number of edges is met
        n_neighbours = random_subset_with_weights_beta(degrees, m)

        # add node with back-edges
        neighbours.append(n_neighbours)
        degrees.append(m)

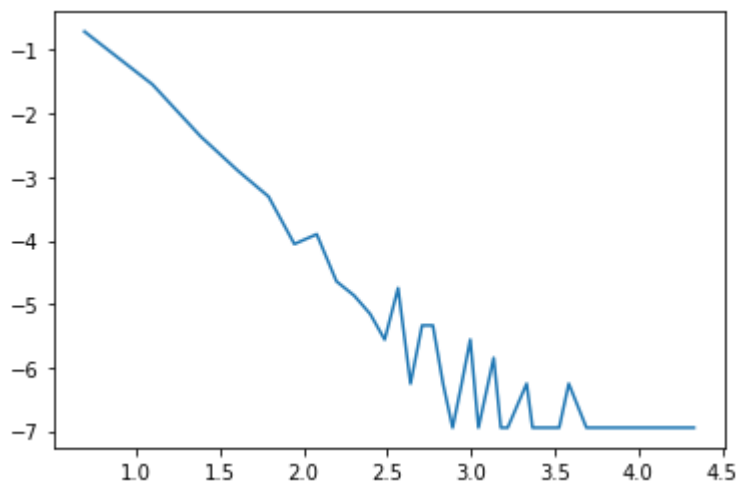
        # add forward-edges
        for j in n_neighbours:
            neighbours[j].add(i)
            degrees[j] += 1
    return neighbours
```

```
In [75]: four = barabasi_albert_one(1038, 2)
a_four = np.zeros((1038, 1038))
for i in range(len(a_four)):
    for item in list(four[i]):
        a_four[i][item] = 1
```

```
In [76]: four_deg = []
for i in range(len(four)):
    four_deg.append(len(four[i]))
```

```
In [83]: get_degree(four_deg)
```

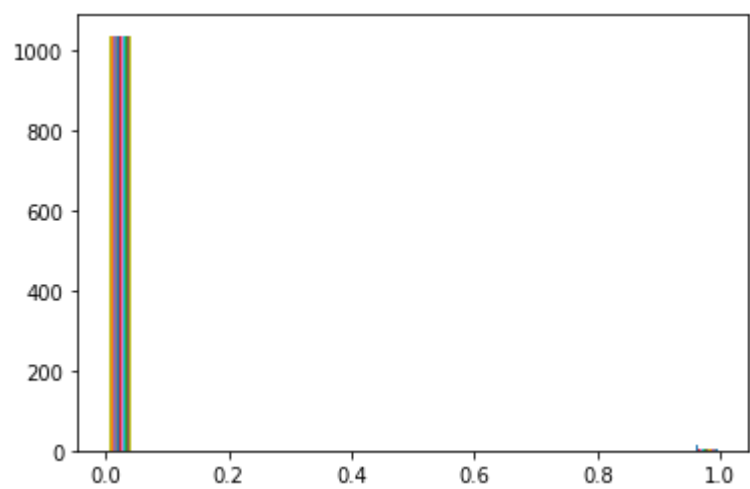
```
[-1.99588874  0.00895811]
Degree distribution
```



There are only slight differences in coefficients but overall the trends are same. It means the randomization process won't revolutionarily change things.


```
In [84]: clustering_coeff(a_four)
```

Total number triangles: 0.0
Global: 0.0
Clustering coefficient, first 10: [0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
Max clustering coefficient: 0.0
Min clustering coefficient: 0.0



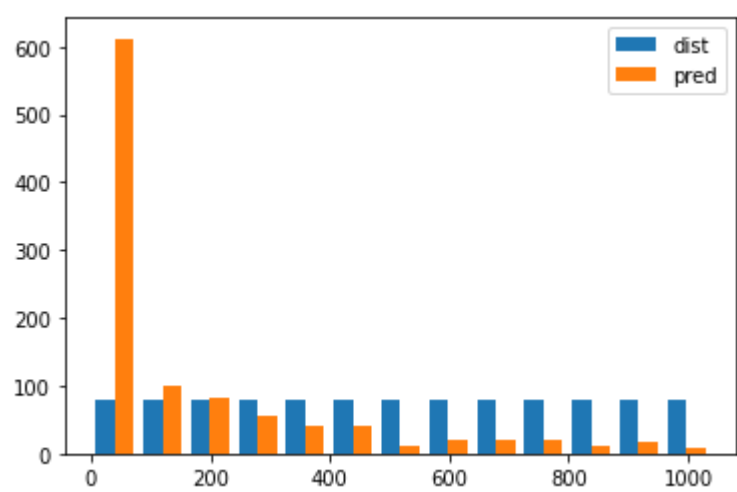
```
In [85]: names2 = ['Four']
mats2 = [a_four]

for i in range(len(names2)):
    graph = mats2[i]
    graph = csr_matrix(graph)
    dist_matrix = breadth_first_order(csgraph=graph, i_start=0)[0]
    predecessors = breadth_first_order(csgraph=graph, i_start=0)[1]
    predecessors[0] = breadth_first_order(csgraph=graph, i_start=1)[1][0]

    for j in range(len(predecessors)):
        if predecessors[j] == -9999:
            predecessors[j] = breadth_first_order(csgraph=graph, i_start=j+1)[1][j]

    print(names2[i])
    print("Distribution vector: ", dist_matrix)
    print("Predecessors: ", predecessors)
    print("Histograms for shortest path distributions and predecessors\n")
    plt.hist([dist_matrix, predecessors], bins = 'auto', label=['dist', 'pred'])
    plt.legend(loc='upper right')
    plt.show()
    print("-----")
```

Four
Distribution vector: [0 1 2 ... 958 798 937]
Predecessors: [1 0 0 ... 31 2 10]
Histograms for shortest path distributions and predecessors

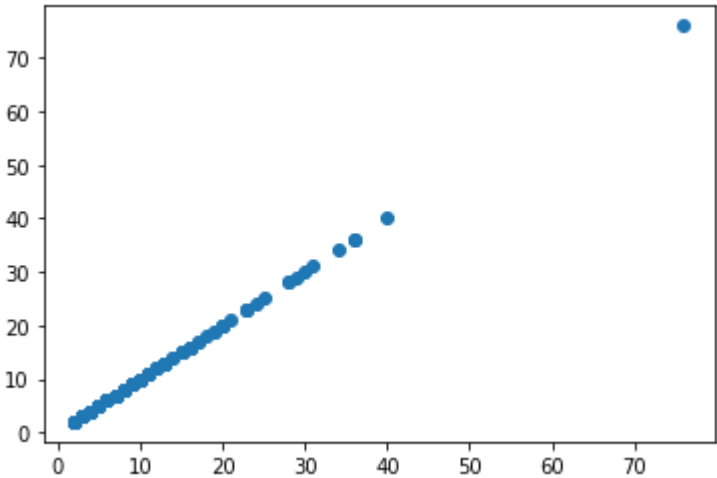


```
In [86]: eigenvalues(a_four)
```

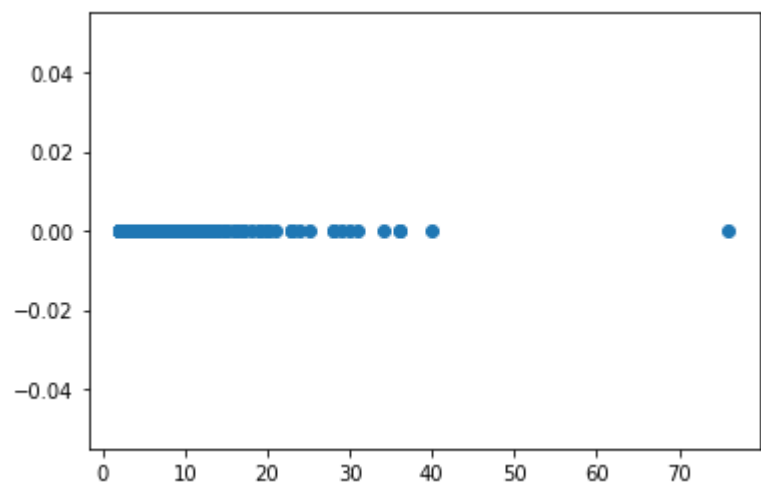
First 100 eigenvalues:
[77.11601743 41.35560575 37.8957354 36.28451538 35.34951753 32.13762735 31.25539453 29.99519244 28.9276927 28.85288126 26.39865573 24.76792543 24.51949542 24.19625225 24.257059 22.1593592 21.97197673 21.10656013 20.5775282 20.44401837 20.04823442 19.94833797 19.43755713 18.55620201 17.54980957 17.37225521 17.31310769 17.21826584 17.13114483 16.33220079 16.28622731 16.13130556 15.93774661 15.89802961 15.75096667 15.29173983 14.91930542 14.23804544 14.24445417 14.01515158 13.95870142 13.82491531 13.68762551 13.66154511 13.60787549 13.41409974 13.21815829 13.09764242 12.97737171 12.90915195 12.85873631 12.48049328 12.05452233 11.87117486 11.83368055 11.55218661 11.34843658 11.06583203 10.93845173 10.89860018 10.85302662 10.81535769 10.55609542 10.48864618 10.46622846 10.40635596 10.37920106 10.26342745 10.12947982 10.11268739 9.96281579 9.93472573 9.84958445 9.53189286 9.48013672 9.39637294 9.36781137 9.3496561 9.23555128 9.1299522 9.10724747 9.09491548 9.06219999 9.00106713 8.94986013 8.94189165 8.90653971 8.85336457 8.78107442 8.64518224 8.62123524 8.54586391 8.50356547 8.4111222 8.42349275 8.27893706 8.26340347 8.22577388 8.15598959 8.09363693]
Spectral Gap, smallest non-zero eigenvalue for the first 100: 8.09363692988137

```
In [87]: scatter(a_four)
```

Pearson Correlation Coefficient: 0.9999999999999998



```
In [88]: d_c(a_four)
```



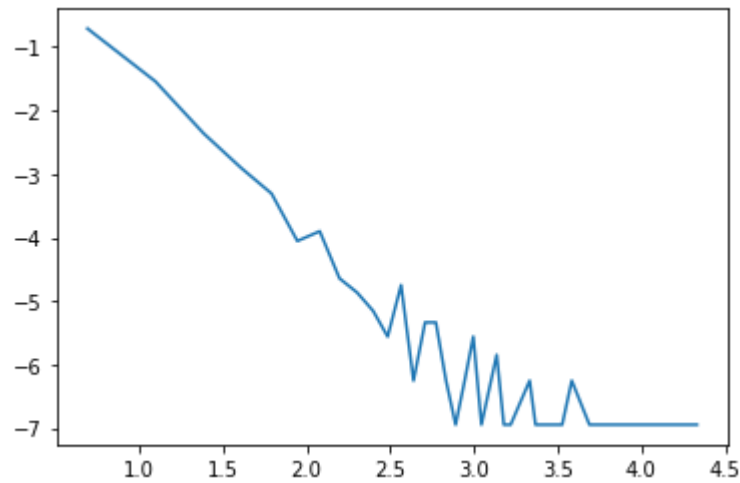
The rest confirm the same story

Try with more initial points. This will increase number of edges.

```
In [93]: five = barabasi_albert(1038, 5)
a_five = np.zeros((1038, 1038))
for i in range(len(a_five)):
    for item in list(five[i]):
        a_five[i][item] = 1
five_deg = []
for i in range(len(five)):
    five_deg.append(len(five[i]))
```

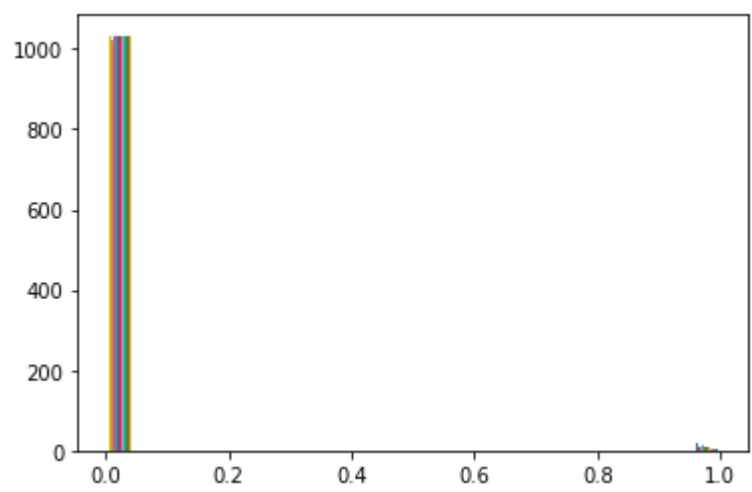
```
In [94]: get_degree(four_deg)
```

`[-1.99588874 0.00895811]`
Degree distribution



```
In [95]: clustering_coeff(a_five)
```

Total number triangles: 0.0
Global: 0.0
Clustering coefficient, first 10: [0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0]
Max clustering coefficient: 0.0
Min clustering coefficient: 0.0

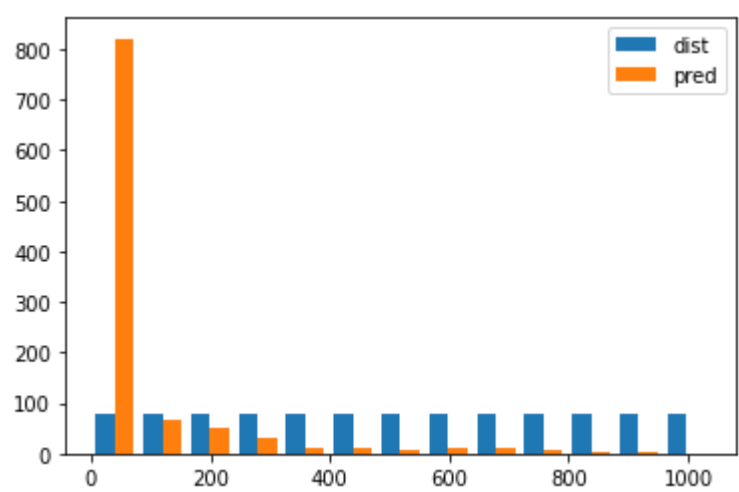


```
In [96]: names3 = ['Five']
mats3 = [a_five]

for i in range(len(names3)):
    graph = mats3[i]
    graph = csr_matrix(graph)
    dist_matrix = breadth_first_order(csgraph=graph, i_start=0)[0]
    predecessors = breadth_first_order(csgraph=graph, i_start=0)[1]
    predecessors[0] = breadth_first_order(csgraph=graph, i_start=1)[1][0]
    for j in range(len(predecessors)):
        if predecessors[j] == -9999:
            predecessors[j] = breadth_first_order(csgraph=graph, i_start=j+1)[1][j]

    print(names3[i])
    print("Distribution vector: ", dist_matrix)
    print("Predecessors: ", predecessors)
    print("Histograms for shortest path distributions and predecessors\n")
    plt.hist([dist_matrix, predecessors], bins = 'auto', label=['dist', 'pred'])
    plt.legend(loc='upper right')
    plt.show()
    print("-----")
```

Five
Distribution vector: [0 1 2 ... 663 456 862]
Predecessors: [1 0 0 ... 530 574 2]
Histograms for shortest path distributions and predecessors



The skewing of degrees exaggerated even more with more nodes

In [97]:

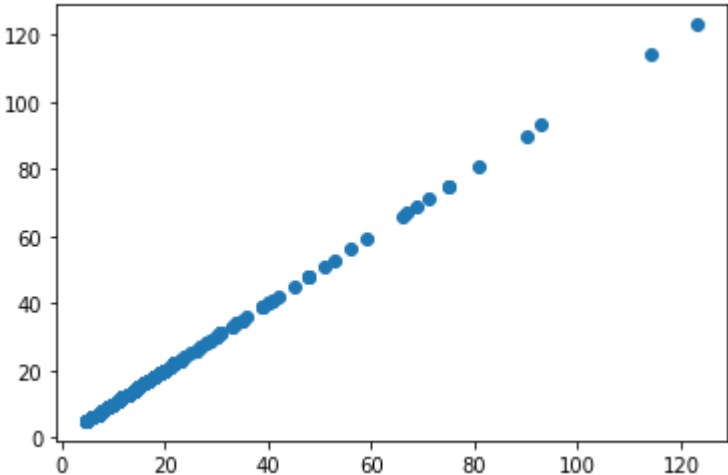
eigenvalues(a_five)

First 100 eigenvalues:
[124.22887067 115.16068029 94.41170626 91.01481836 82.24168858
77.15783924 75.47827567 72.75067796 69.36502789 67.91629187
66.66481085 60.11651922 57.4090516 54.20049168 52.00809445
49.42649727 48.98161201 48.90872014 45.9311437 43.78282396
42.75579451 41.48405842 41.38665976 40.85246906 40.19212343
39.98905024 39.72095697 37.21046704 36.83649917 35.50492699
35.33282906 35.23439422 34.41468564 34.18764281 32.61496679
32.35553226 32.19663452 31.73870394 31.17010135 30.96693402
30.8393308 30.35424825 30.26647945 29.08846335 28.44123645
28.14759022 28.26039002 26.62436503 26.54700912 26.10383611
25.62498629 25.01416254 24.94401722 24.61159249 24.23582853
24.15371713 23.97491169 23.57671387 23.22913071 23.08117118
23.02461132 22.98327628 22.85164819 22.71486874 22.48093979
22.43392112 22.10078718 22.08047149 21.74008494 21.58018326
21.38779709 21.3415254 21.29068757 21.16607359 21.07046099
20.99241076 20.84050532 20.81321449 20.58045199 20.48486304
20.43684547 20.40299455 20.31369432 20.20398685 20.1260494
20.09698878 19.90441796 19.83403782 19.81752823 19.46409177
19.34928685 19.18409641 19.13620225 19.04332625 18.90017103
18.80601259 18.52143205 18.35409761 18.19825412 18.11175009]
Spectral Gap, smallest non-zero eigenvalue for the first 100: 18.111
750087381605

In [98]:

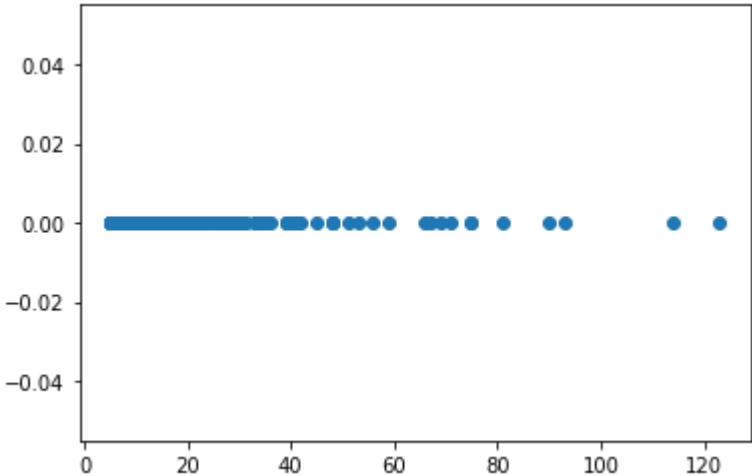
scatter(a_five)

Pearson Correlation Coefficient: 1.0



In [99]:

d_c(a_five)



Overall, there are minor changes but we can see that as the algorithm runs, most of the patterns stay the same.