

Identification of critical connectors in the directed reaction-centric graphs of microbial metabolic networks

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November 18th 2020

Background/Description of Data

- Data is an **adjacency matrix** from a directed microbial metabolic network
 - Nodes are metabolic reactions and edges are metabolites
 - Binary NxN matrix, N is the number of reactions
- Matrices for five microorganisms: *E. coli*, *K. pneumoniae*, *B. subtilis*, *G. metallireducens*, and *S. cerevisiae*
- 4917 total nodes (mean = 983.4, std = 183.3) in the reaction graphs with 42181 total arcs (mean = 8436.2, std = 1311.5) across 5 organisms

	Organism	Nodes	Edges
0	eColi	1251	9099
1	gMetallireducens	900	8049
2	sCerevisiae	881	10460
3	bSubtilis	748	6489
4	kPneumoniae	1137	8084

Analysis Plan

- Recreate the results found in figure 2 of the paper showing that the reaction-centric networks are scale free (degree distribution follows a power law)
- Perform regression analysis (linear model) of node degrees for each microorganism
- Create our own cascade number algorithm
- Calculate correlation matrix with the different centrality metrics using networkx package in Python

Paper's Fig 2.

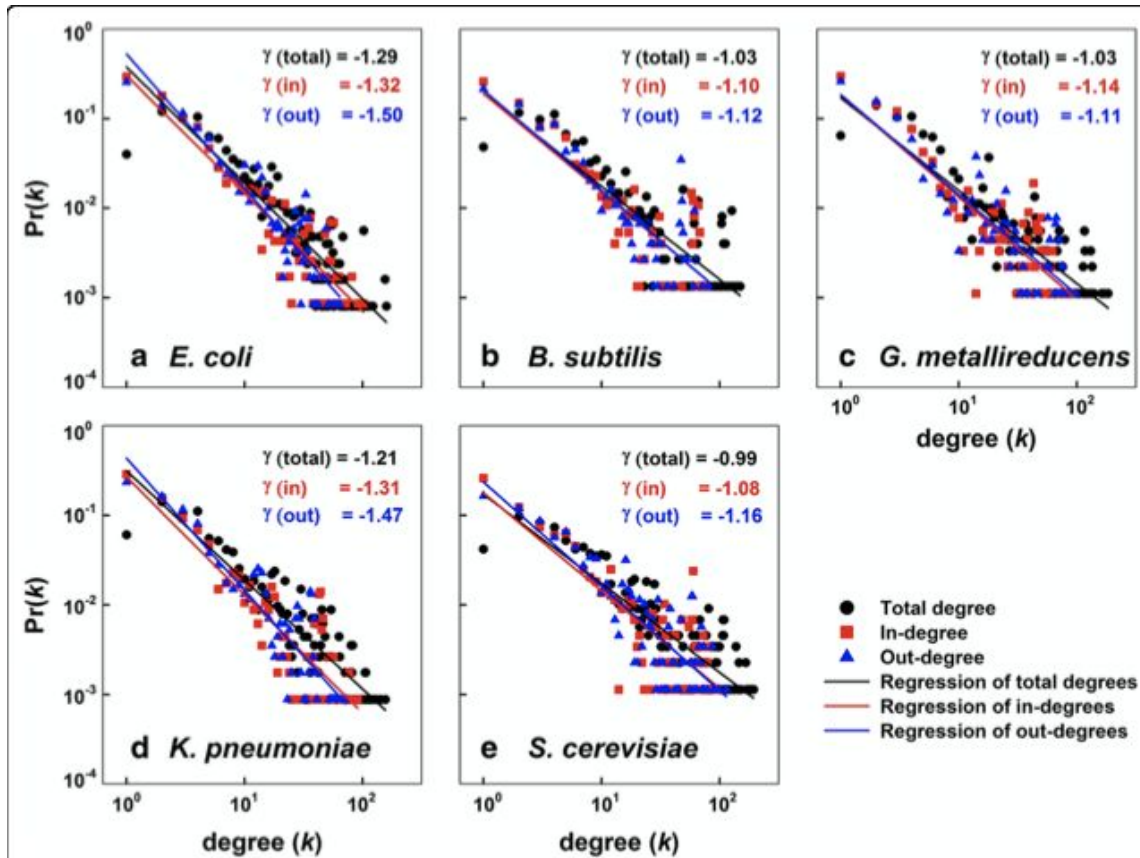


Fig. 2 Degree distribution in the reaction-centric metabolic networks. (a) *Escherichia coli* (IJ01366), (b) *Bacillus subtilis* (J0844), (c) *Geobacter metallireducens* (IAF987), (d) *Klebsiella pneumoniae* (JYL1228), and (e) *Saccharomyces cerevisiae* (JMM904). In-degree (denoted as a red square), out-degree (denoted as a blue triangle), or total degree (denoted as a black circle) was plotted against their probabilities on logarithmic scales.

Recreating Fig 2.

Number of In degrees >>
`k_in = row_sum()`

Number of Out degrees >>
`k_out = col_sum()`

`k_total = k_in + k_out`

Pr(k) obtained from KDE

```
def kde_and_score(vec):
    vec = vec.reshape(-1, 1)
    kde = KernelDensity()
    kde.fit(vec)
    scores = kde.score_samples(vec).ravel()
    return np.exp(scores)

def mat_to_kframe(mat, organism_name='e_coli'):
    in_k = mat.sum(axis = 0).values
    out_k = mat.sum(axis = 1).values
    total_k = in_k + out_k

    frame = []
    for name, k_arr in [("in_k", in_k), ("out_k", out_k), ("total_k", total_k)]:
        k_arr = k_arr[k_arr > 0]
        subframe = pd.DataFrame({
            'k_arr' : k_arr,
            'prob' : kde_and_score(k_arr),
            'k_type' : name
        })
        frame.append(subframe)

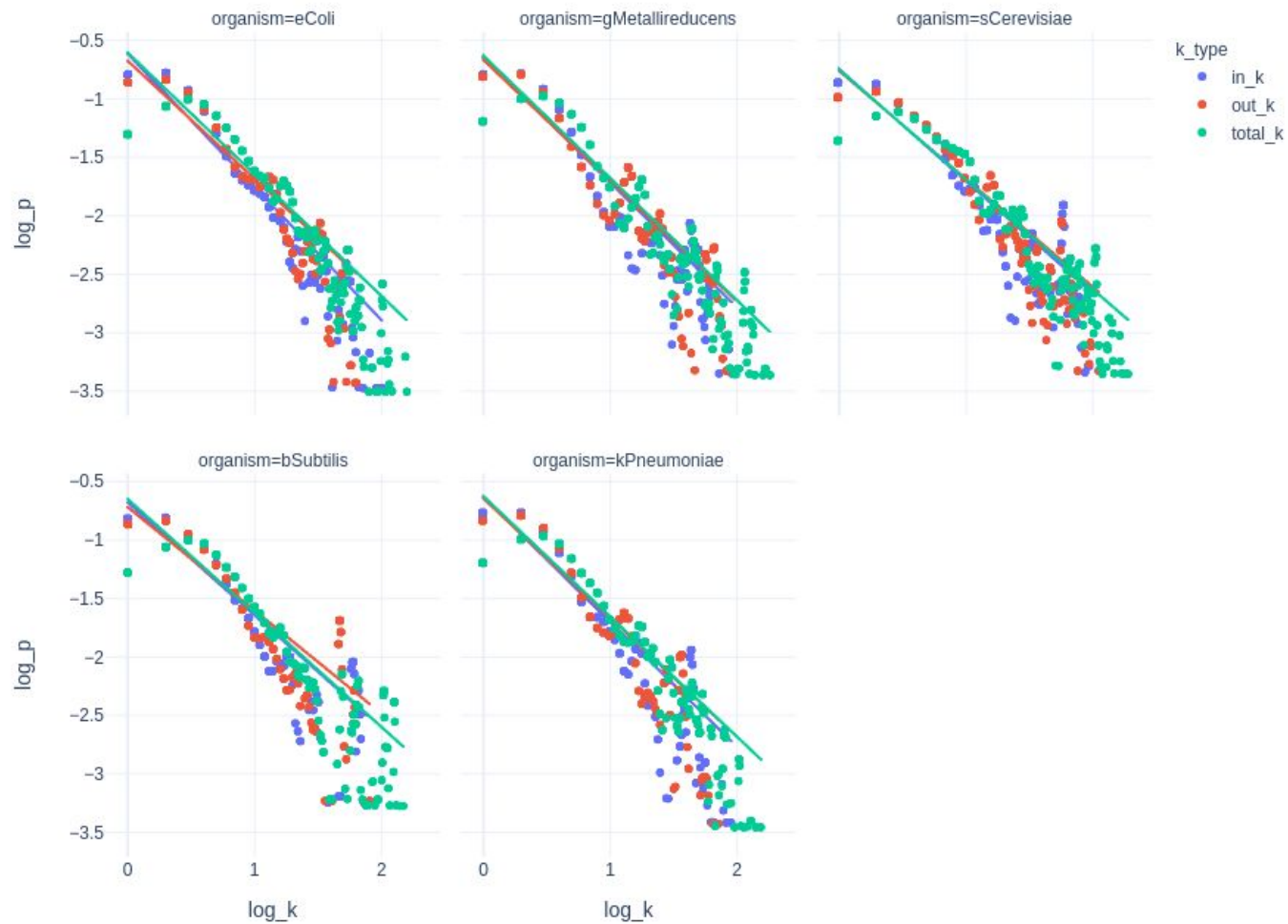
    frame = pd.concat(frame)

    frame['log_k'] = np.log10(frame.k_arr)
    frame['log_p'] = np.log10(frame.prob)
    frame['organism'] = organism_name

    return frame

kframe_list = [mat_to_kframe(m, o) for m, o in zip(mat_list, org_list)]
k_frame = pd.concat(kframe_list)
```

Our Fig 2.



Regression Analysis of Node Degrees (k)

Organism	R-Squared	Intercept	Coefficient	P_val
sCerevisiae	0.8564	-0.73135	-0.93891	< 2e-16
gMetallireducens	0.8586	-0.61384	-1.04682	< 2e-16
KPneumonie	0.8515	-0.61567	-1.02967	< 2e-16
bSubtilis	0.8170	-0.64510	-0.97476	< 2e-16
eColi	0.8379	-0.59247	-1.04100	< 2e-16

$$y = mx + b$$

Probability Distribution

Coefficient(Degree)

Intercept

Paper's Cascade Number Algorithm

Let a directional network be an ordered pair, (V, A) , where V is the set of nodes and A is the set of arcs of the network. Then, the cascade set and cascade number are computed by the following algorithm:

$\text{Cascade}(\text{Node}, \text{Network}(V, A))$

Initialize a queue with the *Node*

Mark *Node* as cut off

Add all nodes v for which (Node, v) in A to the queue

Traverse queue

The node at the front of the queue is q

If q has no ancestors that are not marked as cut off

Mark q as cut off

Add all nodes v for which (q, v) in A to the queue

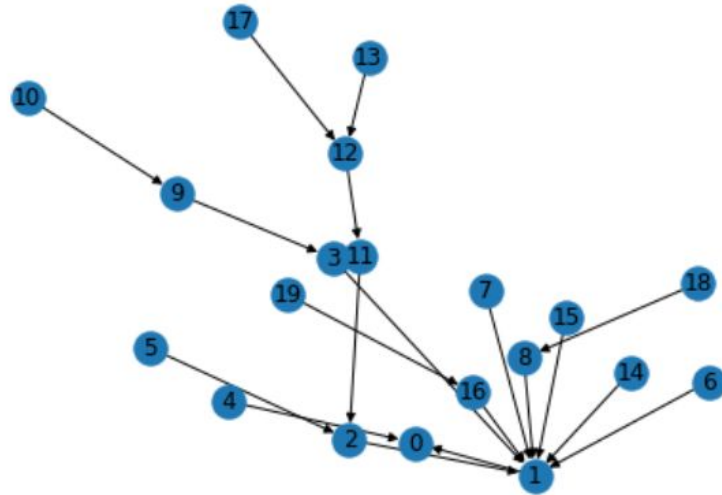
End if

End Traverse

The cascade set of *Node* is the set of nodes marked as cut off.

Cascade number = size of Cascade set

Cascade Number Algorithm



Node	CascadeNumber	NumOut	NumIn
0	0	0	2
1	1	0	8
2	2	0	2
3	3	0	1
4	4	0	0
5	5	0	0
6	6	0	0
7	7	0	0
8	8	0	1
9	9	1	1
10	10	2	0
11	11	0	1
12	12	1	2
13	13	0	0
14	14	0	0
15	15	0	0
16	16	0	1
17	17	0	0
18	18	1	0
19	19	1	0

The Code

```
class CascadeNumber:
```

```
    def __init__(self, dg):
        self.dg = dg
        self.rg = nx.reverse_view(self.dg)
        self.knockouts = set()
        self.cn = 0

    def calculate(self, n, first=True):

        # first recursion
        if first:
            self.knockouts = set()
            self.cn = 0

            self.knockouts.add(n)
            for n in self.dg.neighbors(n):
                self.calculate(n, first=False)
            return self.cn

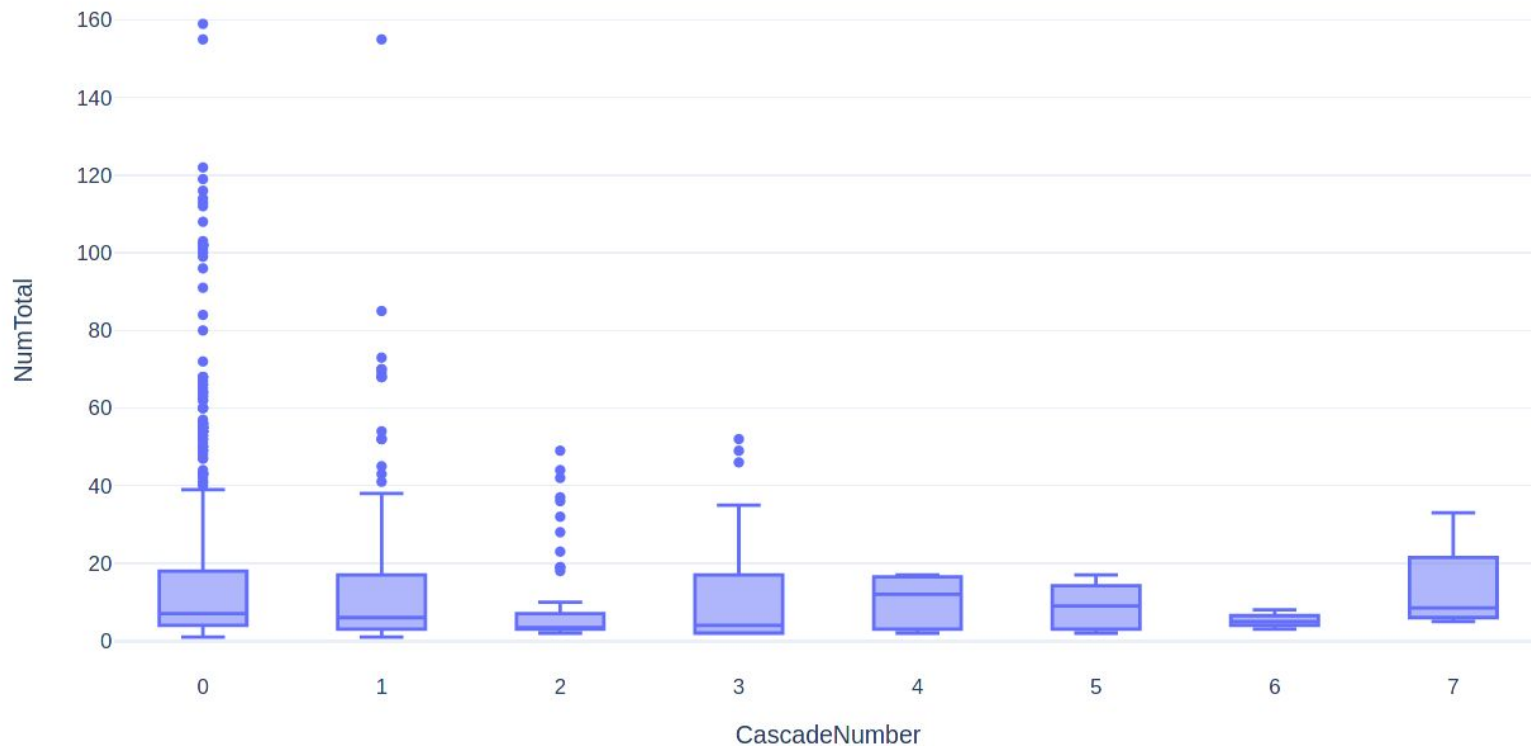
        # every other recursion
        else:
            # stops self loops
            if n in self.knockouts:
                return

            parent_nodes = set(self.rg.neighbors(n))

            # all parent nodes have been knocked out
            if (parent_nodes.intersection(self.knockouts) == parent_nodes):
                self.cn += 1
                self.knockouts.add(n)
                for child in self.dg.neighbors(n):
                    self.calculate(child, first=False)

            # not all parent nodes have been knocked out
            else:
                return
```

Correlation of Cascade Number and Degrees

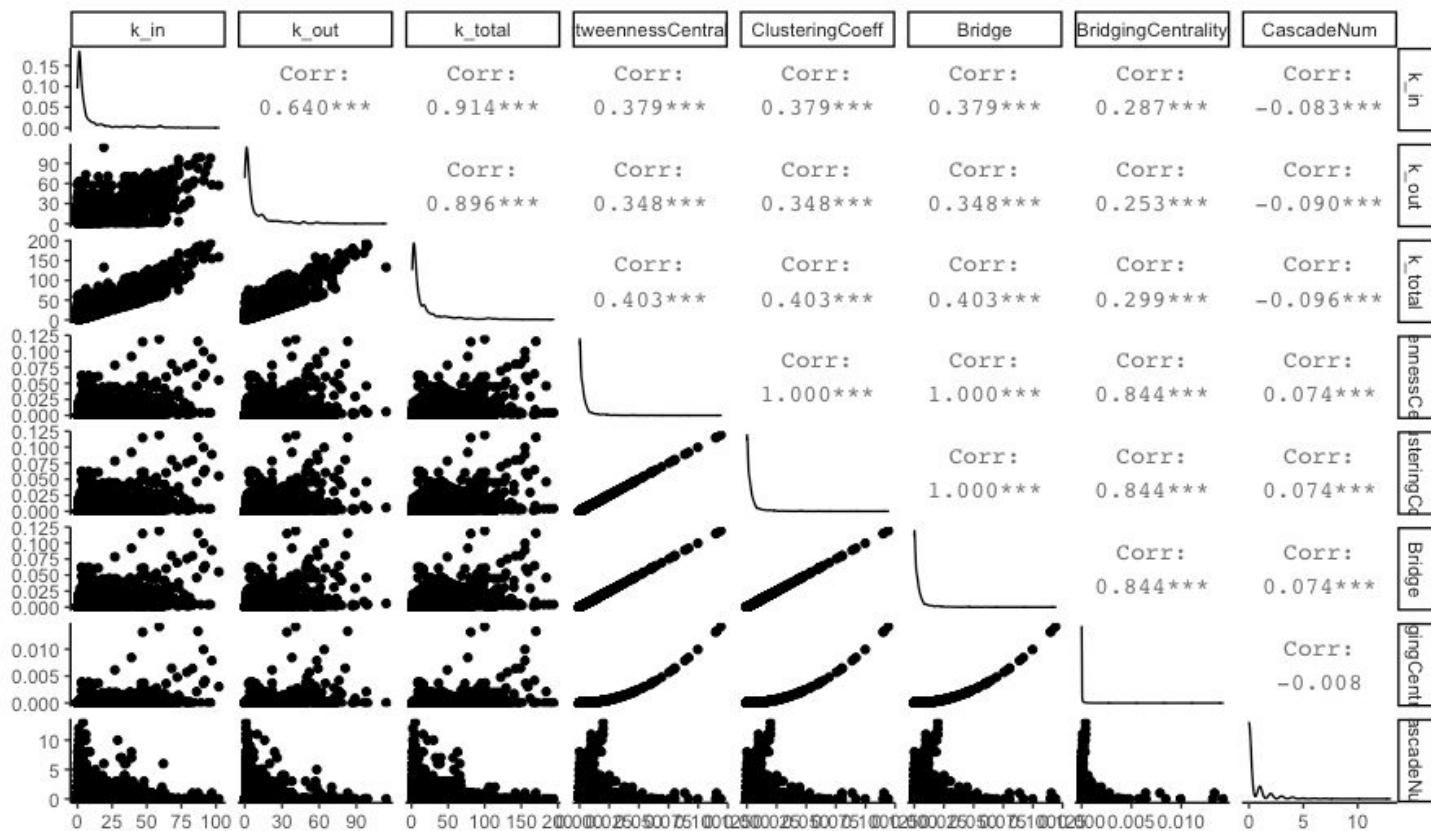


Additional Analysis: Analyzing Centrality Metrics

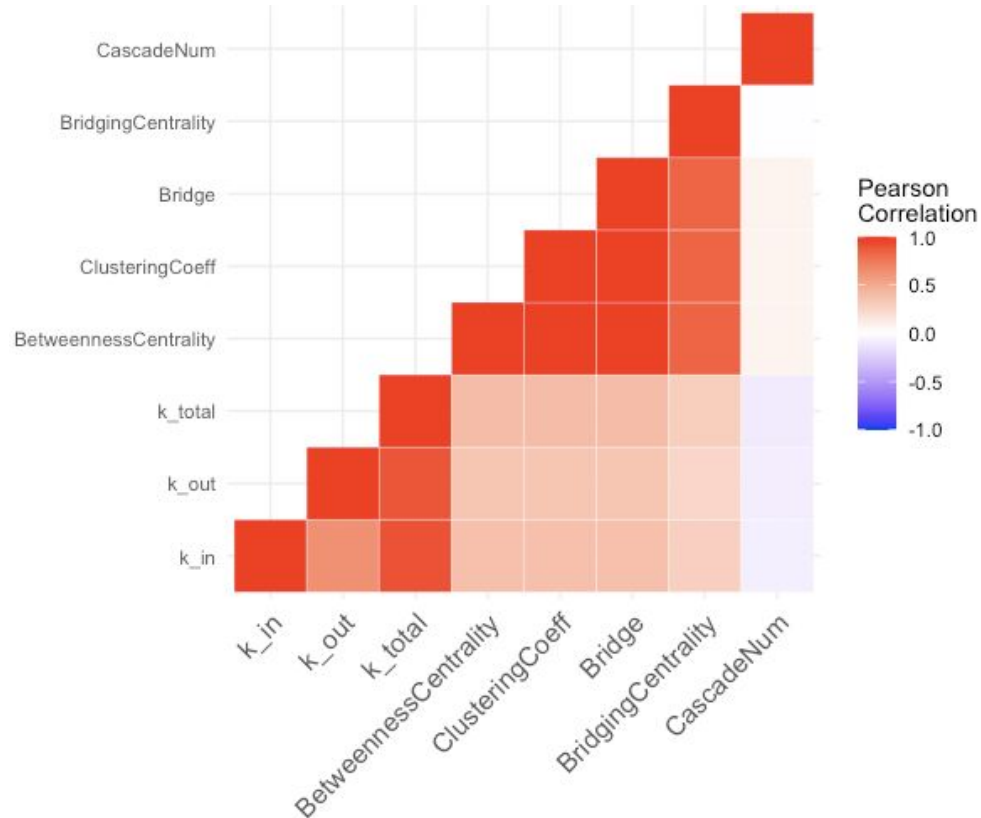
- 5 different organism
- 4917 nodes total

Organism	k_in	k_out	k_total	k_prob	BetweennessCentrality	ClusteringCoeff	Bridge	BridgingCentrality	CascadeNum
1 eColi	6	0	6	0.0580100028	0.000000e+00	0.000000e+00	0.000000e+00	0.000000e+00	0
2 eColi	1	3	4	0.0924816540	7.853140e-06	7.853140e-06	7.853140e-06	6.167180e-11	0
3 eColi	3	14	17	0.0204745832	1.273720e-03	1.273720e-03	1.273720e-03	1.622363e-06	0
4 eColi	2	35	37	0.0055617573	3.341345e-03	3.341345e-03	3.341345e-03	1.116459e-05	0
5 eColi	0	29	29	0.0071321323	0.000000e+00	0.000000e+00	0.000000e+00	0.000000e+00	0
6 eColi	0	4	4	0.0924816540	0.000000e+00	0.000000e+00	0.000000e+00	0.000000e+00	0
7 eColi	0	4	4	0.0924816540	0.000000e+00	0.000000e+00	0.000000e+00	0.000000e+00	0
8 eColi	6	2	8	0.0370412233	1.757579e-03	1.757579e-03	1.757579e-03	3.089085e-06	0
9 eColi	57	6	63	0.0016658922	7.236145e-03	7.236145e-03	7.236145e-03	5.236179e-05	0
10 eColi	3	14	17	0.0204745832	1.643370e-03	1.643370e-03	1.643370e-03	2.700664e-06	1
11 eColi	57	7	64	0.0017141013	1.142245e-02	1.142245e-02	1.142245e-02	1.304723e-04	0
12 eColi	57	5	62	0.0012873496	8.428701e-03	8.428701e-03	8.428701e-03	7.104299e-05	0
13 eColi	57	5	62	0.0012873496	6.898377e-03	6.898377e-03	6.898377e-03	4.758760e-05	0
14 eColi	57	6	63	0.0016658922	9.319659e-03	9.319659e-03	9.319659e-03	6.885605e-05	0
15 eColi	57	3	60	0.0010544001	6.633763e-03	6.633763e-03	6.633763e-03	4.400681e-05	0
16 eColi	57	3	60	0.0010544001	5.846833e-03	5.846833e-03	5.846833e-03	3.418546e-05	0
17 eColi	53	2	55	0.0052129757	1.205446e-03	1.205446e-03	1.205446e-03	1.453099e-06	0

- k_in= Number of In Degrees
- k_out = Number of out Degrees
- k_total=Total Number of Degrees
- BetweennessCentrality= number of times a node acts as the shortest path of the system
- ClusteringCoeff=measure the degree to which nodes will cluster together
- Bridge=measure the number of edges whose removal causes the number of connected components to increase
- BridgingCentrality=Measure the extent of bridging capability. $CC \cdot Br$
- CascadeNumber=Controllability of the graph



Correlation Matrix(pearson), of each centrality metric



Cascade number does not correlate well with any of the other statistics

Create a model to test sensitivity of Cascade Number

Call:

```
lm(formula = CascadeNum ~ k_total + BetweennessCentrality + BridgingCentrality,  
    data = train)
```

Model 1

Residuals:

Min	1Q	Median	3Q	Max
-1.5794	-0.4904	-0.4329	0.1247	10.1167

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	4.554e-01	2.503e-02	18.199	<2e-16 ***
k_total	-7.109e-03	8.061e-04	-8.820	<2e-16 ***
BetweennessCentrality	5.241e+01	4.615e+00	11.357	<2e-16 ***
BridgingCentrality	-5.780e+02	6.574e+01	-8.793	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.166 on 3683 degrees of freedom

Multiple R-squared: 0.04223, Adjusted R-squared: 0.04145

F-statistic: 54.13 on 3 and 3683 DF, p-value: < 2.2e-16

Excluded Bridge, Clustering Coefficient, k_in, k_out due to singularities.

Model 2: Interaction of Variables

Call:

```
lm(formula = CascadeNum ~ k_total * BetweennessCentrality * BridgingCentrality,  
    data = train)
```

Model 2

Residuals:

Min	1Q	Median	3Q	Max
-1.7359	-0.4807	-0.2262	0.1052	9.5596

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	2.250e-01	2.920e-02	7.705	1.67e-14	***
k_total	-2.092e-03	1.100e-03	-1.902	0.0572	.
BetweennessCentrality	1.868e+02	9.975e+00	18.731	< 2e-16	***
BridgingCentrality	-6.137e+03	4.309e+02	-14.242	< 2e-16	***
k_total:BetweennessCentrality	-1.912e+00	2.042e-01	-9.362	< 2e-16	***
k_total:BridgingCentrality	5.990e+01	5.782e+00	10.359	< 2e-16	***
BetweennessCentrality:BridgingCentrality	4.141e+04	3.884e+03	10.664	< 2e-16	***
k_total:BetweennessCentrality:BridgingCentrality	-3.915e+02	4.235e+01	-9.243	< 2e-16	***

Tested to Validate the data

Created 80/20 split of training to test data for these models.

Model 1	58% accuracy
Model 2	59% accuracy

Cascade Number is Discrete!

I need to change my model to predict a discrete feature and not continuous

actuals	predicteds
0	0.361065070
0	0.426998042
0	0.488894358
0	0.356546013
0	0.315562903
1	0.856292563
0	0.008062391
0	0.084495228
0	0.059466466
0	0.117322324
3	0.255136083
0	0.125261105
0	-1.165614635
0	0.447291195
0	0.453288728
0	0.423666182
0	0.507805873
5	0.568314610
4	0.561661470

Creating a GLM under a poisson distribution

```
glm(formula = CascadeNum ~ k_total + BetweennessCentrality +  
    BridgingCentrality, family = poisson(link = "log"), data = train)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.2200	-0.9362	-0.8479	-0.2360	8.3718

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-9.260e-01	3.783e-02	-24.48	<2e-16 ***
k_total	-2.524e-02	1.869e-03	-13.50	<2e-16 ***
BetweennessCentrality	1.914e+02	9.724e+00	19.69	<2e-16 ***
BridgingCentrality	-4.689e+03	3.930e+02	-11.93	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model 3	64% Accuracy
Model 4	64% Accuracy

```
glm(formula = CascadeNum ~ k_total * BetweennessCentrality *  
    BridgingCentrality, family = poisson(link = "log"), data = train)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.3736	-0.8794	-0.7017	-0.2271	6.2964

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.369e+00	4.989e-02	-27.435	< 2e-16 ***
k_total	-1.647e-02	2.970e-03	-5.544	2.96e-08 ***
BetweennessCentrality	4.210e+02	1.565e+01	26.896	< 2e-16 ***
BridgingCentrality	-1.879e+04	9.975e+02	-18.841	< 2e-16 ***
k_total:BetweennessCentrality	-3.402e+00	4.716e-01	-7.213	5.48e-13 ***
k_total:BridgingCentrality	1.458e+02	1.110e+01	13.140	< 2e-16 ***
BetweennessCentrality:BridgingCentrality	1.297e+05	8.055e+03	16.106	< 2e-16 ***
k_total:BetweennessCentrality:BridgingCentrality	-9.868e+02	7.481e+01	-13.190	< 2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Lessons/Challenges

- Data was limited
 - Edge direction was not given in adjacency matrix
 - More network metrics would be helpful
- Translating cascade algorithm from pseudocode
- Discrete vs Continuous predictive modeling

Nice job on the presentation! Clear background and description of the network; good work fitting a linear model and reimplementing cascade number as a recursion. As we discussed in class, the high CV accuracy despite low R-square is a tip-off that there may be leakage between the training and test sets. Unbalanced classes also affect performance metrics.

Grade: 27/30

