Numerical Investigation of Metrics for Epidemic Processes on Graphs

(In Proceedings of 2015 Asilomar Conference on Signals, Systems, and Computers)

Max Goering, Nathan Albin
and Pietro Poggi-Corradini
Department of Mathematics
Kansas State University
Manhattan, KS 66506
Email: mlgoering@gmail.com,
{albin,pietro}@math.ksu.edu

Caterina Scoglio
and Faryad Darabi Sahneh
Department of Electrical and
Computer Engineering
Kansas State University
Manhattan, KS 66506
Email: {caterina,faryad}@ksu.edu

Abstract—This study develops the epidemic hitting time (EHT) metric on graphs measuring the expected time an epidemic starting at node \( a \) in a fully susceptible network takes to propagate and reach node \( b \). An associated EHT centrality measure is then compared to degree, betweenness, spectral, and effective resistance centrality measures through exhaustive numerical simulations on several real-world network data-sets. We find two surprising observations: first, EHT centrality is highly correlated with effective resistance centrality; second, the EHT centrality measure is much more delocalized compared to degree and spectral centrality, highlighting the role of peripheral nodes in epidemic spreading on graphs.

I. INTRODUCTION

Dynamics on graphs has long been a central research topic across many applied disciplines. Several graph related quantities have proven successful in studying different applications. In particular, the effective resistance metric appears to be an important tool for studying a variety of dynamics over graphs, including, but not limited to, random walks on graphs, electrical networks, Markov chains, and averaging networks [4]. It comes as no surprise that effective resistance is important for all these dynamic processes because they are gradient driven processes. The effective resistance is closely related to the Laplacian matrix of the underlying graph. However, epidemic spreading dynamics is a branching process and behaves very differently from gradient driven dynamics.

In this paper, we seek graph quantities that help describe epidemic dynamics. Centralities are frequently used to determine properties of the underlying topology of a network. In fact, comparing different centralities on the same network can be used to classify the network structure [22]. Herein, we compare common centralities as well as graph metrics to see how to best understand epidemic dynamics. We use many of the same real-world data sets as in [22] and conclude that surprisingly, regardless of the underlying network structure, numerics indicate that the effective resistance is the most relevant graph quantity to the epidemic spreading. A partial explanation is offered at the end of the article.

This material is based upon work supported by the National Science Foundation under Grant No. DMS-1201427 and No. DMS-1515810.

II. EPIDEMIC HITTING TIME METRIC FOR GRAPHS

A. The SI model

The SI Epidemic Model is a model where every interaction between an infected and susceptible node can lead the susceptible node to become infected at a rate \( \beta \) called the infection rate. This means, that if two people, say Alice and Bob interact, and at time \( t \) Alice is infected while Bob is susceptible, then the probability that Alice infects Bob in the time interval \( (t, t+h) \) equals \( \beta h + o(h) \). Further, in the SI epidemic model, we assume that infections occur independently and once someone becomes infected they remain infected forever. In particular, by independence, the probability that two separate infections occur during a time interval \( (t, t+h) \) is \( o(h) \).

In realistic models, these interactions are described by links of a contact network \( G = (V, E) \). In order to keep track of the infection, we introduce the state vector \( \omega_t \), where \( \omega_t(i) \) is the state at time \( t \) of the \( i \)-th node in the network. If \( \omega_t(i) = 0 \) we say node \( i \) is susceptible and if \( \omega_t(i) = 1 \) we say node \( i \) is infected. In order to make the scenario with Alice and Bob rigorous, we let \( N = |V| \) and \( A = [A(i,j)]_{1 \leq i,j \leq N} \) be the adjacency matrix representing the network \( G \). Then \( A(i,j) = 1 \) if node \( i \) can be infected by node \( j \) and zero otherwise. Finally, let \( I_t = \{ i : \omega_t(i) = 1 \} \) be the set of nodes that are infected by time \( t \). Since at most one infection occurs during \( (t, t+h) \), we can condition on the possible infection occurrences and obtain:

\[
\mathbb{P} \left[ \omega_{t+h}(i) = 1 \mid \omega_t(i) = 0, I_t \right] = \beta h \sum_{j=1}^{N} A(i,j) \omega_t(j) + o(h)
\]

(II.1)

Next we consider the process \( |I_t| \) which counts the total number of infected nodes in the network at time \( t \). We find the transition probabilities for \( |I_t| \) by summing over all susceptible nodes \( S_t = \{ i : \omega_t(i) = 0 \} \). In other words, writing \( |I_t| = \omega_t \cdot 1 \) where \( 1 = [1 \cdots 1]^T \) is a vector of ones, we have that
for \( h > 0 \) small,
\[
\mathbb{P}[ |I_{h+1}^t| - |I_t^t| = 1 | I_t^t ] = \beta h \left( {\omega_i^T} A^1 - {\omega_i^T} A\omega_t \right) + o(h)
\]

Note that \( A^1 = d \) where \( d(j) \) is the degree of node \( j \). Write \( D = \text{diag}(d) \) for the diagonal matrix of the node degrees. Then,
\[
{\omega_i^T} A^1 = {\omega_i^T} d = {\omega_i^T} D^1 = {\omega_i^T} D\omega_t,
\]
where the last equality follows since \( \sum_{j} \omega_i(j)D(i,j) = \sum_{j} d(i)\omega_i(j) = \sum_{j} d(i)\omega_i(j)^2 = \sum_{j} \omega_i(j)D(i,j)\omega_j(j) \).

So letting \( L = D - A \) be the combinatorial Laplacian, we get that
\[
{\omega_i^T} A^1 - {\omega_i^T} A\omega_t = {\omega_i^T} D\omega_t - {\omega_i^T} A\omega_t = \omega_i^T L\omega_t
\]

Then
\[
\mathbb{P}[ |I_{h+1}^t| - |I_t^t| = 1 | I_t^t ] = \beta h {\omega_i^T} L\omega_t + o(h). \tag{II.2}
\]

We learned to use the Laplacian in this equation from \cite{24}.

The set \( V \) splits into two subsets \( S_t \) and \( I_t \) and \( \omega_t \) is the indicator function of the set \( I_t \). This partition defines a subset of edges called the edge-boundary, \( \partial I_t \), consisting of all the edges that connect a node in \( I_t \) to a node in \( S_t \). With this in mind, the quadratic form
\[
{\omega^T} L\omega_t = \sum_{e \in E} [\nabla \omega_t(e)]^2 = \sum_{e \in \partial I_t} 1 = |\partial I_t|
\]
counts the number of edges in \( \partial I_t \).

So equation (II.2) becomes
\[
\mathbb{P}[ |I_{h+1}^t| - |I_t^t| = 1 | I_t^t ] = \beta h |\partial I_t| + o(h). \tag{II.3}
\]

Now we determine the probability that a susceptible node \( i \) will be the next node infected after time \( t \), given \( \omega_t \) and given that an infection occurs. Using the definition of conditional probability,
\[
\mathbb{P}[ \omega_{t+h}^i \sim \omega_t^i = 1 | I_t^t, |I_{t+h}^t| - |I_t^t| = 1 ] = \frac{\mathbb{P}[ \omega_{t+h}^i \sim \omega_t^i = 1, |I_{t+h}^t| - |I_t^t| = 1 | I_t^t ]}{\mathbb{P}[ |I_{t+h}^t| - |I_t^t| = 1 | I_t^t ]} = \frac{\beta h (A\omega_t^i)(i) + o(h)}{\beta h |\partial I_t| + o(h)} = (A\omega_t^i)(i) + o(1)
\]
where the last line follows from (II.1) and (II.3).

Letting \( h \downarrow 0 \) yields, we see that \( I_t \) evolves by choosing an active edge in \( \partial I_t \) uniformly at random, and then infecting the susceptible endpoint of the chosen edge. The arrival times \( Y_0, Y_1, \ldots \) of the SI epidemic \( \omega_t \) are defined by \( Y_0 = 0 \) and
\[
Y_k = \inf \{ t \geq 0 : |I_t| = k \} \quad \text{for } k = 1, 2, \ldots
\]
The interarrival times \( T_1, T_2, \ldots \) are the times between successive arrivals,
\[
T_k = Y_k - Y_{k-1} \quad \text{for } k = 1, 2, \ldots
\]
Therefore, given the set of infected nodes \( I_{Y_k} \), the next arrival time \( T_{k+1} \) satisfies
\[
T_{k+1} \sim \text{Exponential}(\beta |\partial I_{Y_k}|).
\]

More precisely,
\[
\mathbb{P}[ T_{k+1} \leq t \mid I_{Y_k} = I ] = 1 - e^{-\beta |\partial I_t|^t}.
\]

This gives rise to an event-based algorithm that picks an active edge uniformly and updates the clock exponentially based on the size of the active set.

B. Epidemic Hitting Time and Variable-Lengths Models

The SI model describes a basic epidemic process which can be thought of as a Markov chain on the set of subsets of \( V \). It is natural to introduce the notion of epidemic hitting time.

Definition II.1. Given two nodes \( a \neq b \), start an SI epidemic \( \omega_t \) at \( a \). Define the hitting time \( T_{a,b} = \inf \{ t \geq 0 : b \in I_t \} \). Then, the epidemic hitting time from \( a \) to \( b \) is the expected hitting time
\[
\tau_{a,b} = \mathbb{E} (T_{a,b}).
\]

The variable-lengths model for the network \( G = (V,E) \) consists of assigning i.i.d. lengths \( X_e \sim \text{Exponential}(\beta) \) for every \( e \in E \). We then let \( d(a,b) \) be the shortest-path distance with respect to these random edge-lengths.

Theorem II.2. For a contact network \( G = (V,E) \) with variable i.i.d. edge-lengths \( X_e \sim \text{Exponential}(\beta) \) for each \( e \in E \), the continuous time process \( Z_t = \{ v \in V : d(a,v) \leq t \} \) is a Markov process that evolves like an SI epidemic.

Remark II.1. Theorem II.2 is folklore in some circle (We thank Brent Werness for pointing out section 1.2.1 of \cite{19} where this remark is made).

C. Properties of Epidemic Hitting Time

Theorem II.3. The epidemic hitting time is a metric (it is non-degenerate, symmetric and satisfies the triangle inequality).

Proof: Theorem II.3 follows directly from Theorem II.2 since \( \tau_{a,b} = \mathbb{E} [d(a,b)] \) and the expected value of a metric is still a metric.

We say that a graph \( G_1 = (V_1, E_1) \) is a refinement of \( G = (V,E) \) if \( V_1 \subset V \) and \( E_1 \subset E \).

Proposition II.4. If \( G_1 \) is a refinement of \( G \), then for all \( a, b \in V \), the epidemic hitting time \( \tau_{a,b}(G) \geq \tau_{a,b}(G_1) \).

Proof: By Theorem II.2 adding more edges can only shorten \( d(a,b) \), and adding new vertices cannot lengthen the shortest walk between \( a \) and \( b \). So \( Z_t(G) \subset Z_t(G_1) \).

Proposition II.5. Assume \( \beta = 1 \). If \( T \) is a tree, then the epidemic hitting time is equal to the graph metric \( d_0 \) (shortest-path metric using number of hops). Furthermore, for an arbitrary graph \( G \), the epidemic hitting time is bounded above by \( d_0 \).

Proof: This also follows from Theorem II.2. On a tree there is a unique simple path from \( a \) to \( b \). So the expectation of the distance \( d(a,b) \) can be computed using linearity. That
is, if $\gamma_{a,b}$ denotes the unique simple path starting at $a$ and ending at $b$, then

$$\mathbb{E}(d(a,b)) = \sum_{a\in\gamma_{a,b}} \mathbb{E}(X_e) = |\gamma_{a,b}| = d_0(a,b).$$

The ‘Furthermore’ statement follows from Proposition II.4.

**Proposition II.6.** For the complete graph $K_N$ on $N$ nodes. Given $a \neq b$ and $\beta = 1$, the epidemic hitting time equals

$$H_N(a,b) = \frac{\log N}{N} + o(1). \quad (II.4)$$

Therefore, for an arbitrary graph $G$, the epidemic hitting time is bounded below by the expression in (II.4).

**Proof:** To compute $\tau_{a,b}$, we condition on the event $T_{a,b} = Y_k$, meaning that $b$ is the $k$th infected node.

$$\tau_{a,b} = \sum_{k=1}^{N-1} \mathbb{E}[T_{a,b} \mid T_{a,b} = Y_k] \mathbb{P}(T_{a,b} = Y_k)$$

Note that by symmetry

$$\mathbb{P}(T_{a,b} = Y_k) = \frac{1}{N-1}.$$ 

Now, if $T_{a,b} = Y_k$ that means that the first interarrival time $T_1$ is distributed like the minimum of $N-1$ exponential variables, $T_2$ like the minimum over $2(N-2)$ variables, etc... and so $\mathbb{E}[T_{a,b} \mid T_{a,b} = Y_k]$ should be equal to:

$$\frac{1}{(N-1)} + \frac{1}{2(N-2)} + \cdots + \frac{1}{k(N-k)}$$

With this we get

$$\tau_{a,b} = \frac{1}{N-1} \sum_{k=1}^{N-1} \sum_{j=1}^{k} \frac{1}{j(N-j)}$$

$$= \frac{1}{N-1} \sum_{j=1}^{N-1} \sum_{k=j}^{N-1} \frac{1}{j(N-j)}$$

$$= \frac{1}{N-1} \sum_{j=1}^{N-1} \frac{1}{j} \log \frac{N}{j}$$

Combining our refinement observation (Proposition II.4) with Propositions II.5 and II.6 we have the following corollary.

**Corollary II.7.** Given a contact graph $G = (V,E)$ and two nodes $a,b$ in $V$. Then

$$H_N(a,b) \leq \tau_{a,b} \leq d_0(a,b).$$

A different lower bound was proved by Lyons, Pemantle and Peres in [18].

**Theorem II.8 (18).** Let $G = (V,E)$ be a contact network with variable i.i.d. edge-lengths $X_e \sim \text{Exponential}(1)$ for each $e \in E$. Let $a,b$ be two nodes in $V$. Then

$$\tau_{a,b} = \mathbb{E}[d(a,b)] \geq R(a,b)$$

where $R(a,b)$ is the effective resistance between $a$ and $b$ when $G$ is an electrical network with edge-conductances equal to 1 Ohm.

Note that for a complete graph $R(a,b)$ is smaller than $H_N(a,b)$, while for a path graph it is larger. In general, the relation between these two bounds depends on the structure of the graph.

**D. The “Dijkstra on the fly” algorithm**

When computing the shortest-path distance $d(a,b)$, one may implement Dijkstra’s algorithm. However, instead of determining all the edge-lengths $X_e$ at the beginning, one may compute the length of an edge as needed. So to obtain the “Dijkstra on the fly” algorithm from Dijkstra’s algorithm it is enough to insert line 8. The advantage is that only the edges in the ball induced by $\{x \in V : d(x,a) \leq d(b,a)\}$ are needed.

**Algorithm 1** Dijkstra on the fly algorithm

**Require:** $(G,s)$

1: $W \leftarrow \emptyset$

2: $\delta(s) \leftarrow 0$

3: $\delta(u) \leftarrow \infty$ and $\text{pred}(u) \leftarrow \emptyset$ for all $u \in V \setminus \{s\}$

4: **while** There exists $u \not\in W$ satisfying $\delta(u) < \infty$ **do**

5: \hspace{0.5cm} $u \leftarrow \text{argmin}\{\delta(u) : u \not\in W\}$

6: \hspace{0.5cm} $W \leftarrow W \cup \{u\}$

7: **for** Each $v \not\in W$ that neighbors $u$ **do**

8: \hspace{1cm} $\ell(u,v) \leftarrow \text{Exponential}(\beta)$

9: \hspace{1cm} **if** $\delta(u) + \ell(u,v) < \delta(v)$ **then**

10: \hspace{1.5cm} $\delta(v) \leftarrow \delta(u) + \ell(u,v)$

11: \hspace{1.5cm} $\text{pred}(v) \leftarrow u$

12: **end if**

13: **end for**

14: **end while**

**III. METRICS AND CENTRALITIES**

A graph centrality is a function $P : V \rightarrow \mathbb{R}$ that assigns a value to each node. This value represents how important a node is with respect to the graph topology. It is often convenient to normalize a centrality so that it can be thought of as a probability distribution.

A graph metric is a symmetric, non-degenerate function $d : V \times V \rightarrow [0, \infty]$ that satisfies the triangle inequality. Every graph metric induces a centrality denoted

$$P_d(v_i) := \frac{1}{N} \sum_{v_j \neq v_i} \frac{1}{d(v_i,v_j)}. \quad (III.1)$$

Heuristically, this induced centrality measures how close node $v_i$ is to the rest of the network.

**A. Metrics**

**Epidemic Hitting Time:** This is the expected time it takes for an infection starting at node $i$ to infect node $j$. Theorem II.3 establishes that the epidemic hitting time is actually a graph metric. For numerical approximations, one can run an
\[\mathcal{R} = \text{diag}(L^\dagger) + \text{diag}(L^\dagger)^T - 2L^\dagger \quad (\text{III.2})\]

Effective resistance has been shown to be closely related to many properties of random Markov processes \([2]\), including escape probabilities and commuting times of random walks \([6]\), as well as recurrence/transience properties of random walks \([7]\).

**B. Centralities**

**Spectral Centrality:** The spectral centrality \((S)\) is based on the idea that the importance of a node depends on the importance of its neighbors. Spectral centrality does well in characterizing simple dynamics like diffusion, and is the basis of the PageRank algorithm \([5]\). It is defined as

\[S(i) = v_i = \lambda^{-1} \sum_{j \sim i} v_j,\]

where \(\lambda\) is the largest eigenvalue of the adjacency matrix and \(v_j\) is the \(j\)th component of the corresponding eigenvector.

**Degree Centrality:** The degree centrality \((D)\) of a node is simply the number of neighbors. Therefore it ignores the importance a node’s neighbors and will frequently rank the importance of a large number of nodes to be the same.

**Betweenness Centrality:** The betweenness centrality \((B)\) first introduced in \([3]\) and popularized by Freeman \([9]\) is a method of measuring the importance of a node based on the fraction of shortest paths that it lies on. It measures the influence of a node over the spread of information through the network. It is defined as

\[B(i) = N^{-1} \sum_{j \neq i \neq k} \frac{\sigma_{jk}(i)}{\sigma_{jk}},\]

where \(\sigma_{jk}\) denotes the number of shortest paths between \(j\) and \(k\) and \(\sigma_{jk}(i)\) is the number of shortest paths from \(j\) to \(k\) that visit node \(i\). Betweenness centrality is good for determining bottlenecks.

**Communicability Centrality:** The communicability centrality \((C)\) is an adaptation of Freeman’s betweenness centrality that takes into account all independent walks between two nodes, instead of just the geodesic paths. The pairwise communicability can be computed from the spectrum of the adjacency matrix \([8]\) as

\[C(i) = \sum_{j=1}^{N} (v_{j,i})^2 e^{\lambda_j},\]

where \(\lambda_1 \geq \lambda_2 \geq \ldots \geq \lambda_N\) are the eigenvalues of the adjacency matrix, and \(v_{k,\ell}\) is the \(\ell\)th element of the eigenvector corresponding to the \(k\)th eigenvector.

**IV. Real-World Networks**

In our simulations, we have used several real-world networks, available for download at [http://ece.k-state.edu/netse/projects/sprojects/proj2-products.html](http://ece.k-state.edu/netse/projects/sprojects/proj2-products.html).

| Network     | Number of Nodes | Number of Edges | Average Node Degree | Average Clustering Coefficient | Diameter |
|-------------|-----------------|-----------------|---------------------|--------------------------------|----------|
| Adinoun     | 112             | 425             | 7.589               | 0.1569                         | 5        |
| Dolphins    | 62              | 159             | 5.129               | 0.309                          | 8        |
| Facebook    | 2106            | 2915            | 2.768               | 0.117                          | 12       |
| Football    | 115             | 615             | 10.695              | 0.407                          | 4        |
| GRQC        | 4158            | 13422           | 6.456               | 0.357                          | 17       |
| Hep         | 8361            | 15751           | 3.768               | 0.329                          | 19       |
| Karate      | 34              | 78              | 4.588               | 0.286                          | 5        |
| Lesmis      | 17              | 254             | 6.597               | 0.499                          | 5        |
| Netscience  | 1589            | 2742            | 3.451               | 0.693                          | 17       |
| Polblogs    | 1490            | 19090           | 25.624              | 0.226                          | 9        |
| Power       | 4941            | 6594            | 2.569               | 0.103                          | 46       |

![Fig. 1. Summary of Network Structure Properties](image-url)

**V. Numerical Methods and Results**

For each network described above, the epidemic hitting time was approximated by averaging the results of 100 SI simulations. Then a corresponding centrality was created using (III.1). These results were compared to the centrality obtained from effective resistance as well as the spectral, degree, betweenness, and communicability centralities. Comparisons were done in two ways.

**Total variation distance of probability measures:** One comparison was to compute the total variation between two centralities after normalizing the centralities so that they can be interpreted as a probability measure on the nodes. Given two centralities \(P\) and \(Q\) this amounts to computing (see \([16]\)),

\[\frac{1}{2} \sum_{v \in V} |P(v) - Q(v)|.\]

In particular, the total variation distance of probability measures is a value between zero and two, where zero means the distributions overlap completely, and two means they are mutually singular.

**Spearman’s Rank Correlation Coefficient:** The Spearman Rank coefficient takes values between negative one and one and should be interpreted like the Pearson correlation coefficient \([14]\). Below are the results of these comparisons.

This data indicates that effective resistance is a good measure of the influence that a node has over the spread of an epidemic throughout a contact network. However, the tables give little insight as to why effective resistance outperforms the other quantities. To gain intuition, we look at the heatmaps of the Lesmis network \([23]\) in Figure 4 representing the importance of each node according to the respective graph quantity. We see that effective resistance and the epidemic hitting time are the only two graph quantities that assign relative importance to peripheral nodes of the network.
Fig. 2. A table of values of the Spearman Rank coefficient between each centrality and the epidemic hitting time centrality. We note that in every network except the Karate club network, the Effective Resistance outperforms every other centrality. We also remark that in [22], there was a similar observation of the Karate club network not behaving like the other networks, likely due its being a small network with a few dominating nodes.

VI. CONCLUSION

In this paper, we propose the epidemic hitting time (EHT) as a relevant metric on graphs to study epidemic processes. Epidemic hitting time between node \(a\) and node \(b\) measures the expected time it takes for an infection process starting at node \(a\) in a fully susceptible network to propagate and reach node \(b\). We develop the theory based on the susceptible-infected (SI) model, and show its equivalence with a variable link-length shortest-path model based on exponentially distributed random edge weights. As a result, we develop several efficient numerical methods for the EHT metric computation. Then,
we conduct an exhaustive numerical experiment where we compute node centralities based on the EHT metric and compare the resulting ranking with the ones obtained using several other common node centralities including node degree, spectral, betweenness, communicability, and effective resistance centrality. We observe two surprising findings: first, EHT centrality is highly correlated with effective resistance centrality; second, EHT highlights the role of peripheral nodes in epidemic spreading unlike most other common centrality measures.

The variable-lengths model is useful to establish various properties of epidemic hitting time, but it also offers a partial explanation as to why our numerics show effective resistance as being closely correlated to the epidemic hitting time. In the work of Lyons, Pemantle, and Peres [18], it was shown that the expected shortest path on a graph with i.i.d. exponentially distributed random lengths of mean one is bounded below by the effective resistance on the graph with unit resistance. In particular, this shows that the epidemic hitting time is bounded below by the effective resistance. This result confirms the recent finding of other authors (for example Sikic et al. [23]) that the impact of peripheral nodes is typically underestimated in epidemic models. In summary, the computation of EHT-based node centrality provides novel information on the infection process on a graph, complementing the knowledge provided by common metrics.

REFERENCES

[1] L. A. Adamic and N. Glance, The political blogosphere and the 2004 us election: divided they blog. In Proceedings of the 3rd international workshop on Link discovery, pages 36–43. ACM, 2005.
[2] D. Aldous and J. Fill, Reversible markov chains and random walks on graphs, Unfinished monograph, recompiled 2014, available at http://www.stat.berkeley.edu/$\sim$aldous/RWG/book.html.
[3] A. Bavelas, A mathematical model for group structures. Human organization, 7(3):16–30, 1948.
[4] A. Ghosh, S. Boyd, and A. Saberi, Minimizing effective resistance of a graph. SIAM Rev. 50 (2008), no. 1, 3766.
[5] S. Brin and L. Page, The anatomy of a large-scale hypertextual web search engine. Computer networks and ISDN systems, 30(1):107–117, 1998.
[6] A. K. Chandra, P. Raghavan, W. L. Ruzzo, R. Smolensky, and P. Tiwari, The electrical resistance of a graph captures its commute and cover times. Computational Complexity, 6(4):312–340, 1996.
[7] P. G. Doyle and J. L. Snell, Random walks and electric networks. AMC, 10:12, 1984.
[8] E. Estrada and N. Hatano, Communicability in complex networks. Physical Review E, 77(3):036111, 2008.
[9] L. C. Freeman, A set of measures of centrality based on betweenness. Sociometry, pages 35–41, 1977.
[10] M. Girvan and M. E. J. Newman, Community structure in social and biological networks. Proceedings of the National Academy of Sciences, 99(12):7821–7826, 2002.
[11] D. J. Klein and M. Randić, Resistance distance. Journal of Mathematical Chemistry, 12(1):81–95, 1993.
[12] D. E. Knuth, The Stanford GraphBase: a platform for combinatorial computing, volume 37. Addison-Wesley Reading, 1993.
[13] D. Lusseau, K. Schneider, O. J. Boisseau, P. Haase, E. Slooten, and S. M. Dawson, The bottlenose dolphin community of doubtful sound features a large proportion of long-lasting associations. Behavioral Ecology and Sociobiology, 54(4):396–405, 2003.
[14] A. Lehman, JMP for basic univariate and multivariate statistics: a step-by-step guide. SAS Institute, 2005.
[15] J. Leskovec and J. J. Mcauley, Learning to discover social circles in ego networks. In Advances in neural information processing systems, pages 539–547, 2012.
[16] D. A. Levin, Y. Peres, and E. L. Wilmer. Markov chains and mixing times. 2009.
[17] J. Leskovec, J. Kleinberg, and C. Faloutsos, Graph evolution: Den- sification and shrinking diameters. ACM Transactions on Knowledge Discovery from Data (TKDD), 1(1):2, 2007.
[18] R. Lyons, R. Pemantle, and Y. Peres, Resistance bounds for first-passage percolation and maximum flow. Journal of Combinatorial Theory, Series A, 86(1):158–168, 1999.
[19] J. Miller and S. Sheffield, Quantum loewner evolution. preprint, 2013. http://arxiv.org/abs/1312.5745
[20] M. E. J. Newman, The structure of scientific collaboration networks. Proceedings of the National Academy of Science, 98(2):404–409, 2001.
[21] M. E. J. Newman, Finding community structure in networks using the eigenvectors of matrices. Physical review E, 74(3):036104, 2006.
[22] J. Miller and S. Sheffield, Quantum loewner evolution. preprint, 2013. http://arxiv.org/abs/1312.5745
[23] M. Šikić, A. Lančić, N. Antalov-Fantulin, and H. Štefančič, Epidemic centrality is there an underestimated epidemic impact of network peripheral nodes? The European Physical Journal B, 86(1):1–13, 2013.
[24] J. Miller and S. Sheffield, Quantum loewner evolution. preprint, 2013. http://arxiv.org/abs/1312.5745
[25] M. Šikić, A. Lančić, N. Antalov-Fantulin, and H. Štefančič, Epidemic centrality: is there an underestimated epidemic impact of network peripheral nodes? The European Physical Journal B, 86(1):1–13, 2013.
[26] P. Van Mieghem, Exact markovian SIR and SIS epidemics on networks and an upper bound for the epidemic threshold. arXiv preprint arXiv:1402.1731 2014.
[27] D. J. Watts and S. H Strogatz, Collective dynamics of small-world networks. Nature, 393(6684):440–442, 1998.
[28] W. W. Zachary, An information flow model for conflict and fission in small groups. Journal of anthropological research, pages 452–473, 1977.