Abstract—We study how the behavior of viral spreading processes is influenced by local structural properties of the network. For a wide variety of spreading processes, the largest eigenvalue of the adjacency matrix of the network plays a key role on their global dynamical behavior. For many realistic large-scale networks, it is unfeasible to exactly retrieve the complete network structure to compute its largest eigenvalue. Instead, one usually have access to myopic, egocentric views of the network structure, also called egonets. In this paper, we propose a mathematical framework, based on algebraic graph theory and convex optimization, to study how local structural properties of the network constrain the interval of possible values in which the largest eigenvalue must lie. Based on this framework, we present a computationally efficient approach to find this interval from a collection of egonets. Our numerical simulations show that, for several social and communication networks, local structural properties of the network strongly constrain the location of the largest eigenvalue and the resulting spreading dynamics. From a practical point of view, our results can be used to dictate immunization strategies to tame the spreading of a virus, or to design network topologies that facilitate the spreading of information virally.

Index Terms—Complex Networks, Virus Spreading, Algebraic Graph Theory, Convex Optimization.

I. INTRODUCTION

Understanding the behavior of viral spreading processes taking place in large complex networks is of critical interest in mathematical epidemiology [1], [2]. Spreading processes are relevant in many real scenarios, such as disease spreading in human populations [3]–[5], malware propagation in computer networks [6]–[7], or information dissemination in online social networks [8]–[9]. To study viral spreading processes, a variety of stochastic dynamical models has been proposed in the literature [10]–[14]. In these models, the steady-state infection of the network presents two different regimes depending on the virulence of the infection and the structure of the network of contacts. In one of the regimes, an initial infection dies out at a fast (usually exponential) rate. In the other regime, an initial infection becomes an epidemic. Both numerical and analytical results show that these two regimes are separated by a phase transition at an epidemic threshold determined by both the virulence of the infection and the topology of the network. One of the most fundamental questions in mathematical epidemiology is to find the value of the epidemic threshold in terms of the virus model and the contact network.

In many cases of practical interest it is unfeasible to exactly retrieve the complete structure of a network of contacts. In these cases, it is impossible to exactly compute the epidemic threshold. On the other hand, in most cases one can easily retrieve the structure of egocentric views of the network, also called egonet[1]. To estimate the value of the epidemic threshold, researchers have proposed a variety of random network models in which they can prescribe structural properties that can be retrieved from these egonets, such as the degree distribution [15], [16], local correlations [17], [18], or clustering [19].

Although random networks are the primary tool to study the impact of local structural features on the epidemic threshold [20], this approach presents a major flaw: Random network models implicitly induce many structural properties that are not directly controlled but can have a strong influence on the value of the epidemic threshold. For example, it is possible to find two networks having the same degree distribution, but with opposite dynamical behavior [21]. Therefore, it is difficult (if not impossible) to isolate the role of a particular structural property in the network performance using random network models. Furthermore, many real networks present weighted edges representing, for example, bandwidth in communication networks or resistance in electric networks. Current random networks fail to faithfully recover both the structure of the network and the distribution of weights over the links. In this paper, we develop a mathematical framework, based on algebraic graph theory and convex optimization, to study how the structure of local egonets constrain the interval of possible values in which the epidemic threshold must lie. As a result of our analysis, we present a computationally efficient approach to find this interval from a collection of egonets extracted from a (possibly) weighted network. Our numerical simulations show that the resulting interval is very narrow for several social and communication networks. This illustrates the fact that, for many real networks, local structural properties of the network strongly constrain the location of the viral epidemic threshold.

The rest of this paper is organized as follows. In Section I, we review terminology and existing results relating the dynamical behavior of a virus model with spectral properties of the network of contacts. In Section II we introduce an approach, based on algebraic graph theory and convex optimization,
to find upper and lower bounds on the epidemic thresholds from local egonets. In Subsection III-A we introduce an approach to related these egonets to the so-called spectral moments of the adjacency matrix. In Subsection III-B we propose an optimization framework to derive bounds on the epidemic threshold from a collection of spectral moments. In Section IV we illustrate the quality of our approach by computing bounds on the epidemic threshold for real-world social and communication networks.

II. Notation & Preliminaries

Let $G = (V, E)$ be an undirected, unweighted graph, where $V = \{1, \ldots, n\}$ denotes a set of $n$ nodes and $E \subseteq V \times V$ denotes a set of undirected edges linking them. If $(i, j) \in E$, we call nodes $i$ and $j$ adjacent (or first-neighbors), which we denote by $i \sim j$. We define the set of first-neighbors of a node $i$ as $N_i = \{ j \in V : (i, j) \in E \}$. The degree $d_i$ of a vertex $i$ is the number of nodes adjacent to it, i.e., $d_i = |N_i|$. A graph is weighted if there is a real number $w_{ij} \neq 0$ associated with every edge $(i, j) \in E$. More formally, a weighted graph $H$ can be defined as the triad $H = (V, E, W)$, where $V$ and $E$ are the sets of nodes and edges in $H$, and $W = \{ w_{ij} \in \mathbb{R} \setminus \{ 0 \} \}$, for all $(i, j) \in E$ is the set of possibly negative weights.

The adjacency matrix of a simple graph $G$, denoted by $A_G = [a_{ij}]$, is an $n \times n$ symmetric matrix defined entry-wise as $a_{ij} = 1$ if nodes $i$ and $j$ are adjacent, and $a_{ij} = 0$ otherwise. For weighted graphs, the entry $a_{ij}$ is equal to the weight $w_{ij}$ for $(i, j) \in E$; otherwise, for undirected graphs, $A_G$ is a symmetric matrix; thus, $A_G$ has a full set of $n$ real and orthogonal eigenvectors with real eigenvalues $\lambda_1 \geq \lambda_2 \geq \ldots \geq \lambda_n$. The largest eigenvalue of $A_G$, $\lambda_1$, is called the spectral radius of $A_G$. If $A$ has nonnegative entries and is irreducible (i.e., $G$ is connected), then the Perron-Frobenius theorem [22] can be used to show that the spectral radius $\lambda_1$ is unique, real, and positive. We also define the $k$-th spectral moment of $G$ as:

\[ m_k(G) \triangleq \frac{1}{n} \sum_{i=1}^{n} \lambda_i^k. \] (1)

A walk of length $k$ from node $i_1$ to node $i_{k+1}$ is an ordered sequence of nodes $(i_1, i_2, \ldots, i_{k+1})$ such that $i_j \sim i_{j+1}$ for $j = 1, 2, \ldots, k$. One says that the walk touches each of the nodes that comprises it. If $i_1 = i_{k+1}$, then the walk is closed. A closed walk with no repeated nodes (with the exception of the first and last nodes) is called a cycle. Given a walk $p = (i_1, i_2, \ldots, i_{k+1})$ in a weighted graph $H$, we define the weight of the walk as, $\omega(p) = w_{i_1i_2}w_{i_2i_3}\cdots w_{i_{k}i_{k+1}}$.

A. Stochastic Modeling of Viral Spreading

A wide variety of stochastic models has been proposed in the literature to study the dynamics of virus spreading processes. In most models, the steady-state level of infection in the network presents two different regimes separated by a phase transition taking place at an epidemic threshold. This epidemic threshold is determined by both the virulence of the infection and the network topology. A series of papers study the value of this epidemic threshold as a function of the network structure, in both random [23–27] and real topologies [10–14]. A spreading model widely considered in the literature is the so-called SIS (Susceptible-Infectected-Susceptible) model. In this model, each individual in the network can be in one of two possible states: susceptible or infected. Given an initial set of infected individuals, the virus propagates through the edges of an undirected graph $G$ at an infection rate $\beta$. Simultaneously, infected nodes recover at a rate $\delta$, returning back to the susceptible state (see [10] for a formal description of this model). In [10–12], we find different (and complementary) approaches to find an expression for the SIS epidemic threshold. In all of these papers, the authors are able to decouple the effect of the network topology from the dynamics of individual nodes. On the one hand, the effect of the node dynamics is completely characterized by the ratio $\tau_{SIS} = \delta/\beta$. On the other hand, the effect of the network topology depends exclusively on the largest eigenvalue of the network adjacency matrix, $\lambda_1 (A_G)$, such that if the threshold condition $\lambda_1 (A) < \tau_{SIS} = \delta/\beta$ is satisfied, a ‘small’ initial infection dies out exponentially fast [10–12].

Many extensions to the SIS model have been proposed to capture different characteristics of viral processes, such as permanent or temporal immunity of a recovered individual, or virus incubation time [13, 14]. As shown in [14], the decoupling argument that allows to separate the role of the network topology from the node dynamics in the SIS model still holds for a variety of other virus models. Similarly, a ‘small’ initial infection dies out exponentially fast in these models if the condition $\lambda_1 (A_G) < \tau_{VM}$ is satisfied, where the threshold $\tau_{VM}$ measures the virulence of the infection (and is independent of the network structure). As a bottom line, all of the above results remark the key role played by the largest eigenvalue of the adjacency matrix, $\lambda_1 (A_G)$, in virus spreading processes. In particular, the larger $\lambda_1 (A_G)$, the more efficient a network is to spread a disease (or a piece of information) virally.

B. Spectral Estimators Based on Random Graphs

Random network models are currently the primary tool to study the relationship between local structural properties of a network and its epidemic threshold. Although many random networks have been proposed in the literature [15–19], only random networks including a very limited amount of structural information are currently amenable to analysis. The original random graph model is the Erdős-Rényi graph, denoted by $G(n, p)$, in which each edge in a graph with $n$ nodes is independently chosen with probability $p$. In this model, the distribution of degrees in the network follows a Poisson distribution with expectation $\mathbb{E}[d_i] = (n-1)p$. Furthermore, the largest eigenvalue of its adjacency matrix is almost surely $\lambda_1 = [1 + o(1)] np$ (assuming that $np = \Omega (\log n)$). Although very interesting from a theoretical point of view, the original random graph presents very limited modeling capabilities, since the degree distributions of real-world networks almost never follow a Poisson distribution.
In order to increase the modeling abilities of random graphs, Chung et al. proposed in [16] a random graph \( G(\omega) \) in which one can prescribe a desired expected sequence of degrees, \( \omega = (w_1, \ldots, w_n) \). In this random graph, edges are independently assigned to each pair of vertices \((i, j)\) with probability \( w_i w_j / \sum_{k=1}^n w_k \). Chung et al. proved in [16] that if \( \sum_{j=1}^n w_j^2 / \sum_{j=1}^n w_j > \sqrt{\max \{ w_j \} \log n} \), then the largest eigenvalue \( \lambda_1 \) converges almost surely
\[
\lambda_1 (G(\omega)) \rightarrow [1 + o(1)] \sum_{j=1}^n w_j^2 / \sum_{j=1}^n w_j,
\]
for large \( n \). Despite its theoretical interest, random graphs with a given degree distribution are by far not enough to faithfully model the structure of real complex networks. In particular, it is well-known that the degree distribution alone is not a sufficient statistic to analyze the performance of many networks. For example, Alderson et al. introduce in [21] a collection of networks, including random graphs, presenting the same degree distribution and radically different dynamical performance.

Although random graph models with more elaborated structural properties can be found in the literature [15]–[19], these models are usually hard (if not impossible) to analyze from a spectral point of view. The source of this intractability is the presence of strong correlations among the entries of the (random) adjacency matrix. These strong correlations prevent the resulting random adjacency matrix from being analytically tractable. In the next section, we present a novel approach to analyze the effect of local structural properties on the largest eigenvalue of a network without making use of random graphs.

III. SPECTRAL ANALYSIS FROM EGOCENTRIC SUBNETWORKS

In this section, we study the relationship between local structural properties of a network and its eigenvalue spectrum. In our analysis, we assume that we do not have access to the complete topology of the network, due to, for example, privacy and/or security constraints. Instead, we assume that we are able to access local egocentric views of the network topology. In this setting, we propose an approach to extract global spectral information from local structural properties of the network. This spectral information will be used in Subsection III-B to compute upper and lower bounds on the epidemic threshold.

We now provide graph-theoretical and algebraic elements to characterize the information contained in these egocentric views of the network. Let \( \delta(i, j) \) denote the distance between two nodes \( i \) and \( j \) (i.e., the minimum length of a walk from \( i \) to \( j \)). By convention, we assume that \( \delta(i, i) = 0 \). We define the \( r \)-th order neighborhood around node \( i \), denoted by \( G_{i,r} = (N_{i,r}, E_{i,r}) \), as the subgraph \( G_{i,r} \subseteq G \) with node-set \( N_{i,r} \triangleq \{ j \in V : \delta(i, j) \leq r \} \), and edge-set \( E_{i,r} = \{(v, w) \in E \text{ s.t. } v, w \in N_{i,r}\} \). Notice that \( G_{i,r} \) provides a graph-theoretical description of the egocentric view of the network from node \( i \) within a radius of \( r \) hops. Motivated by this interpretation, we also call \( G_{i,r} \) the egonet of radius \( r \) around node \( i \). Egonets can be algebraically represented via submatrices of the adjacency matrix \( A_G \), as follows. Given a set of \( k \) nodes \( K \subseteq V \), we denote by \( A_G(K) \) the \( k \times k \) submatrix of \( A_G \) formed by selecting the rows and columns of \( A_G \) indexed by \( K \). In particular, we define the adjacency submatrix \( A_{i,r} \triangleq A_G(N_{i,r}) \). Notice that \( A_{i,r} \) is itself an adjacency matrix representing the structure of the egonet \( G_{i,r} \). By convention, we associate the first row and column of the submatrix \( A_{i,r} \) with node \( i \in V \), which can be done via a simple permutation of the rows and columns of \( A_{i,r} \).

A. Spectral Moments from Local Egonets

In this subsection, we derive expressions for the spectral moments of the adjacency from the knowledge of local egonets using tools from algebraic graph theory. The following lemma provides an interesting connection between the number of closed walks in \( G \) (a combinatorial property) and its spectral moments (an algebraic property) [29].

**Lemma 3.1:** Let \( G \) be a simple graph with adjacency matrix \( A_G = [a_{ij}] \). Then
\[
[A_G^k]_{ii} = |W_{i,k}|,
\]
where \( W_{i,k} \) is the set of closed walks of length \( k \) starting and finishing at node \( i \).

Using the above result, one can prove the following well-known result in algebraic graph theory [29].

**Corollary 3.2:** Let \( G \) be a simple graph. Denote by \( e \) and \( \Delta \) the number of edges and triangles in \( G \), respectively. Then,
\[
m_1(A_G) = 0, \quad m_2(A_G) = 2e / n, \quad \text{and} \quad m_3(A_G) = 6\Delta / n.
\]

We can generalize Lemma [3.1] to weighted graphs as follows.

**Lemma 3.3:** Let \( H = (V, E, W) \) be a weighted graph with weighted adjacency matrix \( A_H \). Then,
\[
[A_H^k]_{ii} = \sum_{p \in P_{k,i}} \omega(p),
\]
where \( P_{k,i} \) is the set of closed walks of length \( k \) from \( v_i \) to itself in \( H \).

**Proof:** By recursively applying the multiplication rule for matrices, we have the following expansion
\[
[A_H^k]_{ii} = \sum_{i_1=1}^n \sum_{i_2=1}^n \cdots \sum_{i_k=1}^n w_{i_1, i_2} w_{i_2, i_3} \cdots w_{i_k, i}. \tag{3}
\]

Using the graph-theoretic nomenclature introduced in Section II, we have that \( w_{i_1, i_2} w_{i_2, i_3} \cdots w_{i_k, i} = \omega(p) \), for \( p = (v_{i_1}, v_{i_2}, v_{i_3}, \ldots, v_{i_k}, v_i) \). Hence, the summations in (3) can be written as \( [W_H^k]_{ii} = \sum_{1 \leq i_1, i_2, \ldots, i_k \leq n} \omega(p) \). Finally, the set of closed walks \( p = (v_{i_1}, v_{i_2}, v_{i_3}, \ldots, v_{i_k}, v_i) \) with indices \( 1 \leq i_1, i_2, \ldots, i_k \leq n \) is equal to the set of closed walks of length \( k \) from \( v_i \) to itself in \( H \) (which we have denoted by \( P_{k,i} \) in the statement of the Proposition).
Using Lemma 3.3 we can extend Lemma 3.2 to higher-order moments of weighted graphs as follows:

**Theorem 3.4:** Consider a weighted, undirected graph $\mathcal{H}$ with adjacency matrix $A_{\mathcal{H}}$. Let $A_{i,r}$ be the (weighted) adjacency matrix of the egonet of radius $r$ around node $i$. Then, for a given $r$, the spectral moments of $A_{\mathcal{H}}$ can be written as

$$m_k (A_{\mathcal{H}}) = \frac{1}{n} \sum_{i=1}^{n} [A_{i,r}^{k}]_{11},$$

for $k \leq 2r + 1$.

**Proof:** Since the trace of a matrix is the sum of its eigenvalues, we can expand the $k$-th spectral moment of the adjacency matrix as follows:

$$m_k (A_{\mathcal{H}}) = \frac{1}{n} \text{Trace} (A_{\mathcal{H}}^k) = \frac{1}{n} \sum_{i=1}^{n} [A_{i,r}^k]_{ii}.$$  

From Lemma 3.3 we have that $[A_{i,r}^k]_{11} = \sum_{p \in P_{k,i}} \omega (p)$. Notice that for a fixed value of $k$, closed walks of length $k$ in $\mathcal{H}$ starting at node $i$ can only touch nodes within a certain distance $r$ of $i$, where $r$ is a function of $k$. In particular, for $k$ even (resp. odd), a closed walk of length $k$ starting at node $i$ can only touch nodes at most $k/2$ (resp. $[k/2]$) hops away from $i$ (see Fig. 1). Therefore, closed walks of length $k$ starting at $i$ are always contained within the neighborhood of radius $[k/2]$. In other words, the egonet $\mathcal{H}_{i,r}$ of radius $r$ contains all closed walks of length up to $2r + 1$ starting at node $i$. We can count these walks by applying Lemma 3.3 to the local adjacency matrix $A_{i,r}$. In particular, $\sum_{p \in P_{k,i}} \omega (p)$ is equal to $[A_{i,r}^k]_{11}$ (since, by convention, node 1 in the local egonet $\mathcal{H}_{i,r}$ corresponds to node $i$ in the graph $\mathcal{H}$). Therefore, for $k \leq 2r + 1$, we have that

$$[A_{i,r}^k]_{11} = \sum_{p \in P_{k,i}} \omega (p) = [A_{i,r}^k]_{ii}.$$  

Then, substituting (6) into (5), we obtain the statement of our Theorem.

**Remark 3.1:** The above theorem allows us to compute a truncated sequence of spectral moments $\{m_k (A_{\mathcal{H}}), k \leq 2r + 1\}$, given a collection of local egonets of radius $r$, $\{\mathcal{H}_{i,r}, i \in \mathcal{V}\}$. According to (4), we can compute the $k$-th spectral moment by simply averaging the quantities $[A_{i,r}^k]_{11}, i = 1, \ldots, n$. For a fixed $k$, each value $[A_{i,r}^k]_{11}, i = 1, \ldots, n$, can be computed in time $O (|\mathcal{N}_{i,r}|^3)$, where $|\mathcal{N}_{i,r}|$ is the number of nodes in the local egonet $\mathcal{H}_{i,r}$. The sparse structure of most real networks implies that $|\mathcal{N}_{i,r}| \ll n$ (for moderate values of $r$). In particular, if $|\mathcal{N}_{i,r}| = o (n^\epsilon)$ for any $\epsilon > 0$, we can compute the $k$-th spectral moments in quasi-linear time (with respect to the size of the network) using (4). This result provides a clear computational advantage compared to computing the spectral moments via an explicit eigenvalue decomposition, which can be prohibitively expensive to compute for large complex networks.

### B. SDP-Based Bounds on the Spectral Radius

Using Theorem 3.4 we can compute a truncated sequence of the spectral moments of a network $\mathcal{H}$, $(m_1 (A_{\mathcal{H}}), m_2 (A_{\mathcal{H}}), \ldots, m_{2r+1} (A_{\mathcal{H}}))$, from a set of local egonets of radius $r$, $\{\mathcal{H}_{i,r}, i \in \mathcal{V}\}$. We now present a convex optimization framework to extract information about the largest eigenvalue of the adjacency matrix, $\lambda_1 (A_{\mathcal{H}})$, from this sequence of moments. We can state the problem solved in this subsection as follows:

**Problem 1:** Given a truncated sequence of spectral moments of a weighted, undirected graph $\mathcal{H}$, $m_{2r+1} = (m_0, m_1, \ldots, m_{2r+1})$, find tight upper and lower bounds on the largest eigenvalue $\lambda_1 (A_{\mathcal{H}})$.

Our approach is based on a probabilistic interpretation of the eigenvalue spectrum of a given network. To present our approach, we first need to introduce some concepts:

**Definition 3.1:** Given a weighted, undirected graph $\mathcal{H}$ with (real) eigenvalues $\lambda_1, \ldots, \lambda_n$, the spectral density of $\mathcal{H}$ is defined as

$$\mu_{\mathcal{H}} (x) = \frac{1}{n} \sum_{i=1}^{n} \delta (x - \lambda_i),$$

where $\delta (\cdot)$ is the Dirac delta function.

The spectral density can be interpreted as a discrete probability density function with support on the set of eigenvalues $\{\lambda_i, i = 1 \ldots n\}$. Let us consider a discrete random variable $X$ whose probability density function is $\mu_{\mathcal{H}}$. The moments of this random variable satisfy the following:

**Lemma 3.5:** The moments of a r.v. $X \sim \mu_{\mathcal{H}}$ are equal to the spectral moments of $A_{\mathcal{H}}$, i.e.,

$$E_{\mu_{\mathcal{H}}} (X^k) = m_k (A_{\mathcal{H}}),$$

for all $k \geq 0$.

Recall that the support of a finite Borel measure $\mu$ on $\mathbb{R}$, denoted by $\text{supp} (\mu)$, is the smallest closed set $B$ such that $\mu (\mathbb{R} \setminus B) = 0$. 

This result provides a clear computational advantage compared to computing the spectral moments via an explicit eigenvalue decomposition, which can be prohibitively expensive to compute for large complex networks.
whenever clear from the context.

\[ \int x^k \delta(x - \lambda_i) \, dx \]

For univariate distributions, necessary and sufficient conditions for feasibility can be given in terms of certain Hankel matrices being positive semidefinite [30] as follows [31]:

**Theorem 3.6:** [31] Let \( M_{2r+1} = (M_0, M_1, ..., M_{2r+1}) \) \( \in \mathbb{R}^{2r+2} \). Then,

(a) The sequence \( M_{2r+1} \) corresponds to a sequence of moments feasible in \( \Omega = \mathbb{R} \) if and only if \( H_{2r} \geq 0 \).

(b) The sequence \( M_{2r+1} \) is feasible in \( \Omega = [\lambda_{\min}, \infty) \) if and only if

\[ H_{2r} \geq 0 \text{ and } H_{2r+1} - a H_{2r} \geq 0. \]

(c) The sequence \( M_{2r+1} \) is feasible in \( \Omega = (-\infty, \lambda_{\max}] \) if and only if

\[ H_{2r} \geq 0 \text{ and } b H_{2r} - H_{2r+1} \geq 0. \]

Using Theorem 3.6 we have the following result:

**Theorem 3.7:** Let \( \mu \) be a probability density function on \( \mathbb{R} \) with associated sequence of moments \( M_{2r+1} = (M_0, M_1, ..., M_{2r+1}) \), all finite, and let \( [a, b] \) be the smallest interval which contains the support of \( \mu \). Then, \( b \geq \beta^*_r(M_{2r+1}) \), where

\[ \beta^*_r(M_{2r+1}) \triangleq \min_x \left\{ x \mid H_{2r} \geq 0, x H_{2r} - H_{2r+1} \geq 0 \right\}. \]

**Proof:** Since \( M_{2r+1} \) is the moment sequence of a probability density function \( \mu \) with support on \( [a, b] \), we have from Theorem 3.6(c) that \( M_{2r+1} \) satisfy \( H_{2r} \geq 0 \) and \( b H_{2r} - H_{2r+1} \geq 0 \). Since \( \beta^*_r(M_{2r+1}) \) is, by definition, the minimum value of \( x \) such that \( H_{2r} \geq 0 \) and \( x H_{2r} - H_{2r+1} \geq 0 \), we have that \( \beta^*_r(M_{2r+1}) \leq b \).

**Remark 3.2:** Observe that, for a given sequence of moments \( M_{2r+1} \), the entries of \( x H_{2r} - H_{2r+1} \) depend affinely on the variable \( x \). Then \( \beta^*_r(M_{2r+1}) \) is the solution to a semidefinite program [30] (SDP) in one variable. Hence, \( \beta^*_r(M_{2r+1}) \) can be efficiently computed using standard optimization software, e.g. [33], from a truncated sequence of moments.

Applying Theorem 3.7 to the spectral density \( \mu_\mathcal{H} \) of a given graph \( \mathcal{H} \) with spectral moments \( (m_0, m_1, ..., m_{2r+1}) \), we can find a lower bound on its largest eigenvalue, \( \lambda_1(A_\mathcal{H}) \), as follows:

**Theorem 3.8:** Let \( \mathcal{H} \) be a weighted, undirected graph with (real) eigenvalues \( \lambda_1 \geq ... \geq \lambda_n \). Then, given a truncated sequence of the spectral moments of \( \mathcal{H} \), \( m_{2r+1} = (m_0, m_1, ..., m_{2r+1}) \), we have that

\[ \lambda_1(A_\mathcal{H}) \geq \beta^*_r(m_{2r+1}), \]

(10)

where \( \beta^*_r(m_{2r+1}) \) is the solution to the SDP in (9).

**Proof:** Let us consider the spectral density of \( \Omega, \mu_\mathcal{H}, \) in Definition 3.1. According to Lemma 3.5, the density \( \mu_\mathcal{H} \) has associated moments \( m_{2r+1} \). Also, the smallest interval which contains the support of \( \mu_\mathcal{H} \) is \( [a, b] = [\lambda_n, \lambda_1] \). Therefore, applying Theorem 3.7 to \( \mu_\mathcal{H} \), we obtain that \( \beta^*_r(m_{2r+1}) \leq b = \lambda_1 \).

Furthermore, for \( r = 1 \), we can analytically solve the SDP in (9) to derive a closed-form solution for \( \beta^*_1(m_3) \), as follows:

**Corollary 3.9:** Let \( \mathcal{G} \) be a simple graph with adjacency matrix \( A_\mathcal{G} \). Denote by \( n, e, \) and \( \Delta \) the number of nodes, edges, and triangles in \( \mathcal{G} \), respectively. Then,

\[ \lambda_1(A_\mathcal{G}) \geq \frac{3\Delta + \sqrt{9\Delta^2 + 8e^2}}{2e}. \]

(11)

**Proof:** In the Appendix.

Using the optimization framework presented above, we can also compute upper bounds on the spectral radius of \( \mathcal{H} \) from a sequence of its spectral moments, as follows. In this case, our formulation is based on the following set of Hankel matrices:

\[ A = \begin{bmatrix} a_{0}\, a_{1} \ldots \, a_{t}\, a_{t+1} \ldots \, a_{2t+1} \end{bmatrix} \]

A semidefinite program is a convex optimization problem that can be solved in time polynomial in the input size of the problem; see e.g. [32].
Given a weighted, undirected graph $\mathcal{H}$ with $n$ nodes and spectral moments $m_{2r+1} = (m_0, m_1, ..., m_{2r+1})$, let $T_{2r}(y; m_{2r+1}, n)$ and $T_{2r+1}(y; m_{2r+1}, n) \in \mathbb{R}^{(r+1) \times (r+1)}$ be the Hankel matrices defined by

$$
[T_{2r}]_{ij} = \frac{n}{n-1} m_{i+j-2} - \frac{1}{n-1} y^{i+j-2}, \quad (12)
$$

$$
[T_{2r+1}]_{ij} = \frac{n}{n-1} m_{i+j-1} - \frac{1}{n-1} y^{i+j-1}.
$$

Given a sequence of spectral moments, we can compute upper bounds on the largest eigenvalue $\lambda_1(A_{\mathcal{H}})$ using the following result:

**Theorem 3.10:** Let $\mathcal{H}$ be a weighted, undirected graph with (real) eigenvalues $\lambda_1 \geq ... \geq \lambda_n$. Then, given a truncated sequence of its spectral moments $m_{2r+1} = (m_0, m_1, ..., m_{2r+1})$, we have that

$$
\lambda_1 \leq \delta_r^*(m_{2r+1}, n),
$$

where

$$
\delta_r^*(m_{2r+1}, n) \triangleq \max_s \ y 
\text{s.t.} \ T_{2r} \geq 0, \ yT_{2r} - T_{2r+1} \geq 0, \ T_{2r+1} + yT_{2r} \geq 0. \quad (13)
$$

**Proof:** Let us define the bulk of the spectrum as the set of eigenvalues $\{\lambda_2, ..., \lambda_n\}$, and the bulk spectral density as the probability density function:

$$
\tilde{\mu}_H \triangleq \frac{1}{n-1} \sum_{i=2}^n \delta(x - \lambda_i).
$$

We also define the bulk spectral moments as the moments of the bulk spectral density, which satisfy:

$$
\tilde{m}_k(A_{\mathcal{H}}) \triangleq \int_{\mathbb{R}} x^k \tilde{\mu}_H(x) \, dx
$$

$$
= \frac{1}{n-1} \sum_{i=2}^n \int_{\mathbb{R}} x^k \delta(x - \lambda_i) \, dx
$$

$$
= \frac{1}{n-1} \sum_{i=1}^n \lambda_i^k - \frac{1}{n-1} \lambda_1^k
$$

$$
= \frac{n}{n-1} m_k(A_{\mathcal{H}}) - \frac{1}{n-1} \lambda_1^k.
$$

Therefore, the moment matrices associated to the sequence of bulk spectral moments $\tilde{m}_{2r+1} = (\tilde{m}_0, \tilde{m}_1, ..., \tilde{m}_{2r+1})$, satisfy

$$
H_s(\tilde{m}_{2r+1}) = T_s(\lambda_1; m_{2r+1}, n), \quad (14)
$$

for $s \in \{2r, 2r+1\}$, where $H_s$ and $T_s$ were defined in [8] and [12], respectively.

Since $|\lambda_i| \leq \lambda_1$ for $i \geq 2$, the support of the bulk spectral density $\tilde{\mu}_H$ is contained in the interval $[-\lambda_1, \lambda_1]$.

We shall omit the arguments from $T_{2r}$ and $T_{2r+1}$ whenever clear from the context.

Hence, according to Theorems 3.6(b)-(c), the sequence of bulk spectral moments $\tilde{m}_{2r+1}$ must satisfy:

$$
T_{2r}(\lambda_1; m_{2r+1}, n) \geq 0,
$$

$$
\lambda_1 T_{2r}(\lambda_1; m_{2r+1}, n) - T_{2r+1}(\lambda_1; m_{2r+1}, n) \geq 0,
$$

$$
T_{2r+1}(\lambda_1; m_{2r+1}, n) + \lambda_1 T_{2r}(\lambda_1; m_{2r+1}, n) \geq 0.
$$

Since $\delta_r^*(m_{2r+1}, n)$ is, by definition, the maximum value of $y$ satisfying the constrains in (13), we have that $\delta_r^*(m_{2r+1}, n) \geq \lambda_1(A_{\mathcal{H}})$.

**Remark 3.3:** The optimization program in (13) is not an SDP, since the entries of the matrices $T_{2r}(y; m_{2r+1}, n)$ and $T_{2r+1}(y; m_{2r+1}, n)$ are not affine functions, but higher-order polynomials, in $y$. Nevertheless, the program can be cast into a convex optimization program, as follows. For the matrices in (13) to be positive semidefinite, all their principal minors must be nonnegative, where each minor is a polynomial in $y$. In other words, positive semidefiniteness of the matrices in (13) is equivalent to a collection of polynomials in $y$ being nonnegative. Hence, we can substitute the semidefinite constrains in (13) by a collection of polynomials in $y$ being nonnegative. The resulting optimization problem is a Sum-Of-Squares (SOS) program [34], which is a type of convex program that can be efficiently solved using off-the-shelf software [35].

In summary, using Theorems 3.4, 3.8 and 3.10, we can compute upper and lower bounds on the largest eigenvalue of a weighted, undirected network, $\lambda_1(A_{\mathcal{H}})$, from the set of local egonets with radius $r$, as follows: (1) Using (4), compute the truncated sequence of moments $(m_0, m_1, ..., m_{2r+1})$ from the set of egonets, $\{A_{i,r}, i \in V\}$, and (2) using Theorems 3.8 and 3.10, compute the upper and lower bounds, $\delta_r^*(m_{2r+1}, n)$ and $\beta_r^*(m_{2r+1})$, respectively.

**IV. NUMERICAL SIMULATIONS**

In this section, we analyze real data from several social and communication networks to numerically verify the tightness of our bounds. In our first set of simulations, we study a regional network of Facebook that spans 63,731 users (nodes) connected by 817,090 friendships (edges) [36]. In order to corroborate our results in different network topologies, we extract multiple medium-size social subgraphs by running a Breath-First Search (BFS) around a collection of starting nodes in the Facebook graph. Each BFS induces a social subgraph spanning all nodes 2 hops away from a starting node. As a result, we generate a set of 100 different social subgraphs, $G = \{G_i\}_{i=1}^{100}$, centered around 100 randomly chosen nodes. For each social subgraph $G_i \in G$, we compute its first five spectral moments $m_5(G_i) = (m_1(G_i), ..., m_5(G_i))$ and use Theorems 3.8 and 3.10 to compute lower and upper bounds on the spectral radius, $\beta_2^*(G_i) = \delta_2^*(m_5(G_i))$ and $\delta_2^*(G_i) = \delta_2^*(m_5(G_i), n_i)$, where $n_i$ is the size of $G_i$. Since we have access to the complete network topology, we can also numerically compute the exact value of the largest eigenvalue $\lambda_1(G_i)$, for comparison purposes. It is worth remarking that, in many real applications, we do not have access to the complete network topology, due to privacy and/or security...
constraints; therefore, we would not be able to compute the exact value of $\lambda_1$. It is in those cases when our approach is most useful.

Fig. 2 represents a scatter plot where each red circle above the dashed diagonal line has coordinates $(\lambda_1(G_i), \beta_2^*(G_i))$, and each blue circle below the dashed diagonal line has coordinates $(\lambda_1(G_i), \beta_2^*(G_i))$, for all $G_i \in G$. We have also included a black line connecting every pair of circles associated to the same subgraph $G_i$. This black line represents the interval of possible values in which the largest eigenvalue, $\lambda_1(G_i)$, must lie. (Notice how the dashed diagonal line cut through all those segments.) For all the social subnetworks in $G$, the spectral radii $\lambda_1(G_i)$ are remarkably close to the theoretical bounds $\beta_2^*(G_i)$ and $\delta_2^*(G_i)$. In other words, in our collection of social subgraphs, local structural properties of the network strongly constrain the location of the largest eigenvalue, and consequently the ability of a social network to disseminate information virally.

Our bounds are also tight for other important social and communication networks. In the following, we the compare the values of $\beta_2^*$ and $\delta_2^*$ with the largest eigenvalue $\lambda_1$ of an e-mail and an Internet network:

Example 4.1 (Enron e-mail network): In this example we consider a subgraph of the Enron e-mail communication network [37]. Nodes of the network are e-mail addresses and the network contains an edge $(i, j)$ if $i$ sent at least one e-mail to $j$ (or vice versa). The total size of the network is 36,692 nodes, which is too large for us to manage computationally. In order to compare our bounds with the exact value of the largest eigenvalue, we analyze a subgraph obtained by a BFS of depth 2 around a randomly chosen node. The resulting subgraph has $n = 3,215$ nodes and $e = 36,537$ edges. We also compute the value of its largest eigenvalue to be $\lambda_1 = 95.18$. Using (4), we have the following values for the first five spectral moments of the adjacency matrix: $m_1 = 0$, $m_2 = 22.47$, $m_3 = 394.7$, $m_4 = 33,491$, and $m_5 = 2,603,200$. From (9) and (13), we obtain the following upper and lower bounds on the largest eigenvalue: $\beta_2^* = 78.53 < \lambda_1 < 98.74 = \delta_2^*$. Notice that the numerical value of $\lambda_1$ is remarkably close to the upper bound $\delta_2^*$. Since the spectral radius measures the ability of a network to spread information virally, our numerical results indicate that the e-mail network spreads information very efficiently given its structural constrains imposed by the local egonets. We can also compare our bounds with the estimator in (2), corresponding to a random network with the same degree distribution. The value of the estimator is equal to $\tilde{\lambda}_1 = 124.57$, which is looser than our bounds.

Example 4.2 (AS-Skitter Internet network): In this example, we consider a subgraph of the Internet network at the Autonomous Systems (AS) level. The network topology was obtained from the Skitter data collection in CAIDA [38]. Our subgraph was obtained from the complete AS graph using a BFS of depth 2 around a random node. The resulting subgraph has $n = 2,248$ nodes, $e = 20,648$ edges, and its largest eigenvalue at $\lambda_1 = 91.3$. The spectral moments of its adjacency matrix are $m_1 = 0$, $m_2 = 18.37$, $m_3 = 341.1$, $m_4 = 40,001$, and $m_5 = 2,777,018$. The resulting bounds from (9) and (13) are $\beta_2^* = 74.72 < \lambda_1 < 93.94 = \delta_2^*$. Notice how, the largest eigenvalue is again remarkably close to the upper bound, indicating that the network is able to spread information efficiently, given its local structural constrains. In this case, the estimator based on random networks produces a value of $\tilde{\lambda}_1 = 219.1$, which is very loose. Therefore, using random networks to analyze spreading processes in the Internet graph can be misleading.

In conclusion, our numerical results validate the quality of the lower and upper bounds, $\beta_2^*$ and $\delta_2^*$, on the spectral radius $\lambda_1$ in several social and communication networks. Our bounds provide an interval of values in which the largest eigenvalue is guaranteed to lie. This is in contrast with estimators based on random networks, which can be very misleading and present no quality guarantees.

V. CONCLUSIONS

A fundamental question in the field of mathematical epidemiology is to understand the relationship between a network’s structural properties and its epidemic threshold. For many virus epidemic models, the role of the network topology is characterized by the largest eigenvalue of its adjacency matrix, such that the larger the eigenvalue, the more efficient a network is to spread a disease (or a piece of information) virally. In many cases of practical interest, it is not possible to retrieve the complete structure of a network of contacts due to privacy and/or security constrains. Thus, it is not possible to exactly compute the largest eigenvalue of the network. On the other hand, it is usually easy to retrieve local views of a network, also called egonets, by extracting the structure of neighborhoods around a collection of chosen nodes. To estimate the value of the spectral radius when only egonets are available, researchers usually use random network models in which they prescribe local structural features that can be extracted from the egonets, such as the degree distribution. This approach, although very common in practice, presents a major flaw: Random network models implicitly induce many
structural properties that are not directly controlled and can be relevant to the spreading dynamics.

In this paper, we have presented an alternative mathematical framework, based on algebraic graph theory and convex optimization, to study how egonets constrain the interval of possible values in which the largest eigenvalue (and, therefore, the epidemic threshold) must lie. Our approach provides an interval of values in which the largest eigenvalue is guaranteed to lie and is applicable to weighted networks. This is in contrast with estimators based on random networks, which can be very misleading and present no quality guarantees. Our numerical simulations have shown that the resulting interval in which the largest eigenvalue can be very misleading and present no quality guarantees. Our introduction to lie and is applicable to weighted networks. This is in contrast with estimators based on random networks, which can be very misleading and present no quality guarantees. Our numerical simulations have shown that the resulting interval in which the largest eigenvalue is guaranteed to lie is very narrow for several social and communication networks. This indicates that, for an important collection of networks, the viral epidemic threshold is strongly constrained by local structural properties of the network.

APPENDIX

Corollary 3.9 Let $G$ be a simple graph with adjacency matrix $A_G$. Denote by $n$, $e$, and $\Delta$ the number of nodes, edges, and triangles in $G$, respectively. Then,

$$\lambda_1(A_G) \geq \frac{3\Delta + \sqrt{9\Delta^2 + 8e^2}/n}{2e}.$$  

Proof: From Corollary 3.2 we have that the first three moments of $G$ are $m_1(A_G) = 0$, $m_2(A_G) = 2e/n$, and $m_3(A_G) = 6\Delta/n$ (by definition, $m_0(A_G) = 1$). Substituting the sequence of moments, $m_3 = (1, 0, 2e/n, 6\Delta/n)$, into (9), we have that $\beta_3^n(m_3)$ is the solution to the following SDP:

$$\min \ x$$

s.t. $R(x) \triangleq \begin{bmatrix} x & -2e/n \\ -2e/n & 2ex/n - 6\Delta/n \end{bmatrix} \succ 0.$$

The characteristic polynomial of $R(x)$ can be written as $\phi(s; x) = \det (sI - R(x)) = s^2 - s \tr (R(x)) + \det (R(x))$. Then, $R(x) \succ 0$, if and only if both roots of $R(x)$ are nonnegative. By Descartes’ rule, this happens if and only if the following two conditions are satisfied:

1. $\tr (R(x)) = x(1 + 2e/n) - 6\Delta/n \geq 0$, which implies

$$x \geq \frac{6\Delta}{2e} + n \equiv x_1.$$  

2. $\det (R(x)) = 2ex^2/n - 6\Delta x/n - 4e^2/n^2 \geq 0$, which implies

$$x \geq \frac{3\Delta + \sqrt{9\Delta^2 + 8e^2}/n}{2e} \equiv x_2.$$  

We also have that, $x_2 > \frac{3\Delta + \sqrt{9\Delta^2 + 8e^2}/n}{2e} = \frac{3\Delta}{e} > \frac{6\Delta}{2e+n} = x_1$. Therefore, the minimum value of $x$ satisfying (15) and (16) is equal to the right hand side of (11).

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