A preferential attachment approach to community structure and the structure of communities

Jean-Gabriel Young,1 Laurent Hébert-Dufresne,1,2 Antoine Allard,1,3 and Louis J. Dubé1
1Département de Physique, de Génie Physique, et d’Optique, Université Laval, Québec (Québec), Canada, G1V 0A6
2Santa Fe Institute, Santa Fe, NM 87501, USA
3Departament de Física Fonamental, Universitat de Barcelona, Marçà i Franqués 1, 08028 Barcelona, Spain

We introduce an intuitive mechanism to describe both the emergence of community structure and the evolution of the internal structure of communities in social networks. Our idea is based on the simple assumption that each individual can, for every social group to which it belongs, develop connections and introduce new members. Complex behaviors emerge from opposing time scales for the activities of individuals and for the sum of individuals gathered in groups. We show how the resulting model reproduces behaviors observed in real social networks and in the anthropological theory known as Dunbar’s number, i.e., the empirical observation of a maximal number of ties which an average individual can sustain within its social groups. Using this growth process, we organically reproduce the micro and mesoscopic structure of social networks. In so doing, we highlight two interesting properties of the community structure of social networks. First, strong correlations between the number of communities to which a node belong and the number of connections therein; correlating the role of a node in the community structure and its role in the structure of the communities. Second, Dunbar’s number in the structure of communities implies a vanishing group density regardless of the nature of the network or of the detection algorithm.

I. INTRODUCTION

Networks are at the center of the quantitative analysis of social systems [1]. They encode the links between different individuals within a mathematical construct that allows quantification of the role of individuals in social networks through multiple metrics, and the analysis of correlations among them [1,2]. One instance of these correlations, the similarity between the neighborhoods of different nodes (individuals), has received particular attention since links tend to be clustered in tightly connected groups [3,4]. Networks are often expressed as a superposition of such densely connected groups, and we refer to this decomposition as the community structure of a network [5,6]. This structure not only informs us about the current state of a network, but also helps predict missing or future links [7,8], and leads to better models of many dynamical processes on networks [9,10]. This arises because the community structure encapsulates possible correlations between nodes [13], or possible origins for the links (e.g., groups of individuals with similar interests or sharing a workplace) [14].

Information pertaining to the community structure of a network is only valuable if it is known to some degree of certainty. This leads to the problem of community detection. How can one efficiently decompose a network in a set of meaningful communities, by using its structure and no other prior knowledge? The number and diversity of available approaches [4,10,11,22] only serve to illustrate both the difficulty of answering the question, and the absence of consensus on the very definition of communities. Although, the multiplicity of definitions is not problematic per se, the implications of such diversity are far reaching, since diverging definitions of the structure of communities entail different community structures, and vice-versa. This reciprocal dependence is at the core of our paper.

Erdős-Rényi (ER) graphs are perhaps the most prevailing approximation for the structure of communities, both in the context of community detection [22,23] and of network modeling [7,8,24,25]. These random graphs are generated either by randomly distributing m links among the n nodes of a graph [G(n,m) ensemble] or by setting a probability p of existence to every possible link [G(n,p) ensemble] [26,27]. Erdős-Rényi graphs are mostly used because of their simplicity, but also because it is often argued that the lowest level of description of a network should not exhibit any structure [24].

While this sound statistical principle has yielded stunning results in both community detection and network modeling [7,8,24], one can hardly expect ER graphs to realistically describe communities as the basic building blocks of social system, since random graphs ensemble with uncorrelated links contain communities with disconnected subsets of nodes, in direct violation of one of the basic tenets of the concept of community. A subtle and even more serious issue also becomes apparent when one views networks as snapshots of growing complex systems. Indeed, it has been shown time and time again that heterogeneity stems from the history of growing systems [13,28,30]. Since communities are the basic building blocks of such systems, they must in turn exhibit heterogeneity, both in their sizes and in their internal structures. Sophisticated random graphs models that incorporate inhomogeneities [9,12,31] are closer to reality, but still not completely suitable models for the structure of communities, because having hardwired internal structures make the problem of detection exponentially harder, and yield no temporal information or insights on the growth process. The Preferential Attachment model [28] does not suffer from these issues, but highly heterogeneous degree distributions at all community sizes make it unsuitable for our purpose; while big communities might exhibit some inhomogeneity, one expects small communities (e.g. families, working groups) to be uniformly connected.

In this paper, we provide a solution to these problems by introducing a simple, organic and realistic growth process that reproduces both the local structure of communities and the global statistical properties of overlapping community structures. Power-law-like behavior has been found to be a good
approximation for many of the statistical properties at the community structure level. It follows that the evolution of the degree distribution (links per node), the membership distribution (groups per node) and the size distribution (nodes per group) can be modeled through preferential attachment.

We will focus on the recently introduced Structural Preferential Attachment (SPA) model, where nodes join new communities at a rate proportional to their current membership number and communities gain new members at a rate proportional to their size (i.e., preferentially). We show how SPA not only ensures an heterogeneous community structure akin to the observed structure of real networks, but also how it is compatible, both in practice and in spirit, with a local growth model for the structure of communities. This local model generates small, homogeneous and connected communities which, when they are allowed to grow larger, become increasingly inhomogeneous.

The structure of the paper is as follows. In Sec. II we describe the process by which a single community and its structure may grow (further details are presented in Appendix A). In Sec. III we incorporate this process within a preferential attachment model at the community structure level and provide a recipe for its implementation. In Sec. IV we compare our model with real social networks, and investigate its implications. We then present our conclusions in Sec. V. Sections II and IV C provide a succinct overview of how our work relates to the theory of Dunbar's number, while the other sections are

II. GROWTH OF THE STRUCTURE OF COMMUNITIES

Our model for the structure of communities is based on the hypothesis that community growth is governed by preferential attachment (i.e., we assume that a community grows with a rate proportional to its current size). This hypothesis is known to reproduce the statistical properties of the community structure of real networks, and can be interpreted as if each member of a community introduces a new member at a given rate. The more members, the faster the community grows. In this section, we obtain a complete model of the growth of a community by combining this simple node creation mechanism to an elementary link creation mechanism.

A. Description of the model and mean-field analysis

The model is simply stated. Each member of a community of size $n$ recruits new members at rate $\rho_n$, such that the growth rate $\dot{n}(t)$ of a community of size $n$ is proportional to $n\rho_n$. A new member is initially connected to the individual who introduced it within the group (its degree $k$, i.e., number of neighbors, therefore equals 1 within this community). This first link ensures the connectedness of the community. To allow for denser communities, we introduce another mechanism whereby each member creates new links at a rate $\rho_k$ until it is connected to every other member, i.e., until its degree is equal to $n - 1$. A receiving individual is selected randomly among the unconnected members (self-loops or doubled links are forbidden). Consequently, the degree of a single member grows faster than the link creation rate $\rho_k$, because it can both create and receive (undirected) links.

The average number $n_k(t)$ of nodes (members) with degree $k$ within an average community of size $n$ can be followed through time $t$ with the interdependent rate equations

$$\dot{n}_k(t) = \rho_n(n_{k-1} - n_k) + \rho_k(n_{k-1} - n_k) + \rho_l X \left[ \frac{(|n| - k)n_{k-1}}{Z} - \frac{(|n| - k - 1)n_k}{Z} \right],$$

where $|n|$ is the integer part of $n$, where $X := \sum_{k'=1}^{\lfloor|n|\rfloor - 1} n_{k'}(t)$ is the number of nodes that can create new links, and where $Z := \sum_{k'=1}^{\lfloor|n|\rfloor - 2} (|n| - 1 - k') n_{k'}$ is the total number of potential links. The first term accounts for the arrival of new nodes: each existing node recruits at rate $\rho_n$, and gain new connections accordingly. This creates a flow that brings a node of degree $k - 1$ to degree $k$ [positive effect on $n_k(t)$], and node of degree $k$ to degree $k + 1$ [negative effect]. The second term is due to the creation of internal links, and behaves exactly like the first term. The third term accounts for the receiving end of links created by existing nodes: these events occur at rate $\rho_l X$ and affect nodes of degree $k$ with probability $\frac{(|n| - k - 1)n_k}{Z}$.

We take the integer part of the community size $n$ to capture the fact that the maximal degree $|n| - 1$ only increases when a new node is recruited, i.e., when the integer part of $n$ jumps from $x$ to $x + 1$.

Some events do not influence the number of nodes of degrees $k = 0, 1, |n| - 1$, and $|n|$, and the following set of rate equations is needed to cover all special cases.

$$\dot{n}_0(t) = 0 \tag{1b}$$
$$\dot{n}_1(t) = \rho_n(n - n_1) - \rho_k \left( n_1 + X \frac{(|n| - 2)n_1}{Z} \right) \tag{1c}$$
$$\dot{n}_{|n|-1}(t) = n_{|n|-2} \left( \rho_n + \rho_k + \rho_l \frac{X}{Z} \right) - \rho_n n_{|n|-1} \tag{1d}$$
$$\dot{n}_{|n|}(t) = \rho_n n_{|n|-1} \tag{1e}$$

Note that when $|n| \leq 2$, the set of Eqs. should, but do not, collapse into a smaller set of consistent equations. This inconsistency is easily avoided since all the problematic cases – communities which initially contain a single node or a single link – deterministically evolve toward triads (see Fig. I). As a result, one can use the equivalent initial condition $\dot{n}(t_0) = (n_0 = 0, n_1 = 2, n_2 = 1)$ whenever the actual initial configuration would lead to inconsistent equations.

The time $t$ of the process has no physical meaning, since different communities have different “initial times” and are only distinguishable by their sizes. Summing Eqs. (1a)–(1e), one finds

$$\dot{n}(t) \equiv \sum_{k=1}^{|n|} \dot{n}_k(t) = n\rho_n. \tag{2}$$

This last equation, together with the observation that
We assume a uniform and uncorrelated distribution of links among individuals, and we define \( L_{\text{max}}(n) = n(n-1)/2 \), the maximal number of links in a community of size \( n(t) \). A randomly selected node is then of degree \( k \) with probability

\[
\tilde{p}_k = \binom{n-1}{k} \left( \frac{L}{L_{\text{max}}(n)} \right)^k \left( 1 - \frac{L}{L_{\text{max}}(n)} \right)^{n-k-1},
\]

As previously stated, a node will not create new links if its degree equals \( n-1 \) (see Sec. II B). The rest of the nodes create new links at a rate \( \rho_k \). The total link creation rate is therefore approximately given by

\[
\frac{dL(t)}{dt} = n\rho_n + n\rho_\ell \left[ 1 - \left( \frac{L}{L_{\text{max}}(n)} \right)^{n-1} \right],
\]

where \( n\rho_n \) is the contribution of the node recruiting process, and where the second term is equivalent to \( n\rho_\ell (1 - \tilde{p}_{n-1}) \equiv n\rho_\ell \sum_{j<n-1} \tilde{p}_j \).

Again, a straightforward transformation yields \( L(n) \) as a function of the average size at time \( t \):

\[
\frac{dL}{dn} = \frac{dL}{dt} \frac{dt}{dn} = 1 + r \left[ 1 - \left( \frac{L}{L_{\text{max}}(n)} \right)^{n-1} \right].
\]

While the actual link distribution is neither uniform nor uncorrelated in the complete model (see Fig. 2), we will see that our simplification is robust, and that Eq. (6) accurately reproduces the average internal degree of communities (see Sec. II C).

A simple analysis of Eq. (6) highlights an interesting feature of the model. For large sizes \( n \), the factor \( [L/L_{\text{max}}(n)]^{n-1} \) goes rapidly to zero, such that a maximal link creation rate

\[
\frac{dL}{dn} \approx 1 + r
\]

is attained. Hence, the intensive quantity \( L/n \to (1 + r) \) converges toward a constant that depends on the parametrization of the model alone. Considering that one link equals two stubs (or degree), the asymptotic average degree is directly related to the parameter \( r \) through:

\[
\langle k \rangle = \frac{2L}{n} = 2 (1 + r).
\]

This indicates a maximal average number of connections in social group.

\section{C. Relation with Dunbar’s number}

The results of Fig. 3 highlight the two different behaviors for the average number of links per individual in relation to the size of a social group. For low average sizes \( n \), the mean degree \( \langle k(n) \rangle \) scales linearly with the community size \( n \). In other words, the model captures the fact that everybody knows everybody within small groups (e.g. family or close friends).

At larger sizes \( n \), \( \langle k(n) \rangle \) reaches the plateau \( 2 (1 + r) \) given by Eq. (8). From this point onwards, a typical individual will not

\begin{align*}
\left\{ \begin{array}{c}
(0,2,1) \\
(0,1,2,1) \\
(0,1,0, \ldots, 0, s-1, 1)
\end{array} \right.
\end{align*}
FIG. 2. (color online) Degree distributions \(\{p_k\}\) for various community sizes \(n\), with relative event ratios \(r = r_{\text{e}}/p_k = 9\) and \(r = 49\). We compare the results of Eq. (3) (small dots) with the average of 20,000 Monte-Carlo simulations (closed symbols). Lines are added to the analytical results to guide the eye. A bulge appears in the distributions for \(n \gg 1\). It corresponds to the signature of a peloton dynamics [29]. We gather some remarks on this dynamics in Appendix A.

FIG. 3. (color online) Internal degree \(\langle k(n)\rangle\) of an average node as a function of community size \(n\). We compare the prediction of Eq. (5) (lines) with the average of 50,000 Monte-Carlo simulations, for \(r = 4\) (lozenge), \(r = 4\) (inverted triangles), \(r = 8\) (squares), \(r = 16\) (circle), and \(r = 32\) (triangles). Asymptotic agreement is excellent, and only small deviations can be observed near the inflexion points.

to maintain such relationships. While the importance of neocortical sizes [34] and the generality of the results [35] are both disputable, the fact remains that empirical evidence supports the existence of an upper bound in the absolute number of active relationships for an average individual [36].

In our intuitive model, this upper bound naturally emerges and is solely dependent on the parameter \(r\). This parameter can be interpreted as the ratio between the involvement of an individual in a community, in the sense of bonding with other members, and its contribution to the growth rate of the community. For low \(r\) or large community sizes, the rate of change in the population is higher than an individual’s involvement, such that the maximal degree stagnates. Whereas, for high \(r\) and small communities, the individual is able to follow the population changes and hence create relationships with most of its members. Different types of social organizations will feature different \(r\) and consequently different values of “Dunbar’s number” (an online social network, where relationships are easily maintained, will lead to higher values of \(r\) than a co-author network for example). Note that we do not interpret the plateau as an absolute upper bound, but rather as a bound on the maximal number of connections that an average individual can maintain.

In this interpretation, the upper bound for individual degree in social groups is due to the fact that connections and introduction of new members have linear requirements for individuals, but exponential consequences for the group. Other mathematical models exist to describe Dunbar’s number (e.g. [36]), usually based on arguments of priority and/or time resources [37]. However, our model is based on the observed structure of the communities of real world networks and consequently, explains Dunbar’s number in terms of its two basic units, individuals and groups, and the ratio of their respective...
characteristic growth rates. The consequence of this result for the complete community structure of social networks is discussed in Sec. [IVC]

III. GROWTH OF THE COMMUNITY STRUCTURE

We now bridge the gap between the local community growth model of Sec. [II] and the Structural Preferential Attachment (SPA) model of Refs. [14] and [29]. SPA builds upon the idea that networks can be interpreted as projections of higher structural levels, such as communities [33]. From this community-centric point of view, groups do not emerge because links get clustered; instead, individuals join communities and then form links with their other members. SPA thus models network growth by considering that all events consist of a node joining a community.

A. Structural Preferential Attachment

The essence of SPA can be summarized as follows [14]. At every discrete time step, a growth event occurs. An event marks the birth of a new node with probability $q$, and the creation of a new fully connected community of $s$ nodes, with probability $p$. When an existing node or community is involved (with complementary probabilities $1 - q$ and $1 - p$ respectively), it is chosen preferentially to its past activity: A node with $m$ memberships or a community of size $s$ is chosen more frequently than a node/community with fewer memberships or a community of size $s$. SPA thus models network growth by considering that all events consist of a node joining a community.

We can write rate equations to follow the numbers $N_m$ of nodes belonging to $m$ groups and the number $S_n$ of groups with $n$ nodes. These equations are similar to most linear preferential attachment models:

$$N_m(t+1) = N_m(t) + q\delta_{m,1}$$
$$+ \frac{1 - q + p(s - 1)}{t[1 + p(s - 1)]} [(m - 1)N_{m-1}(t) - mN_m(t)]$$

$$S_n(t+1) = S_n(t) + p\delta_{n,s}$$
$$+ \frac{1 - p}{t[1 + p(s - 1)]} [(n - 1)S_{n-1}(t) - nS_n(t)] ,$$

and $N_m, S_n$ can be shown to scale as power laws, i.e. $N_m \sim m^{-\gamma_N}$ and $S_n \sim n^{-\gamma_S}$, with exponents [29]

$$\gamma_N = \frac{2 - q + 2p(s - 1)}{1 - q + p(s - 1)}$$

$$\gamma_S = \frac{2 - p + p(s - 1)}{1 - p} .$$

The interested reader is directed to Refs. [14] [29] for a complete derivation of these results.

B. Coupling discrete and continuous processes

Our goal is to incorporate the simple local mechanism of Sec. [II] within the SPA model for heterogeneous community structures. To do so, we must determine the precise relation between the time scales of SPA and that of the local model, thereby allowing a concurrent simulation of both processes. This is not a simple matter, since one must reconcile the continuous nature of the local growth mechanism with the discrete nature of SPA.

In SPA, time $\tilde{T}$ is measured in number of events. Without loss of generality and for reasons that will become apparent shortly, let us define a rescaled discrete time scale $T$ in which a fraction $\epsilon$ of the time steps lead to SPA events, such that $\epsilon \tilde{T} = T$. The community structure does not change during the remaining $(1 - \epsilon)T$ time steps. Because a time step $T$ marks the birth of a new community (of size $s$) with probability $p$, or the growth of an existing one with complementary probability $1 - p$, we can write the time dependent sum of the sizes $n_i(T)$ of all communities as

$$\sum_i n_i(T) = \epsilon T [ps + (1 - p)] = \epsilon T [1 + p(s - 1)] .$$

The average size $n_i(T)$ of community $i$ in discrete time $T$ is then governed by a rate equation

$$n_i(T + 1) = n_i(T) + \epsilon(1 - p) \frac{n_i(T)}{\epsilon T [1 + p(s - 1)]}$$

$$= n_i(T) \left[1 + \frac{1}{T} \alpha(p, s)\right]$$

where we have defined $\alpha(p, s) := (1 - p)/(1 + p(s - 1))$. Equation (14) merely states that growth events will affect community $i$ with probability $n_i(T)/\sum_j n_j(T)$ (i.e. preferentially to its size). In the limit of large times, (14) can be rewritten as

$$\frac{dn_i(T)}{dT} = \frac{n_i(T)}{T} \alpha(p, s) .$$

Now, recall that the size $n_i(t)$ of a community grows exponentially in continuous time $t$ as

$$\frac{dn_i(t)}{dt} = n_i(t)\rho_n .$$

Combining time derivatives (15) and (16) yields a relation between the continuous time $t$ and the discrete time $T$

$$\frac{dt}{dT} = \frac{dt}{dn_i(t)} \frac{dn_i(T)}{dT} = \frac{n_i(T)}{n_i(t)} \rho_n T = \frac{\alpha(p, s)}{\rho_n T} .$$

This result holds provided that $n_i(t) = n_i(T)$ at all time. As such, Eq. (17) is valid for all communities (i.e. there exists a single time scale for all communities) and it can be used to express both processes on a unified time scale. We choose to
describe the local link creation process of Sec. II in time $T$, since discrete time scales are generally easier to handle.

The first part of the local model (nodes are recruited at rate $np_n$) is easily accounted for: Whenever a node joins a new community, we simply choose a recruiting node uniformly among the current members of that community, and form a new link. The exponential growth of communities in SPA ensures that this process is consistent with the model of Sec. II.

The second part of the local model (internal links are created at rate $\propto np_l$) entails a more involved analysis. Let us define $\tilde{n}_i(t)$ as the effective size of community $i$, i.e. the number of nodes that are allowed to create links (those with less than $n_i(t) - 1$ links within community $i$). Then, in the local model, the number of links $L(t)$ in a community of effective size $\tilde{n}_i(t)$ grows at a rate

$$\frac{dL(t)}{dt} = \rho \tilde{n}_i(t)$$

such that links are introduced in a community at the rate

$$\frac{dL(T)}{dT} = \frac{dL(t)}{dt} \frac{dt}{dT} = \rho \frac{\tilde{n}_i(t)}{n_i} \alpha(p,s)$$

$$= r\epsilon(1-p) \frac{\tilde{n}_i(T)}{\sum_j n_j(T)}.$$  \hfill (19)

The purpose of time transformation $\epsilon T = \tilde{T}$ is then apparent: It can be adjusted to bound $r\epsilon(1-p)$ to the interval $[0,1]$ for all $r \in \mathbb{R}^+$. Since $\epsilon$ is an arbitrary fraction which also lies in $[0,1]$, we adopt the simplest choice, i.e.

$$\epsilon = \begin{cases} \frac{1}{r(1-p)} & \text{if } r(1-p) > 1, \\ 1 & \text{otherwise}. \end{cases}$$  \hfill (20)

Equation (19) can then be interpreted in two ways. Straightforwardly, we may say that at each time step $dT$ of the SPA process, a new link is created between the existing members of the communities of effective size $\tilde{n}_i$ with a probability given by the RHS of (19), for all $i$. Alternatively, we may say that at each time step $dT$ of the SPA process, a new link is created with probability $r\epsilon(1-p)$, in a community selected with a probability proportional to its effective size, $\tilde{n}_i(T)/\sum_j n_j(T)$. Equation (20) ensures that this interpretation is always sensible. In both interpretations, the source of the link is selected uniformly among all the nodes of degree $k < n-1$, and the target node is selected uniformly among all possible targets (the nodes to which the source is not connected).

Note that the ratio $\tilde{n}_i(T)/\sum_j n_j(T)$ is not normalized. In the context of the second interpretation, this implies that at each time step $dT$, there is a probability $1 - \sum_i \tilde{n}_i(T)/\sum_j n_j(T)$ that no link creation event will occur. Alternatively, we may select the community in which the link creation event occurs proportionally to its actual size $n_i(T)$, and select the source node uniformly among all the nodes of that community. The ratio $\tilde{n}_i(T)/\sum_j n_j(T)$ will then be effectively respected if we consider that a link creation simply “fails” whenever the randomly selected source node has the maximal number of connections.

The above analysis yields a straightforward algorithm for the modified version of SPA (hereafter SPA+) \[39\]. Starting with disjoint and fully connected communities of size $s$, at each discrete time step $T$:

1: a new community of size $s$ is created with probability $p_c$, or an existing one (chosen preferentially to its size) grows with probability $(1-p)c$;

1.a: if a community birth event has been selected, one of the $s$ involved nodes is a new one with probability $q$ or an existing one (chosen preferentially to its current memberships) with complementary probability $1-q$. The other $s-1$ nodes are chosen preferentially, among existing nodes;

1.b: if a community growth event has occurred, the involved node is a new one with probability $q$ or an existing one (chosen preferentially to its current membership) with probability $1-q$. This node then randomly selects an existing member of the community (uniformly) and creates a link;

2: with probability $r(1-p)c$, a new link is created in a community chosen preferentially to its size. It connects a uniformly chosen node, and a uniformly chosen potential neighbor, provided that the source node is not already connected to every node in the community.

If $r(1-p) < 1$, link creation occurs on slower time scale than community structure related events, whereas the converse is true if $r(1-p) > 1$.

### C. Parameters estimation

SPA+ efficiently grows networks with heterogeneous community structure and communities with realistic internal structures. We now turn to the problem of parameters fitting. Most of the parameters, e.g. $s$, or the final size $N$, are automatically set by the system that one wishes to model. This leaves three free parameters: $p \in [0,1]$ (size of communities), $q \in [0,1]$ (memberships of nodes), and $r \in [0,\infty)$ (density of communities). In this section, we explain how to fit $r$, since the relation between $p$, $q$ and the community structure is extensively discussed in \[14\]. In the following, all estimated values of the parameters will be affixed with a caret: $\hat{p}$, $\hat{q}$, and $\hat{r}$.

#### 1. Density estimators

There exist two obvious methods to fit $r$ to empirical data. The first is a straightforward least square estimator (LSE); it compares the observed average degree $\langle k(n) \rangle$ in groups of size $n$ and the analytical prediction of Eq. (6) for $\langle k(n; r) \rangle = 2L(n; r)/n$. By minimizing the distance over all $r$, one obtains the estimate $\hat{r}$. The other method relies on likelihood maximization (MLE), and uses the results of the rate equations of Sec. II. Define $\{k_{i,\ell}\}$, the sequence of internal degrees of a real network, where $i$ refers to node...
and \( \ell \) is the index of a community. Assuming uncorrelated communities, the log-likelihood \( \mathcal{L} \) that \( r \) was used to generate the sequence \( \{k_{i,\ell}\} \) is then

\[
\mathcal{L}(r|\{k_{i,\ell}\}) = \sum_{\ell} \sum_{i \in \ell} \log[p(k_{i,\ell}|n_{i,\ell}, r)],
\]

where \( p(k_{i,\ell}|n_{i,\ell}, r) \) is the probability of finding a node of degree \( k_{i,\ell} \) in a community of size \( n_{i,\ell} \), if the growth ratio equals \( r \). This probability is obtained by numerical integration of Eq. (3), and one estimates \( \hat{r} \) by maximizing Eq. (21) over all \( r \).

2. Finite size effects and correction mask

While both estimators work well in theory, a few implementation issues arise because we have developed our internal mechanism in a mean-field framework; we ignore effects that significantly alter the predictions of Eq. (3) and (4), on which our estimators rely. We have assumed that a community grows on its own and draws new members from an infinite reservoir of indistinguishable nodes. In practice, the reservoir is finite and each node therein is tagged. We argue that a systematic bias is introduced by two important finite size effects, and that it can be removed with a procedure explained below.

First, when a community grows by recruiting a new member, the member is selected randomly from all existing nodes. In finite systems, the same node can (and will) be recruited twice by the same community. To respect the relative rates of all events and preserve the mean-field mapping of Sec. III B we consider that this node is effectively a new one. This implies that a node can be connected to multiple copies of itself. When we construct the full system at the end of the growth process, we collapse the redundant memberships into a single membership, which (a) skews the tail of membership and size distribution and (b) removes self-loops from the system. Second, a further finite size effect arises because it is possible for two nodes to share more than one community, such that the internal density of a community can be inflated by links that were created in different communities.

To delineate the finite-size effects at play and their impact on our estimates of \( \hat{r} \), we construct a number of SPA+ networks and obtain their matrices of internal degrees \( \{k_{i,\ell}\} \) using informations that is not available to an observer who does not know the history of the system. We then apply our estimators to these matrices and establish how each finite-size effect influences our estimate of \( \hat{r} \). The numerical results of this investigation are displayed in Fig. 4 for \( N = 10,000 \).

The estimators are first calibrated on pure internal structures (Fig. 4a-b), where we analyze each communities separately, without collapsing memberships. In the pure case, the quality of our estimate of \( \hat{r} \) only depends on \( p \), through its effect on sample size and the time-mapping. As \( p \) increases the inference task becomes harder, because communities mostly live in the fully connected regime, where there are few discriminating effects.

FIG. 4. (color online) Accuracy of the least square (a-c-e) and maximum log-likelihood (b-d-f) estimators of \( r \), in finite size networks generated by SPA+ with \( s = 1 \), \( N = 10,000 \) and \( r = 2 \). The sub-figures display the ratios of the estimates \( \hat{r} \) to the value of \( r \) used to create the data, for all pairs of \( (p,q) \). We use these ratios to quantify the finite-size bias of our estimators. A perfect match is color coded in white, whereas under- (over-) estimates appear in shades of blue (yellow). The ratios are largely independent of \( r \), and qualitatively similar \( \forall N \). Their precise values depend however on \( N \).

(a-b) Estimators computed using the pure internal average degree distributions. (c-d) Estimators computed using the collapsed internal average degree distributions. (e-f) Estimators computed using the collapsed and overlapping internal average degree distributions. See the main text for a definition of the finite size effects involved in each case.

FIG. 5. (color online) Parameters \((\hat{p}, \hat{q})\) used for the reproduction of arXiv (blue lozenge), Enron (orange circles), and MathSci (green squares). Our bias measure \( m(\hat{p}, \hat{q}; N) \) of the MLE is shown in the background for \( N = 10,000 \) and \( r_m = 2 \) to illustrate the qualitative corrections that must be applied to \( r_0 \) (see main text for the definition). The color map is only indicative of the actual corrections that are calculated separately for each \( N \). We find the following values of \( m \): 1.27 (arXiv, CCPA), 6.84 (arXiv, LCA), 5.00 (Enron, LG), 1.03 (Enron, OSLOM) and 1.04 (MathSciNet, GCE).
As shown by our results, the bias is more pronounced in the estimated value of $N$ over the number of SPA+ networks realizations), and take the estimated parameter $\hat{m}(\hat{p}, \hat{q}; \hat{r})$ appears at the bottom of each figure, and is determined using the procedure described in Secs. III C and IV A. Simulated networks grow from an initial size ranging from $N/100$ to $N/10$, with final sizes $N = 3561$ for arXiv (a-b), $N = 36692$ for Enron (c-d), $N = 391529$ for MathSciNet (e). All reproductions are realized with $s = 1$ because empirical datasets feature disconnected components.

We then consider collapsed internal structures (Fig. 4(c-d)), which are obtained by merging duplicate nodes into single entities, and then removing self-loops and parallel links. Communities that contain multiple copies of a same node decrease both in size and number of links. The membership collapsing procedure only affects our estimate of $r$ at very low $(p, q)$, i.e. for parameters that yield highly redundant communities. For the majority of $(p, q)$ pairs, the bias is small for both estimators: The estimated value $\hat{r}$ deviates from the true value by at most 25%, for 60.9% (LSE) and 80.1% (MLE) of the $(p, q)$ pairs.

A significant bias is however introduced when one does not assign links to specific communities. This is what we call the collapsed & overlapping structures, where links increase the density of all the communities to which they belong, rather than a single one. This final case encompasses all the finite size biases, and makes use of the information that should be recovered by mean of a perfect community detection algorithm. As shown by our results, the bias is more pronounced in the significantly overlapping regime $p < q$, where communities grow slower than the node reservoir (see Sec. II B).

While not a problem per se, this bias must nevertheless be removed when fitting SPA+ to empirical data. Since most overlapping community detection algorithms do not explicitly assign links, we are often placed in the “collapsed and overlapping” case. We use the following modeling procedure to account for the finite-size bias: (i) obtain the parameters $(\hat{p}, \hat{q})$ that best model the community structure, (ii) compute an initial estimate $\hat{r}_0$ of the strength of the internal connectivity of communities, and (iii) finally obtain the corrected estimated parameter $\hat{r}$, as $\hat{r} = \hat{r}_0/m(\hat{p}, \hat{q}; \hat{N})$. The correction $m(\hat{p}, \hat{q}; \hat{N})$ is the value of the bias removal mask for networks of $N$ nodes, at point $(\hat{p}, \hat{q})$ (see Fig. 5). Since the mask depends on the network size $N$, it is computed for each network separately. In practice, we obtain $m(\hat{p}, \hat{q}; \hat{N})$ by first generating a number of SPA+ networks of $N$ nodes with fixed parameters $(\hat{p}, \hat{q}, \hat{r} = \hat{r}_m)$. We have found that the final results are almost independent on the precise value of $\hat{r}_m$; we have used $\hat{r}_m = 2$ but $\hat{r}_m = \hat{r}_0$ is an equally good choice. We then extract $\hat{r}_m$ from the collapsed and overlapping communities (averaged over the number of SPA+ networks realizations), and take $m(\hat{p}, \hat{q}; \hat{N}) = \hat{r}_m/r_m$. This bias removal mask accounts for finite size effects and allows us to generate networks with mean internal degrees on a $\langle k(n) \rangle$ curve that resemble the empirical data.

IV. RESULTS AND DISCUSSION

The SPA model has previously been shown to capture several properties of the community structure of real networks. We now investigate these properties anew by modeling three social networks: Co-authorship networks obtained from the arXiv circa 2005 and from MathSciNet circa 2008, as well as the email exchange network from Enron. We detect their community structure with five different algorithms: A link clustering algorithm (LCA), a greedy clique expansion algorithm (GCE), the order statistics local optimization method (OSLOM), a greedy modularity optimization of line-graphs algorithm (LG), and a cascading approach to clique percolation (CCPA). This provides us with a total of 15 systems, from which we have selected 5 representative examples. Note that three of the above algorithms (LCA, LG, CCPA) identify link partitions, while the other two directly find overlapping node communities. We translate link partitions into node communities to analyze every algorithm on a common basis, where the true community of a link is unknown.

A. Modeling real networks

As discussed in Sec. III C, we model a real network by choosing a value for the tuple of parameters $(p, q, r)$. The parameters $p$ and $q$ are fitted using the memberships and size distributions of the empirical data. In practice, we obtain a first approximation for $p$ and $q$ using a systematic method for estimating power-law exponents by likelihood maximization. We then adjust $(p, q)$ to account for the fact that empirical distributions are not pure power-law. We use the MLE of Sec. III C to fit $r$ to the the sequence of internal degrees $\{k_i, \epsilon\}$.
In Fig. 6, we compare the statistical properties of SPA+ networks with their empirical counterparts. We obtain good agreement in general. However, it is immediately clear that the empirical distributions are not all pure power laws, such that our model is bound to fail in some cases. Our model produces heterogeneous community structure with scale-free behavior, and we aim to stay within this framework; as long as we consider scale-free systems, we can fit both the size and membership distribution robustly and independently [29, 45]. This is why we obtain good agreements in sizes [see Fig. 6(a)-(d)] and memberships [Fig. 6(a)-(e)] for most analyzed community structures. However, when the empirical distributions decay erratically [e.g. Fig. 6(a)] or too slowly, [e.g. Fig. 6(e)], we only obtain an approximate agreement.

Due to the nature of our model, the quality of the predicted degree distribution is inherently connected to the quality of the predicted size and membership distributions. It can be shown that the global degree distribution of SPA+ networks cannot decay more slowly than the membership and size distributions. The reason is that links are created within communities, such that the number and size of the communities of a node limit its maximal degree (See Ref. [29] for a full discussion). If the community structure is properly described by the SPA model [see Fig. 6(a)-(d)], we expect SPA+ to reproduce the global degree distributions to some extent. When it is not the case, SPA+ generates network with a global degree distribution that falls too rapidly [see Fig. 6(d)-(e)], and inaccuracies in the community structure are reflected in the global degree distributions, even if our internal model fits the empirical data nicely [see Fig. 8]. This effect explains why we cannot model the degree distribution of Enron network as described by OSLOM [notice the abnormally large and densely connected communities of size \(n \approx 10^3\) in Fig. 6(d)], and of the MathSciNet network as described by GCE [see Fig. 6(e)].

### B. Correlations between community structure and the structure of communities

Additional properties are also captured by SPA+. The results shown in Fig. 7 investigate correlations between the organization within communities and the overarching community structure. We obtain the relation between the average internal degree of a node within communities of size \(n\) (i.e. the “social involvement” of an individual within a group), and its membership number \(m\), in empirical datasets and the corresponding simulated networks. We quantify this relationship by the ratio \(\langle k(n, m) \rangle / \langle k(n, 1) \rangle\).

Generally, all algorithms except GCE find that nodes active in the community structure (high number \(m\) of memberships) tend to be also active within communities (high average internal degree \(\langle k \rangle\)). Even though agreement is not perfect, our model reproduces this effect through age-memberships and age-degree correlations. While the available data does not tell whether these correlations are indeed age-related, it is natural to assume that authors or employees who have been active for a longer time within the archive or the company, tend to have more groups and more relations within them. To the best of our knowledge, these correlations are not considered in other growth models, but naturally emerge from our link creation mechanism. In essence, this means that individuals acting as hubs in the community structure (many memberships), tend to act also as hubs within the structure of their communities.
FIG. 8. (color online) Dunbar’s number in empirical data. (a-c) Average number of connections \(\langle k(n) \rangle\) for individuals within a group of size \(n\). (d-f) Average density \(\langle \rho(n) \rangle = \langle k \rangle / [n(n-1)]\) of groups of size \(n\). A line \(\langle \rho(n) \rangle \propto n^{-1}\) is traced to guide the eye. Rough (uncorrected) estimates of \(\hat{r}_0\) using the LSE are, from bottom to top, (arXiv) \(\hat{r}_0 = 2.18, 2.61, 2.89, 5.20, 5.99\) (Enron) \(\hat{r}_0 = 1.69, 2.27, 4.97, 7.96\) and (MathSci) \(\hat{r}_0 = 0.77, 1.33, 1.47, 2.68\).

C. Some implications of Dunbar’s number

In Sec. II C we have discussed the theoretical relation between our model for the structure of communities and a cognitive limit in an individual’s social relationships known as Dunbar’s number. In our model, this limit stems from the ratio of effort put in building new connections \(\rho_n\) and in increasing group size \(\rho_t\), which constrains the average internal degree in large groups. In Fig. 8 we observe a similar behavior in our social network datasets. The empirical results are also compared with our model using our least square estimates for \(\hat{r}_0\).

The observed plateau implies a vanishing average density \(\langle \rho(n) \rangle\), i.e. fraction of potential links that exist, for large communities. Regardless of the nature of the network, of the community detection algorithm and of the parameters \((p, q, r, s)\), the simple existence of the plateau implies that community density vanishes as \(\langle \rho(n) \rangle \sim n^{-1}\). This is obviously true in our model, and observed for our datasets in Fig. 8. Only the community structure of Enron as detected by LG stands out from the prediction. One could argue that this limit is in fact universal, since non-vanishing densities would imply overly dense communities at large sizes. Further empirical studies would however be required to support this claim.

V. CONCLUSION

We have introduced a simple model for the growth of the internal structure of communities which is consistent with empirical observations (vanishing density, varying heterogeneity). As a by-product, we have shown how this model offers a simple explanation of the theory of Dunbar’s number.

Furthermore, we have shown how our local model fits in the broader context of structural preferential attachment, and how the resulting model reproduces the well-known heterogeneity of the membership, size, degree and internal degree distributions, independently of the network and of our detection algorithm. This led to better insights on the relation between the community structure and the structure of communities. As a result, we have identified a seldom studied ubiquitous properties of the internal structure of network, namely the correlation between the activity of a node within communities (i.e. its role in the structure of its communities) and within the network (i.e. its role in bridging communities).

Due to its universality, we argue that SPA+ could be used as a high-quality proxy for realistic network structures. In fact, because it grows realistic and varied networks with full community structure metadata, we are presently applying our model as a benchmarking tool for community detection algorithms. SPA+ offers the possibility to create networks with communities of vanishingly small link density. The point will be to test the robustness of algorithms in these controlled situations. We can expect that algorithms will only be able to detect communities up to a certain size, since the density of larger
communities becomes increasingly similar to that of the full network.

ACKNOWLEDGMENTS

The authors would like to thank Calcul Qu´ebec for the computing facilities. This work has been supported by the Institutes de recherche en sant´e du Canada, the Conseil de recherches en sciences naturelles et en g´enie du Canada, the Fonds de recherche du Qu´ebec-Nature et technologies, and the James S. McDonnell Foundation Postdoctoral Fellowship. J.-G.Y and L.H.-D contributed equally to this work.

Appendix A: Peloton dynamics

This Appendix presents our preliminary analysis of the results of Fig. 2 which are reminiscent of the peloton dynamics studied in Ref. [29]. It is a finite-size effect related to the leaders dynamics: groups of highly connected individuals result in a clearly identifiable bulge in the internal degree distribution. Averaging over multiple realizations of the growth of a community leads to the creation of a peloton where one is significantly more likely to find entities than predicted by the asymptotic distribution. Because the same peloton evolves with growing n, it is expected to retain its shape across a large range of community sizes. The simplest scaling Ansatz takes the form

\[ p_k(n; r) \approx k^{-\alpha(r)} G(k/n^{\beta(r)}) \quad \text{for} \quad n \gg 1, \quad (A1) \]

where \( G(x) \) is a universal function. The construction is clear: \( k^{-\alpha} \) takes care of the power law decreases and the scaled variable \( k/n^\beta \) aligns all curves together. This exercise is carried out in Fig. 9 for the case \( r = 49 \). The procedure is inspired by Ref. [46] and is called quite appropriately data collapse.

Although, we have not investigated the exact form of \( G(x) \), its general behavior is characteristic of a number of self-organized critical systems observed thus far (Ref. [45]): A flat curve sharply rising to a well defined maximum followed by a rapid exponential decrease as a function of the rescaled variable. The scaling information is captured by the exponents \( \alpha \) and \( \beta \). They can be extracted numerically from the positions \( k_0(n; r) \) of the maxima of the bulges of the individual probability distributions, together with the values of the probabilities \( p_k \) at these maxima (see Fig. 9(a)], and the scaling Ansatz of Eq. (A1). The search for the best scaling exponents \( \alpha(r) \) and \( \beta(r) \) is done separately under the assumption that they are independent. This is coherent with our scaling Ansatz. In practice, one obtains \( \alpha(r) \) from the asymptotic slope of the distributions (i.e., the initial dependence on \( k \) before the peloton), and \( \beta(r) \) from a power law fit \( n^{\beta(r)} \) to \( k_0(n; r) \) versus \( n \). Our initial findings, based only on two values of \( r \), reveal that the exponents have only a mild dependence on \( r \) and in particular that \( \beta \) seems to be close to 0.3. In view of our small datasets, it is not expected that the numerical values of \( (\alpha, \beta) = (1.87, 0.285) \) used in Fig. 9 are the absolute best scaling exponents. A complete analytical justification of our scaling Ansatz and a derivation of the expected values of the exponents are still lacking. However, the mere existence of a scaling behavior provides useful estimates of how the degrees of the leaders scale with network size. This is a crucial information when one is interested in the statistics of the extremes, both in theory [47] and application [48]. This calls for a more extensive study beyond the scope of the present contribution.

[1] S. Wasserman, Social Network Analysis: Methods and Applications (Cambridge University Press, 1994).
[2] M. E. J. Newman, Networks: An Introduction (Oxford University Press, 2010).
[3] D. J. Watts and S. H. Strogatz, Nature 393, 440 (1998).
[4] M. Girvan and M. E. J. Newman, Proc. Natl. Acad. Sci. U.S.A. 99, 7821 (2002).
[5] S. Fortunato, Phys. Rep. 486, 75 (2010).
[6] J. Xie, S. Kelley, and B. K. Szymanski, ACM Computing Surv. 45, 43 (2013).
[7] A. Clauset, C. Moore, and M. E. J. Newman, Nature 453, 98 (2008).
[8] R. Guimerà and M. Sales-Pardo, Proc. Natl. Acad. Sci. U.S.A. 106, 22073 (2009).
[9] B. Karrer and M. E. Newman, Phys. Rev. E 82, 066118 (2010).
[10] L. Hébert-Dufresne, P.-A. Noël, V. Marceau, A. Allard, and L. J.
[11] A. Hackett and J. P. Gleeson, Phys. Rev. E 87, 062801 (2013).
[12] A. Allard, L. Hébert-Dufresne, J.-G. Young, and L. J. Dubé, Phys. Rev. E 92, 062807 (2015).
[13] J. Yang and J. Leskovec, Knowl. Inf. Syst. 42, 181 (2015).
[14] L. Hébert-Dufresne, A. Allard, V. Marceau, P.-A. Noël, and L. J. Dubé, Phys. Rev. Lett. 107, 1 (2011).
[15] F. Radicchi, C. Castellano, F. Cecconi, V. Loreto, and D. Parisi, Proc. Natl. Acad. Sci. U.S.A. 101, 2658 (2004).
[16] G. Palla, I. Derényi, I. Farkas, and T. Vicsek, Nature 435, 814 (2005).
[17] V. Blondel, J.-L. Guillaume, R. Lambiotte, and E. Lefebvre, Journal of Statistical Mechanics: Theory and Experiment 10, 10008 (2008).
[18] M. Rosvall and C. T. Bergstrom, Proc. Natl. Acad. Sci. U.S.A. 105, 1118 (2008).
[19] Y.-Y. Ahn, J. P. Bagrow, and S. Lehmann, Nature 466, 761 (2010).
[20] C. Lee, F. Reid, A. McDaid, and N. Hurley, arXiv:1002.1827 (2010).
[21] B. Ball, B. Karrer, and M. Newman, Phys. Rev. E 84, 36103 (2011).
[22] T. P. Peixoto, Phys. Rev. E 85, 056122 (2012).
[23] F. W. Holland, K. B. Laskey, and S. Leinhardt, Soc. Networks 5, 109 (1983).
[24] C. Seshadhri, T. G. Kolda, and A. Pinar, Phys. Rev. E 85, 056109 (2012).
[25] J. Yang and J. Leskovec, in IEEE 12th International Conference on Data Mining (IEEE, 2012) pp. 1170–1175.
[26] P. Erdős and A. Rényi, Publicationes Mathematicae 6, 290 (1959).
[27] E. N. Gilbert, Ann. Math. Stat. 30, 1141 (1959).
[28] A.-L. Barabási and R. Albert, Science 286, 509 (1999).
[29] L. Hébert-Dufresne, A. Allard, V. Marceau, P.-A. Noël, and L. J. Dubé, Phys. Rev. E 85, 026108 (2012).
[30] L. Hébert-Dufresne, A. Allard, J.-G. Young, and L. J. Dubé, Phys. Rev. E 93, 032304 (2016).
[31] M. Molloy and B. Reed, Rand. Struct. Alg. 6, 161 (1995).
[32] R. Guimerá, L. Danon, A. Díaz-Guilera, F. Giralt, and A. Arenas, Phys. Rev. E 68, 065103 (2003).
[33] R. Dunbar, J. Hum. Evol. 22, 469 (1992).
[34] J. de Ruiter, G. Weston, and S. M. Lyon, Am. Anthropol. 113, 557 (2011).
[35] S. Shultz and R. I. M. Dunbar, Proceedings of the Royal Society of London B: Biological Sciences 274, 2429 (2007).
[36] B. Gonçalves, N. Perra, and A. Vespignani, PLoS ONE 6, e22656 (2011).
[37] R. I. M. Dunbar and S. Shultz, Science 317, 1344 (2007).
[38] L. Hébert-Dufresne, E. Laurence, A. Allard, J.-G. Young, and L. J. Dubé, Phys. Rev. E 92, 062809 (2015).
[39] A C++11 implementation of SPA is available online at https://github.com/spa-networks/spa.
[40] G. Palla, I. Farkas, P. Pollner, I. Derényi, and T. Vicsek, New J. Phys. 10, 123026 (2008).
[41] B. Klimt and Y. Yang, in Conference on Email and Anti-Spam (2004).
[42] A. Lancichinetti, F. Radicchi, J. J. Ramasco, and S. Fortunato, PLoS ONE 6, e18961 (2011).
[43] T. Evans and R. Lambiotte, Phys. Rev. E 80, 016105 (2009).
[44] J.-G. Young, A. Allard, L. Hébert-Dufresne, and L. J. Dubé, PLoS one 10, e0140133 (2015).
[45] A. Clauset, C. R. Shalizi, and M. E. Newman, SIAM review 51, 661 (2009).
[46] K. Christensen and N. R. Moloney, Complexity and criticality, Vol. 1 (Imperial College Press, 2005).
[47] P. L. Krapivsky and S. Redner, Phys. Rev. Lett. 89, 258703 (2002).
[48] R. Albert, H. Jeong, and A.-L. Barabási, Nature 406, 378 (2000).