# Hyperbolae Are No Hyperbole: Modelling Communities That Are Not Cliques

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#### Abstract

Cliques (or quasi-cliques) are frequently used to model communities: a set of nodes where each pair is (equally) likely to be connected. However, when observing real-world communities, we see that most communities have more structure than that. In particular, the nodes can be ordered in such a way that (almost) all edges in the community lie below a hyperbola. In this paper we present three new models for communities that capture this phenomenon. Our models explain the structure of the communities differently, but we also prove that they are identical in their expressive power. Our models fit to real-world data much better than traditional block models, and allow for more in-depth understanding of the structure of the data.

## 1 Introduction

Community detection in graphs is a data mining problem that has gathered significant research interest in recent years. So far, most approaches have (either explicitly or implicitly) modelled communities as (quasi-) cliques, i.e. sets of nodes where every node is connected to (almost) every other node – or in other words, where every edge between any two nodes in the community is equally likely.

We argue that a clique is often not a realistic model for real-world communities. Consider the adjacency matrix of a community from the YouTube data from the Stanford Large Network Dataset collection [9] as seen in Figure 1a. In its original ordering, the community does indeed look like a quasi-clique. If, however, we re-order the nodes in descending degree order (Figure 1b), we see

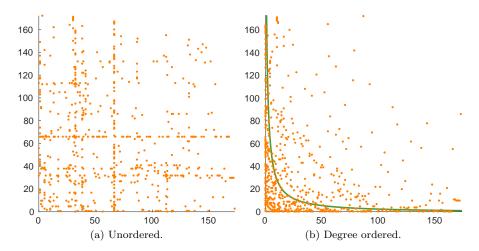


Figure 1: Adjacency matrix of a community from the YouTube data unordered and ordered by induced degree with a model fitted.

immediately that the community takes the shape of a hyperbola: there is a clear curve such that it is much more likely to see an edge below this curve than above it. Accordingly, not every edge between a pair of nodes in a community is equally likely. We have observed this phenomenon in multiple real-world graphs with human-annotated communities [4].

To address this observation, we propose a novel model for communities that explicitly captures the shape of the edge distribution. Importantly, our model contains (quasi-) cliques as a special case; thus, generalizing existing modelling assumptions. In Figure 1b, we see that the curve determined by our model fits very well to the shape of the community, and the likelihood of the community under our model is much higher than under the trivial block model (see Section 4 for the details about the likelihood computation). In fact, in Section 3 we present three different models that allow us to capture different features of the communities and apply different optimization techniques when fitting the model. In Section 3.5 will prove that these three models are equivalent in the sense that a community in one model can be easily transformed to an equivalent community in another model. Yet, the three models are not redundant, as the different views they provide allow for more in-depth understanding of the communities (and the models, as well). In addition to modelling individual communities, we also present a model for the full graph given a set of communities in Section 4. In Section 5 we study the computational complexity of some problems related to the modelling and in Section 6 we present our algorithms for fitting the models to individual communities and full graph alike.

Our experimental evaluation, in Section 7, shows that we can efficiently model real-world graphs with human-annotated communities, yielding significantly more likely models than what we can get by modelling the communities as quasi-

cliques. We will also demonstrate how our models will allow us to gain more understanding on the structure of the communities.

Our main contributions in this paper are

- We present three different but equivalent models for capturing non-uniform edge distributions inside communities.
- We show how to fit the models to the communities, and how to fit a model for the full graph to a graph with a set of communities.
- We show that our approach explains real graphs much better than a traditional quasi-clique based model.

# 2 Related Work

Nodes in real-world networks often organize into communities or clusters. Examples include social networks where people organize in families, clubs and political organizations [17], gene-regulatory networks where groups are formed based on common metabolic function, [14], or the World Wide Web where websites of similar topics show strong clustering structure [7].

For finding such communities, a variety of methods have been introduced in the literature [2]. Even though the proposed approaches seem highly diverse, the vast amount of previous community detection methods have been either explicitly or implicitly aimed at detecting block-shaped areas of uniform density in the adjacency matrix. This includes prominent techniques such as stochastic block-models [3,12], affiliation network models [18,19], pattern based techniques (e.q. detection of quasi-cliques [1]), or cross-associations [5].

In this paper, we argue that communities in real networks do not show such a density profile. As illustrated in Figure 1, they are better represented by using a hyperbolic model. In particular, in contrast to existing works, our model captures that the density within the group is not uniformly distributed – some nodes show stronger connectivity among it peers.

Overlapping community detection The aspect of unequal connectivity structure has also been considered in the area of overlapping community detection. Here, in contrast to classical partitioning approaches, each node might belong to multiple groups. As, e.g., noticed in [18,19], nodes participating in multiple communities lead to areas of higher density. Accordingly, one might conclude that these approaches can handle our scenario of hyperbolic communities. This conclusion, however, is incorrect.

Given a certain community (i.e. a set of nodes), models following the idea of affiliation networks [18, 19], generate edges following the same probability; thus, leading to block-like structures in the adjacency matrix. Similarly, techniques such as mixed-membership block models [3] assume uniform density per community. Indeed, all these methods are highly related to the principle of Boolean Matrix factorization [11] – and its goal of finding overlapping blocks in binary matrices. Clearly, handling overlap and handling hyperbolic structure are two

different aspects. As we will discuss in Section 4, for hyperbolic communities itself, three different types of (non-)overlap can be considered.

So far, the aspect of non-block communities has only been discussed in [4]. The proposed model, however, still does not capture real scenarios. In particular, it assumes a density of 100% inside a community, thus, violating the general property of sparsity. In contrast, our model allows varying density among the different communities.

# 3 Models for Communities

Our goal is to model the aforementioned structure in communities and to that end we present three different models. It should be noted that all these models contain the (quasi-) cliques as special cases; we will prove this later in this section. We will also show that these three different models – with different intuitions behind them – are equivalent representations besides having different parameterizations. These different parameterizations give three different interpretations of the model, and facilitate different types of algorithms for fitting the models to the data.

# 3.1 General modelling decisions

Our input is an undirected graph G = (V, E) with n nodes and m edges. We will assign a number from  $\{0, \ldots, n-1\}$  to the vertices and use (i, j) to denote both a pair of vertices and the (potential) undirected edge between them. We will represent the graph using its adjacency matrix  $\mathbf{A} = (a_{ij}) \in \{0, 1\}^{n \times n}$ .

A community C is a tuple  $(V_C, \pi_C, \Theta_C)$ . The set  $V_C \subseteq V$  contains the nodes in the community, and we write  $n_C = |V_C|$ . The permutation  $\pi: V_C \to \{0, \dots, n_C - 1\}$  orders the nodes. In general, we assume the nodes to be ordered according to their degrees inside the community. The crucial part of our model is the following: not every edge between the nodes in  $V_C$  is necessarily part of our community – that assumption would make all of our communities quasi-cliques. Rather, our community models are defined using a function  $f: \{0, \dots, n_C - 1\} \times \{0, \dots, n_C - 1\} \times \{0, \dots, n_C - 1\} \times \{0, \dots, n_C - 1\}$  if an edge between i and j is part of the community or not. We will define these functions in the subsequent sections.

Notice that the function f only gets the indices relative to the subgraph, not to the full graph, that is, to test a pair  $(i,j) \in V_C \times V_C$ , we need to compute  $f(\pi_C(i), \pi_C(j), \Theta_C)$ . For brevity, we will often omit the permutation and will simply assume that  $i, j \in \{0, \ldots, n_C - 1\}$ .

Every community is associated with two sets of edges: the area of the community,  $A_C$ , defined as  $A_C = \{(i,j) \in V_C \times V_C : f(i,j,\Theta_C) = 1\}$ , and the edges of it,  $E_C = E \cap A_C$ . For notational convenience, we can also define their complements (with respect to the community and the area, respectively):  $\overline{A_C} = (V_C \times V_C) \setminus A_C$  and  $\overline{E_C} = A_C \setminus E$ .

**Probabilistic model for a community** In practice the communities are rarely, if ever, exact. That is, some edges  $(i,j) \in A_C$  are not in  $E_C$ , and some edges  $(i,j) \in E$  that go between the nodes of the community are not in  $A_C$ . To model these imperfect communities, we consider a simple *probabilistic model* of the community. Given a community C, we assume that edges  $(i,j) \in V_C \times V_C$  are drawn from a Bernoulli distribution, that is,  $a_{i,j} \sim \text{Bernoulli}(p_*)$ , where  $A = (a_{ij})$  is the adjacency matrix of the graph, and  $p_*$  is the *density* of the area where the edge belongs to. For a single community, we have two kinds of areas: the area of the community  $A_C$  and its complement  $\overline{A_C}$ . We denote the density of the area of the community by

$$d_C = |E_C| / |A_C| , \qquad (1)$$

and the density of the area outside the community by

$$d_O = |E \cap \overline{A_C}|/|\overline{A_C}| . (2)$$

These densities now correspond to the maximum-likelihood solutions of the variables  $p_*$  for the edges that are inside or outside of the community. We can now consider the likelihood of the subgraph induced by the community  $G|_{V_C}$  given the community C,  $L(G|_{V_C} \mid C)$ . The likelihood of an edge that is in community C is  $d_c$ ; the likelihood of a pair (i,j) that is in the area of C but that is not an edge of G is  $1 - d_C$ ; the likelihood of an edge that is not in the community is  $d_C$ ; and the likelihood of a pair (i,j) that is not in the community's area and is not an edge of G is  $1 - d_C$ . This gives us

$$\log L(G|_{V_C} \mid C) = |E_C| \log(d_C) + |\overline{E_C}| \log(1 - d_C)$$

$$+ |E \cap \overline{A_C}| \log(d_O)$$

$$+ |\overline{A_C} \setminus E| \log(1 - d_O).$$

$$(3)$$

#### 3.2 Area restricted under a hyperbola

For our first model, we can notice from Figure 1 that when the nodes of a community are ordered in the induced degree order, the edges lie under a hyperbolic curve. To define the hyperbola we identify the vertex indices of the community as points in x and y axes. We use i and j instead of x and y to emphasize this connection. We will only consider the area  $[0, n_C - 1] \times [0, n_C - 1]$  from the non-negative quadrant, as that is where the values important to our community are. The equation for a (rectangular) hyperbola is

$$(i+p)(j+p) = \theta , (4)$$

where the hyperbola centre lies at (-p, -p). Figure 2 illustrates one hyperbola. Following the model, an edge (i, j) is considered to be in the community if  $(i + p)(j + p) \leq \theta$ . We call this model hyperbolic $(p, \theta)$  and write  $(i, j) \in \text{hyperbolic}(p, \theta)$  if  $(i + p)(j + p) \leq \theta$ .

From Figure 2 we can gain some intuition to the parameters p and  $\theta$ : different values of p will yield different shapes of the gradient (the coloured background in Figure 2), while different values of  $\theta$  will move the line away from the origin.

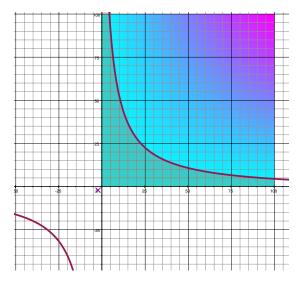


Figure 2: A hyperbola with p=2.06 and  $\theta=673$  (dark red lines). The centre (-p,-p) is marked with a cross. The colours in the background of the nonnegative quadrant indicate the values of (i+p)(j+p) for  $i,j \in [0,99]$ , with higher values moving from cyan to magenta. The area of the community is the solid-coloured area under the curve.

Valid range of parameters The values the Equation (4) assigns to elements (i,j) attain their minimum at the centre (-p,-p). To make sure that all elements  $(i,j) \in \mathbb{N} \times \mathbb{N}$  that are under the curve (4) are always in the community, we must bound p. A simple boundary is to enforce that  $p \geq 0$ , though in Section 3.5 we will derive a more relaxed boundary. Other than this boundary, p and  $\theta$  can be any values.

### 3.3 Fixed points in the curve

The shape of the hyperbola is not easy to interpret from (4), and hence it is not easy to say, by just looking at the parameters p and  $\theta$ , whether the community is 'fat' or 'skinny'. To make the model parameters more interpretable, we can consider two points in the curve: the point at which it crosses the diagonal (i.e. when i=j), and the point at which the hyperbola exits the community (i.e. j for which  $i=n_C$  or vice versa). We call the former  $\gamma$  and the latter H, and we can consider them as two values that define some p and  $\theta$  such that

$$(\gamma + p)(\gamma + p) = \theta \tag{5}$$

$$(H+p)(n_C-1+p) = \theta$$
. (6)

To interpret the parameters, it is helpful to divide every community into two parts: *core* and *tail*. The core consists of nodes that form a (quasi-) clique, while the tail consists of nodes that are mainly connected to the core, and only to few

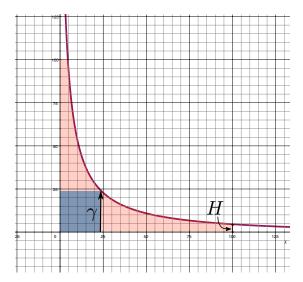


Figure 3: The parameter  $\gamma$  explains the size of the core of the community (dark-shaded box), while H explains the height of the tail at the end of the community.

of each other. This is illustrated in Figure 3 where the core is shaded in dark blue and the tail in light red. The parameter  $\gamma$  is the size of the core (minus 1 to account for zero-based indexing) – the larger, the larger clique the community has – while the parameter H tells how 'fat' the tails are. A (quasi-) clique would have large  $\gamma$  and H, while a star would have  $\gamma = H = 0$ . We will call this model  $\texttt{fixed}(\gamma, H)$  and we will describe the equation for deciding if an edge is in the community later in Section 3.5.

Valid range of parameters Not every  $\gamma$  and H yield valid p and  $\theta$  in (5) and (6), so we have to pay particular attention on the constraints of these parameters. Clearly both  $\gamma$  and H need to be nonnegative. Further, we can restrict them to be integers, as in our application, we are only interested on the value of (i+p)(j+p) in the nonnegative integer grid  $\mathbb{N} \times \mathbb{N}$ . As the hyperbola is monotonic, it must be that  $H \leq \gamma$ , and as the hyperbola is convex, it must be that  $\gamma \leq (n_C - 1 + H)/2$ . Notice that these conditions are necessary, but not sufficient, to make sure that there exists p and  $\theta$  satisfying (5) and (6).

## 3.4 A mixture of a line and a hyperbola

In our third and final model, we consider two restricted models: a simple linear model where an edge (i,j) is in the community if  $i+j \leq \Sigma'$  for some  $\Sigma' \in \mathbb{R}_{\geq 0}$ , and a simple hyperbola  $i \cdot j \leq \Sigma''$ , with  $\Sigma'' \in \mathbb{R}_{\geq 0}$ . Notice that unlike above, here the hyperbola's centre is fixed to the origin. Alone neither of these models can model all different communities that we want to model, but a mixture of

these two is much more powerful: an edge (i, j) is in the community if

$$(1-x)(i\cdot j) + x(i+j) \le \Sigma \tag{7}$$

for some  $x \in [0, 1]$  and  $\Sigma \in \mathbb{R}_{>0}$ .

The meaning of the parameters here is slightly different: the parameter  $\Sigma$  behaves similarly to  $\theta$  in (4), moving the line (or the hyperbola) further from the origin, while the mixture parameter x dictates how much the model looks like a line and how much like a hyperbola centered to the origin. We call this model mixture( $x, \Sigma$ ).

## 3.5 Equivalence and other properties

We will now show that the three models are indeed equivalent. We will first explain how we can map hyperbolic to fixed and vice versa, and then show the equivalence between mixture and hyperbolic.

As we explained above, in  $fixed(\gamma, H)$ ,  $\gamma$  explains the point in which the line (4) crosses the diagonal while H explains the height of the line at the end of the community. From Equations (5) and (6) we can solve p and  $\theta$  given  $\gamma$ , H, and  $n_C$ , the size of the community:

$$p = \frac{\gamma^2 - (n_C - 1)H}{(n_C - 1) + H - 2\gamma} \tag{8}$$

$$\theta = \frac{(\gamma - H)^2 (\gamma - n_C - 1)^2}{(n_C - 1 + H - 2\gamma)^2} \,. \tag{9}$$

Similarly, we can easily work out the equations for  $\gamma$  and H given p and  $\theta$  (and  $n_C$ ).

We will now turn our attention to the equivalence between hyperbolic and mixture.

**Proposition 1.** For any pair  $(p, \theta)$  of valid parameters of the hyperbolic model, there is a pair  $(x, \Sigma)$  of valid parameters of the mixture model that yield exactly the same community, and vice versa.

*Proof.* We have

$$(1+p)(j+p) \le \theta$$

$$\Leftrightarrow \frac{(i+j)p}{1+p} + \frac{ij}{1+p} \le \frac{\theta - p^2}{1+p}$$

$$\Leftrightarrow (i+j)\frac{p}{1+p} + ij\left(1 - \frac{p}{1+p}\right) \le \frac{\theta - p^2}{1+p},$$

$$(10)$$

where the first equivalence is by expanding the left-hand side and re-arranging the terms and the second is by substituting 1/(1+p)=1-p/(1+p). If we now write x=p/(1+p) and  $\Sigma=(\theta-p^2)/(1+p)$ , we get

$$(i+j)x + ij(1-x) \le \Sigma , \qquad (11)$$

concluding the proof.

New constraints for parameters Recall that in Section 3.2 we restricted p to be nonnegative so that it cannot happen that  $(0+p)(0+p) > \theta$  if  $(i+p)(j+p) \le \theta$  for some  $(i,j) \in \mathbb{N} \times \mathbb{N}$ . The motivation for this was that we want element (0,0) to be included in every non-empty community. But we can relax the constraint  $p \ge 0$ :

$$p^2 \le \theta \Leftrightarrow p^2 \le (\gamma + p)^2 \Leftrightarrow p \ge -\frac{\gamma}{2}$$
, (12)

assuming  $\gamma > 0$ . Here, the first equivalence follows by substituting (5) to  $\theta$ . Notice that the p and  $\gamma$  in this inequality are bound together via (8). This constraint also implies the earlier  $H \leq \gamma$ .

Quasi-cliques are a special case An important consideration in our model(s) is that we want to be able to model also the (quasi-)cliques. Clearly this is the case, as we can always set H and  $\gamma$  to  $n_C$  in the fixed model (and solve the parameters for other models accordingly).

# 4 Model for the Full Graph

While the previous section focused on modelling individual communities, we now introduce a principle for describing the full graph – potentially containing multiple communities.

Naturally, when multiple communities are present, we might observe overlapping groups. When communities are modelled as quasi-cliques, there is only one type of overlap we need to consider: if the nodes of two communities overlap, so do their (implicit) edges. With our community models, however, we have to distinguish three types of overlapping behaviour: two communities C and D are node-disjoint if they do not share any nodes  $(V_C \cap V_D = \emptyset)$ ; area-disjoint (but node-overlapping) if they do share nodes but no (implicit) edges  $(V_C \cap V_D \neq \emptyset)$  but  $A_C \cap A_D = \emptyset$ ); and area-overlapping (or overlapping for short) if also their (implicit) edges overlap  $(A_C \cap A_D \neq \emptyset)$ .

For the purposes of this work, we will not allow are a-overlapping communities. Though, instead of enforcing this a priori, we solve it a posteriori: in our model for the full graph, we assign every potential edge  $(i,j) \in V \times V$  to at most one community.

For defining the quality of a set of communities, we refer to a probabilistic approach, i.e. we aim to find the set of models  $\mathcal C$  leading to the highest *likelihood* of the input graph G. For this purpose, notice that in real-graphs it is unlikely to find communities where every edge is present, i.e.  $|E_C| = |A_C|$  rarely holds; instead the communities' densities are likely smaller – and each community might show a different density.

We use the model from Section 3.1 as the basis for modelling a community. That is, the density of a community C,  $d_C$ , is defined as in (1), with every community having its own density. To define the outside density  $d_O$ , we have to consider not only the 'outside area' of a single community, but the whole area of the graph that does not belong to any community. That is, if we let

 $A_{\mathcal{C}} = \bigcup_{C \in \mathcal{C}} A_C$  be the area that belongs to the communities and  $\overline{A_{\mathcal{C}}} = (V \times V) \setminus A_{\mathcal{C}}$  be its complement, then

$$d_O = |E \setminus A_C| / |\overline{A_C}|.$$

We can now model the full graph similarly to how we modelled a single community to obtain the overall likelihood  $L(G \mid \mathcal{C})$  of a graph G given the set of communities  $\mathcal{C}$ .

**Definition 1.** Given a graph G and a collection of its communities C, where every edge belongs to at most one community, the log-likelihood  $log L(G \mid C)$  is defined as

$$\log L(G \mid \mathcal{C}) = \sum_{C \in \mathcal{C}} \left( |E_C| \log(d_C) + |\overline{E_C}| \log(1 - d_C) \right) + |E \setminus A_C| \log(d_O) + (|\overline{A_C}| - |E \setminus A_C|) \log(1 - d_O) .$$
(13)

# 5 Computational Complexity

Before we present our algorithms, let us briefly study the computational complexity of the problems related to the modelling. Instead of dealing directly with the likelihood, in this section our target is to minimize the number of non-edges inside the communities while simultaneously maximizing the number of non-edges outside (i.e. to maximize the community density while minimizing the outside-area density). This is a natural surrogate for the likelihood that allows us to avoid some issues in the analysis caused by the likelihood function (e.g. that the likelihood model is oblivious to the 'inside' and 'outside'; very sparse communities with dense outside area are also good models in likelihood's sense).

We will first consider problems involving only a single community. We will first show that finding the node sets for communities is (still) hard in our model:

**Proposition 2.** Given a graph G = (V, E) and a pair of parameters  $(p, \theta)$ , it is NP-hard to find

- the largest set of nodes  $V_C \subset V$  and a permutation  $\pi_C : V_C \to \{0, \ldots, |V_C| 1\}$  such that the area  $A_C$  defined by  $V_C$ ,  $\pi_C$ , and hyperbolic $(p, \theta)$  is exact, that is  $A_C = E_C$ ;
- the set of nodes  $V_C \subset V$  and a permutation  $\pi_C : V_C \to \{0, \dots, |V_C| 1\}$  such that  $d_C \geq c$  for some given constant  $c \in (0,1)$  and  $d_O$  is minimized.

*Proof.* These results follow from the fact that the clique is a special case of our model. Hence, if  $(p,\theta)$  are set so that they encode a clique, the first case is equivalent to the well-known NP-hard problem of finding the largest clique [8, Problem GT19], while the second is equivalent to the problem of finding the maximum c-quasi-clique, which is also NP-hard [13].

On the other hand, if we are given the nodes (and their ordering), finding the best model for a single community is rather easy:

**Proposition 3.** Given a graph G = (V, E), a set of vertices  $V_C \subseteq V$ , and a permutation  $\pi_C : V_C \to \{0, \dots, |V_C| - 1\}$ , finding the pair of parameters  $(p, \theta)$  that maximizes the function  $d_C + (1 - d_O)$  (or the likelihood of (3)) is doable in time polynomial to  $|V_C|$ .

*Proof.* We utilize here the  $(\gamma, H)$  parameterization, which is equivalent to the  $(p, \theta)$  parameterization. As  $\gamma$  and H are nonnegative integers bounded by  $|V_C|$ , there are at most  $|V_C|^2$  different configurations of them. We can simply try every configuration exhaustively to find the optimal solution.

We use Proposition 3 in the next section to design our algorithms. Importantly, we will show that we do not need to try all the  $\left|V_{C}\right|^{2}$  different configurations.

Let us now turn our attention to the case where we are already given a collection  $\mathcal{C}$  of communities (with fitted models), and we want to find a subcollection  $\mathcal{S} \subseteq \mathcal{C}$  that minimizes the number of edges in the outside area plus the number of non-edges inside the communities. That is, we want to minimize

$$|E \cap \overline{A_{\mathcal{S}}}| + |A_{\mathcal{S}} \setminus E| . \tag{14}$$

For these results, we use the general framework of Miettinen [10]. First note, that our communities are (symmetric) generalized rank-1 matrices in the sense of Miettinen: the functions f of our models define the outer product in Definition 1 of [10], while the adjacency matrix is the data matrix. For this problem, we only care about the union of the areas of the communities, and consequently, we take the element-wise disjunction of the matrices representing their areas. Now, Propositions 6 and 10 of [10] directly furnish us with the following result:

**Proposition 4.** Given a graph G = (V, E) and a collection C of communities of G,

- it is NP-hard to find the subcollection  $S \subseteq C$  that minimizes (14);
- it is NP-hard to approximate the error (14) to within a factor of  $\Omega\left(2^{\log^{1-\varepsilon}|V|}\right)$  and quasi-NP-hard to approximate it within  $\Omega\left(2^{(4\log|\mathcal{C}|)^{1-\varepsilon}}\right)$  for any  $\varepsilon > 0$ ;
- the error (14) can be approximated to within a factor of  $2\sqrt{(|\mathcal{C}| + |V|) \log |V|}$  in polynomial time.

The situation of Proposition 4 can easily arise as the consequence of the following simple idea of finding the communities: first, find many subset of nodes (e.g. by sampling or by enumerating all dense subgraphs), then fit the community models to them, and then select the final subset of communities from the potentially highly redundant set of communities. As Proposition 4 demonstrates, the last step of this approach is computationally very hard. We do not use this approach in this paper due to this.

# 6 Algorithms

Next we present an algorithm for fitting our model to a graph. We assume the algorithm is given as an input the graph and a collection of sets of nodes that determine the communities. These node sets can be found using any existing community-detection algorithm.

We will first present the algorithm to fit the model to a single community, and then how to use that to fit the model for the full graph.

#### 6.1 Modelling a single community

Based on Proposition 3, we will use the fixed model to fit our communities, as it facilitates an easy exhaustive search while being equivalent to the other two models. While on a first sight, this solution seems expensive, due to the constraints we impose on the parameter ranges, searching exhaustively can be done very efficiently.

To gain intuition on how much of the search space the constraints remove, let us consider Figure 4. The area of the plot is the area of all possible combinations of  $\gamma$  and H for some community size  $n_C$ . The yellow area, however, can be ignored as in that area  $H > \gamma$ , violating the trivial constraint from Section 3.3. But also both of the green areas can be ignored, as in those areas, the constraint  $p \geq -\gamma/2$  is violated (see (12)). As we can see, this significantly reduces the different parameter configurations we need to test in the exhaustive search.

**Likelihood-Computation** Given a pair of parameters  $(\gamma, H)$ , we need to evaluate its fit by computing the log-likelihood of the resulting model. According to the model proposed in Section 3.1, this requires to determine the area inside and outside the current community as well as the corresponding number of edges (and non-edges) in these areas. Obviously, testing each position in the community is not a practical solution since it would lead to a running time quadratic in the community's size; instead we derive a solution which is linear in the number of edges.

The computation of the area can be done in time linear in the number of nodes by referring to the functional form of the hyperbola, i.e. evaluating

$$i = \frac{\theta}{j+p} - p$$

for each column j. Here we can compute p and  $\theta$  from  $\gamma$  and H using (8) and (9). Alternatively, we can approximate the area in constant time by taking the integral of this function from 0 to  $n_C - 1$ . Counting how many edges are inside the community requires a pass over the edges. Thus, this step dominates the time complexity.

It is easy to optimize this procedure further: First, we can compute the area faster by noticing that at the bottom we have a rectangle of size  $n_C$ -by-H. Second, when we test a succession of parameter values, we can re-use part of the information about the edges: by increasing the values of H or  $\gamma$  only edges

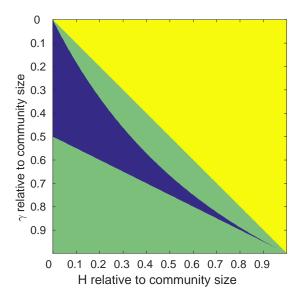


Figure 4: The blue area shows feasible values for parameters  $\gamma$  and H relative to a given community size. The green and yellow area are infeasible. The yellow part violates the trivial requirement of  $H \leq \gamma$  and the green areas violate the condition  $p \geq -\frac{\gamma}{2}$ , where p is given by Equation (8).

previously outside the community need to be evaluated. All remaining edges will still be located within the community.

### 6.2 Modelling a full graph

To obtain a model for a graph consisting of multiple potentially overlapping communities, we aim to optimize the log-likelihood  $L(G \mid \mathcal{C})$  for the full graph (i.e. (13)). Our main problem is to determine how to deal with overlapping communities; indeed, if there are no node-overlapping communities, we can simply optimize every community separately using the above approach. If the communities do overlap, however, we do need to decide the order of the communities so that we can assign every edge to at most one community.

As computing the log-likelihood for the full graph for each possible order of the communities is infeasible, we optimize the log-likelihoods of each community individually following an alternating optimization strategy. When optimizing one community, we keep track of the area that was already covered by other communities, and ignore that area in the computations of the subsequent communities. In concordance with the log-likelihood we want to optimize for, we consider the global density for the whole outside community area (see Section 4) in the log-likelihood computation of the model, instead of just the local outside density, as in Section 3.1.

	nodes	edges	comm	communities	
			all	100-1000	
Amazon	334,863	925,872	75,149	1,380	
DBLP	317,080	1,049,866	13,477	805	
Friendster	65,608,366	1,806,067,135	$957,\!154$	19,763	
LiveJournal	3,997,962	34,681,189	287,512	8,769	
Orkut	3,072,441	117,185,083	6,288,363	80,251	
YouTube	1,134,890	2,987,624	8,385	129	

Table 1: Sizes of the datasets used for evaluation and their total number of communities as well as the number of communities of size 100 to 1000.

The algorithm, shown as Algorithm 1, comprises an initialization phase and an update phase. In the initialization phase of the algorithm (lines 1–6), we compute an individual model for each community, leaving out those edges that have already been covered in a previous step by another community. Note that during this step, each community uses its individual outside density. Next, we order the obtained models by their log-likelihood starting with the best and we compute the global outside density  $d_O$  for the further updates.

Now that we have established an order of the communities, the alternating optimization starts (line 8): Each time a community  $C_i$  is selected and a new model is fit to it – now not only excluding edges already covered in previous communities but also using the global outside density to determine the true log-likelihood for each community. After fitting the new model, we update the global outside density (line 14) if the new model is different to the old one.

All communities that have node overlap with  $C_i$  are marked: due to the update of  $C_i$  also the parameters of the overlapping communities might change. Thus, we mark the communities that overlap with  $C_i$  for a re-update (line 15). We iterate over this process of updating the community models until there are no more communities to be updated.

The output of this algorithm is a list of models for all communities, ordered by their log-likelihoods.

# 7 Experiments

We use the Stanford Large Network Dataset collection [9] to evaluate our method. It provides various networks with ground-truth communities ranging from 300,000 to 65 million nodes. Table 1 provides a summary of the employed datasets. As neither very small nor very large communities are particularly interesting, we restrict our analysis to communities with 100 or more nodes and at most 1000 nodes. Notice that the ground-truth information for the communities is only provided with respect to the nodes.

Algorithm 1 An algorithm to fit the fixed models to a set of communities.

```
Input: Undirected graph G = (V, E), a collection of sets of nodes \mathcal{V} = \{V_i \subset V\}
     describing the communities
Output: Ordered set of communities C
 1: for every set V_i \in \mathcal{V} do
          C \leftarrow \text{best model describing } G|_{V_i}
 2:
          \mathcal{C} \leftarrow \mathcal{C} \cup \{C\}
 3:
 4: end for
 5: Order \mathcal{C} based on the likelihoods of the communities
 6: Compute the global outside density d_O
 7: \mathcal{F} \leftarrow \mathcal{C}
 8: repeat
          \mathcal{T} \leftarrow \mathcal{F}; \mathcal{F} \leftarrow \emptyset; M \leftarrow \emptyset
 9:
          for all C \in \mathcal{T} do
                                                                             ▶ In decreasing likelihood
10:
               Update the model of C ignoring areas in M
11:
               M \leftarrow M \cup A_C
12:
               if the likelihood of C improved then
13:
                    Update d_O
14:
                    \mathcal{F} \leftarrow \mathcal{F} \cup \{D \in \mathcal{C} : V_D \cap V_C \neq \emptyset\}
15:
                    Update the position of C in C
16:
17:
               end if
          end for
18:
19: until \mathcal{F} = \emptyset
20: return C
```

#### 7.1 Obtained models

For a sample of 500 communities per dataset, with the exception of DBLP where we used a sample size of 100, we compute a hyperbolic model and compare the shape of the obtained communities with each other. Figures 5 and 6 summarize the distributions of the parameters  $\gamma$  and H for different data sets, respectively. The boxplots indicate the median as the central mark and the edges of each box are the 25 and 75 percentiles. The whiskers extend to the most extreme data points not considered outliers. We observe a characteristic shape for each data set: While Amazon, DBLP, and Friendster show rather thick communities with  $\gamma$  on median being more than 50% of the community size, LiveJournal, Orkut, and YouTube communities mostly have thin cores. While Orkut also has communities with big cores, LiveJournal is at the other extreme and its communities mostly exhibit a star-like shape.

A few exemplary models are displayed in Figures 7 and 8, respectively for the Amazon and YouTube data.

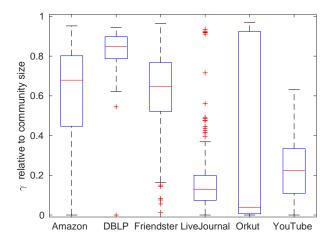


Figure 5: Distribution on  $\gamma$  after fitting a hyperbolic model to sampled communities of size 100 to 1000 from each dataset. The sample size was 500 for all datasets except DBLP where 100 communities were sampled.

#### 7.2 Comparison to block models

As the model we propose is novel, the only comparison we can provide to assess the benefit of describing communities by their hyperbolic structure is to compare how much better this description is compared to describing the same communities by block models. To do so, we compute the log-likelihood as in (13) for the model we obtain for each of the datasets and compare it to the log-likelihood obtained when each community is considered as a block. Blocks are a special case of our proposed model and hence we can employ the same computation and only restrict  $H = \gamma = n_C$  to model each community as a block.

To compare the log-likelihoods against each other, we use the likelihood ratio test [16, Ch. 10.6]. Its test statistic is  $\chi^2$  distributed and hence allows for computing a p-value: We test the null hypothesis  $H_0$  that all parameters, i.e. all H and  $\gamma$  of all communities, are fixed to create the blocks versus the alternative hypothesis  $H_1$  that the parameters are not fixed. The likelihood ratio test statistic is given by  $\lambda = 2\log(L(\text{hyperbolic model})/L(\text{block model}))$  and their values for every dataset are shown in Table 2. The derived p-values are always essentially zero and confirm that the hyperbolic model is statistically significantly better than the block model.

# 7.3 Finding communities

To find the communities, we can use any existing community-finding method. In this section, we test how well we can fit our model to communities returned by methods that look for more clique-like communities. We used spectral clustering and Boolean matrix factorization on various real-world data sets from

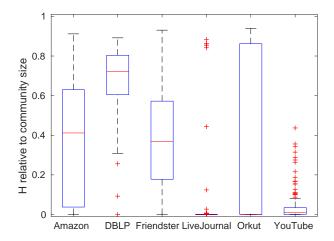


Figure 6: Distribution on H after fitting a hyperbolic model to sampled communities of size 100 to 1000 from each dataset. The sample size was 500 for all datasets except DBLP where 100 communities were sampled.

	LL ratio
Amazon	26450.6
DBLP	3148.5
Friendster	200627.6
LiveJournal	154982.4
Orkut	10867.6
YouTube	75689.6

Table 2: Test statistic of the likelihood ratio test between hyperbolic models and block models. The result for DBLP is based on a sample size of 100, for the other datasets 500 communities were sampled.

the University of Florida Sparse Matrix Collection [6]. These data sets have no ground-truth communities provided.

A summary of the used datasets is given in Table 3. They are significantly smaller than the datasets we examined in the previous experiments to allow the community detection algorithms work efficiently.

#### 7.3.1 Spectral clustering

We first used spectral clustering with the normalized Laplacian [15] to cluster the nodes of the graph. The resulting communities are non-overlapping. Still, in the examined datasets, we notice a significant benefit of modelling the obtained result by means of hyperbolic models, as the log-likelihood ratio test confirms for all examined datasets (see Table 4). Also these results yielded p-values that were essentially zero, confirming that the results are statistically significant.

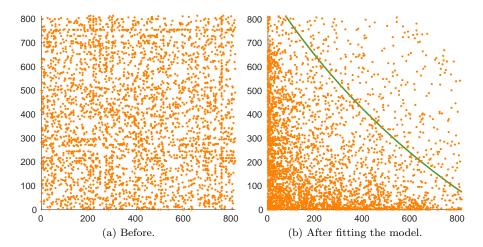


Figure 7: Example of a community obtained from Amazon data.

<u> </u>	nodes	non-zeros	content
Email	1,133	10,902	University email network
Erdős	472	2,628	Erdős collaboration network
Jazz	198	$5,\!484.6$	Network of Jazz musicians
PolBooks	105	882	Books about US politics

Table 3: Datasets used for the community finding experiments.

We have used k=10 clusters for Email, k=8 for Erdős, k=5 for Jazz, and k=6 for PolBooks. We display examples of modelled communities in Figures 9 and 10. These example communities show relatively large cores but thin tails, with most edges being in the lower triangular area. Our models clearly capture this phenomenon.

#### 7.3.2 Boolean matrix factorization

For another community detection algorithm, we used Boolean matrix factorization (BMF) [11]. We used the Asso algorithm [11] with the same number of communities as with spectral clustering. We set the threshold parameter  $\tau$  of Asso to 0.6 and the weight w to 10. We again find that our models resemble the data significantly better than the corresponding block models (see Table 4). Figures 11 and 12 show some example communities for the PolBooks and Jazz data.

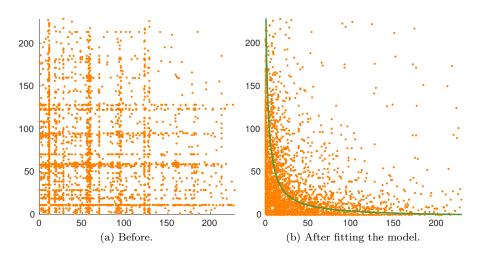


Figure 8: Example of a community obtained from YouTube data.

	LL ratio	
	spectral clustering	BMF
Email	10895.8	3552.0
Erdős	1797.0	949.0
Jazz	3003.8	4435.0
PolBooks	648.0	303.3

Table 4: Statistic of the likelihood ratio test between hyperbolic models and block models (using results of spectral clustering and Boolean matrix factorization as input).

# 7.4 Discussion

Our experiments have verified our intuition that the communities in real-world graphs are better modelled using our models than the traditional quasi-clique models. This holds true for a variety of data sets, both with ground-truth communities, and with communities detected with existing methods. It is important to notice that the existing methods, especially the BMF, aim at finding clique-like communities. Still, our results show that our models provide statistically significantly better fit, even when we take into account the increased number of free parameters for our model.

Not only is our model a better fit for the data, it also provides interesting insights to the shape of the communities. The easy interpretability of the parameters  $\gamma$  and H mean that we can simply study a summary of their distributions to gain an understanding on how the communities in a data look like, whether the cores are small or big and whether the tails are fat or skinny. This allows

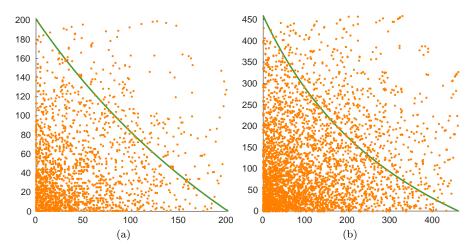


Figure 9: Examples of communities from the Email data fitted by our model. The initial communities were obtained using spectral clustering with k=10 clusters.

a data analyst to obtain a fast general understanding about the data without having to look at any particular community.

Finally, our experiments also demonstrate the scalability of our method. It had no problem of handling even the largest graph, Friendster, with approximately 65.6 million nodes and 1.8 billion edges.

# 8 Conclusions

We have proposed three novel models to describe hyperbolic communities. Based on the observation that communities in real-world graphs do not correspond to blocks of uniform density, our models capture the density distributions per community more accurate. We have shown that all models have the same expressive power, and we proposed an algorithm how to fit these models to a given community – and likewise, how to fit multiple, potentially overlapping, communities to represent the full graph.

In our experimental study, we have analysed a large variety of real-world dataset leading to interesting insights about the data's inherent community structure – showing variations from star-like data to data with patterns similar to quasi-cliques. Our hyperbolic model captures all these scenarios as special cases and is significantly better suited to represent communities than a block model.

Last, comparing the likelihood obtained by our model w.r.t. block-modelling approaches clearly shows the superiority of hyperbolic community models for real-world data.

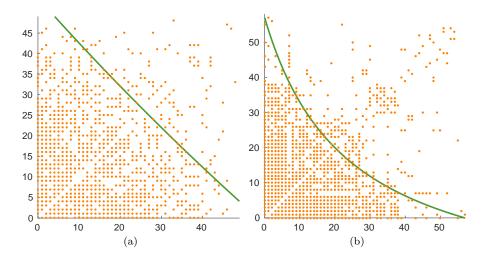


Figure 10: Examples of communities from the Jazz data fitted by our model. The initial communities were obtained using spectral clustering with k=5 clusters.

**Future work** As future work, we plan to develop further optimization principles allowing to efficiently fit the parameters of our model to the given data. While our current model allows node overlapping communities, we have restricted edges to be part of at most one community. Extending our models and algorithms to handle edge overlaps is a further important research direction we aim to investigate.

Furthermore, we aim to investigate how to make use of hyperbolic models in community detection. This also involves to determine the number of communities in a graph automatically.

# References

- [1] J. Abello, M. G. Resende, and S. Sudarsky. Massive quasi-clique detection. In *LATIN 2002: Theoretical Informatics*, pages 598–612. Springer, 2002.
- [2] C. C. Aggarwal, H. Wang, et al. Managing and mining graph data, volume 40. Springer, 2010.
- [3] E. M. Airoldi, D. M. Blei, S. E. Fienberg, and E. P. Xing. Mixed membership stochastic blockmodels. In *Advances in Neural Information Processing Systems*, pages 33–40, 2009.
- [4] M. Araujo, S. Günnemann, G. Mateos, and C. Faloutsos. Beyond blocks: Hyperbolic community detection. In *Machine Learning and Knowledge Discovery in Databases*, pages 50–65. Springer, 2014.

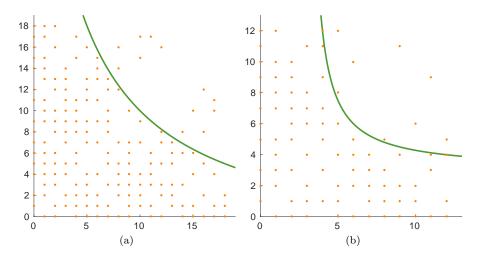


Figure 11: Examples of communities from the PolBooks data fitted by our model. The initial communities were obtained using Boolean matrix factorization with k=6 clusters.

- [5] D. Chakrabarti, S. Papadimitriou, D. S. Modha, and C. Faloutsos. Fully automatic cross-associations. In KDD, pages 79–88, 2004.
- [6] T. A. Davis and Y. Hu. The university of florida sparse matrix collection. *ACM Trans. Math. Softw.*, 38(1):1:1–1:25, Dec. 2011.
- [7] G. W. Flake, S. Lawrence, and C. L. Giles. Efficient identification of web communities. In *KDD*, pages 150–160, 2000.
- [8] M. R. Garey and D. S. Johnson. Computers and intractability: A guide to the theory of NP-Completeness. W. H. Freeman, New York, 1979.
- [9] J. Leskovec and A. Krevl. SNAP Datasets: Stanford large network dataset collection. http://snap.stanford.edu/data, June 2014. Accessed 11 February 2016.
- [10] P. Miettinen. Generalized Matrix Factorizations as a Unifying Framework for Pattern Set Mining: Complexity Beyond Blocks. In *ECMLPKDD '15*, pages 36–52, 2015.
- [11] P. Miettinen, T. Mielikäinen, A. Gionis, G. Das, and H. Mannila. The discrete basis problem. *IEEE Trans. Knowl. Data Eng.*, 20(10):1348–1362, 2008.
- [12] K. Nowicki and T. A. B. Snijders. Estimation and prediction for stochastic blockstructures. *Journal of the American Statistical Association*, 96(455):1077–1087, 2001.

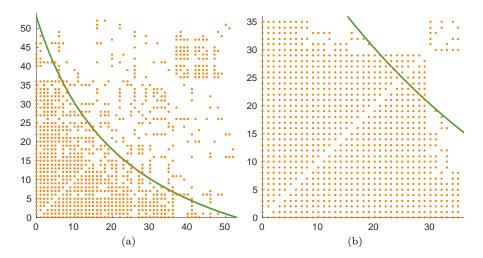


Figure 12: Examples of communities from the Jazz data fitted by our model. The initial communities were obtained using Boolean matrix factorization with k=5 clusters.

- [13] J. Pattillo, A. Veremyev, S. Butenko, and V. Boginski. On the maximum quasi-clique problem. *Discrete Appl. Math.*, 161(1-2):244–257, Jan. 2013.
- [14] T. Sen, A. Kloczkowski, and R. Jernigan. Functional clustering of yeast proteins from the protein-protein interaction network. *BMC Bioinformatics*, 7:355–367, 2006.
- [15] U. von Luxburg. A tutorial on spectral clustering. Stat Comput, 17(4):395–416, Aug. 2007.
- [16] L. Wasserman. All of Statistics: A Concise Course in Statistical Inference. Springer Publishing Company, Incorporated, 2010.
- [17] S. Wasserman and K. Faust. Social Network Analysis: Methods and Applications. Cambridge University Press, 1994.
- [18] J. Yang and J. Leskovec. Community-affiliation graph model for overlapping network community detection. In *ICDM*, pages 1170–1175, 2012.
- [19] J. Yang and J. Leskovec. Overlapping community detection at scale: a nonnegative matrix factorization approach. In Sixth ACM International Conference on Web Search and Data Mining (WSDM '13), pages 587–596, 2013.