Local Treewidth of Random and Noisy Graphs with Applications to Stopping Contagion in Networks

Hermish Mehta
Citadel Securities, Chicago, IL, USA

Daniel Reichman
Department of Computer Science, Worcester Polytechnic Institute, MA, USA

Abstract

We study the notion of local treewidth in sparse random graphs: the maximum treewidth over all k-vertex subgraphs of an n-vertex graph. When k is not too large, we give nearly tight bounds for this local treewidth parameter; we also derive nearly tight bounds for the local treewidth of noisy trees, trees where every non-edge is added independently with small probability. We apply our upper bounds on the local treewidth to obtain fixed parameter tractable algorithms (on random graphs and noisy trees) for edge-removal problems centered around containing a contagious process evolving over a network. In these problems, our main parameter of study is k, the number of initially "infected" vertices in the network. For the random graph models we consider and a certain range of parameters the running time of our algorithms on n-vertex graphs is $2^{o(k)}\,\mathrm{poly}(n)$, improving upon the $2^{\Omega(k)}\,\mathrm{poly}(n)$ performance of the best-known algorithms designed for worst-case instances of these edge deletion problems.

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1 Introduction

Treewidth is a graph-theoretic parameter that measures the resemblance of a graph to a tree. We begin by recalling the definition of treewidth.

▶ **Definition 1** (Tree Decomposition). *A tree decomposition of a graph $G = (V, E)$ is a pair (T, X), where X is a collection of subsets of V, called bags, and T a tree on vertices X satisfying the properties below:*

1. *The union of all sets $X_i \in X$ is V.*
2. *For all edges $(u, v) \in E$, there exists some bag X_i which contains both u and v.*
3. *If both X_i and X_j contain some vertex $u \in V$, then all bags X_k on the unique path between X_i and X_j in T also contain u.*

▶ **Definition 2** (Treewidth). *The width of a tree decomposition (T, X) is one less than cardinality of the largest bag. More formally, we can express this as*

$$\max_i |X_i| - 1.$$

The treewidth of a graph $G = (V, E)$ is the minimum width among all tree decompositions of G.

Many graph-theoretic problems that are NP-hard admit polynomial-time algorithms on graph families whose treewidth is sufficiently slowly growing as a function of the number of vertices [32]. There is vast literature concerned with finding methods to relate the treewidth of graphs to other well-studied combinatorial parameters and leveraging this to devise efficient algorithms for algorithmic problems in graphs with constant or logarithmic treewidth. An excellent introduction to the concept of treewidth as well as brief survey of the work of Robertson and Seymour in establishing this concept can be found in Chapter 12 of [16].

These treewidth-based algorithmic methods, however, have historically found limited applicability in random graphs. Sparse random graphs $G(n, d/n)$ where every edge occurs independently with probability d/n, for some $d > 1$, exhibit striking contrast between their local and global properties – and this contrast is apparent when looking at treewidth. Locally, these graphs appear tree-like with high probability[1] (w.h.p.): the ball of radius $O(\log_d n)$ around every vertex looks like a tree plus a constant number of additional edges. Globally, however, these graphs have w.h.p. treewidth $\Omega(n)$. For example, the super-critical random graph $G(n, \frac{1+\delta}{n})$ has w.h.p. treewidth $\Omega(n)$ [17, 46, 38]. As a result of this global property, conventional techniques used to exploit low treewidth to derive efficient algorithms do not apply directly for random graphs.

In this paper, we take advantage of the local tree-like structure of random graphs by analyzing the *local* behavior of treewidth in random graphs. Central to our approach is the following definition.

▶ **Definition 3** (Local Treewidth). *Let G be an undirected n-vertex graph. Given $k \leq n$ we denote by $t_k(G)$ the largest treewidth of a subgraph of cardinality k of G.*

In words, the local treewidth of an n-vertex graph, with locality parameter k, is the maximum possible treewidth across all subgraphs of size k. We study two models of random graphs, starting with the familiar binomial random graph $G(n, p)$. While the binomial random graph $G(n, p)$ lacks many of the characteristics of empirically observed networks such as skewed degree distributions, studying algorithmic problems on random graphs can nevertheless lead to interesting algorithms.

▶ **Definition 4** (Noisy Trees). *Let T be an n vertex tree. The noisy tree T' obtained from T is a random graph model where every non edge of T is added to T independently, with probability $1/n$.*

Here we assume $p = 1/n$ for convenience; all our results regarding noisy trees also hold when the perturbation probability p satisfies $p = \epsilon/n$ for $\epsilon < 1$. Noisy trees are related to small world models of random networks [45, 44], where adding a few random edges to a graph of high diameter such as a path results with a graph of logarithmic diameter w.h.p. [36].

[1] Given a random graph model, we say an event happens with high probability if it occurs with probability tending to 1 as n tends to infinity.

Below, we give an informal description of the concepts we study and sketch our main results; we defer discussion of formal results until Section 2 and later in the paper. Our main result is a nearly tight bound holding w.h.p. for the maximum treewidth of a k-vertex subgraph of $G(n,p)$ assuming $k \leq n^{1-\epsilon}$ for $\epsilon \in (0,1)$ and $p = d/n$ where $d > 1$. In the notation introduced earlier, this provides a bound for $t_k(G)$. Assuming $k \leq n^{\epsilon}$ for a sufficiently small ϵ we obtain nearly tight bounds for the local treewidth of noisy trees as well.

Our upper bounds on the local treewidth are motivated by algorithmic problems related to containing the spread of a contagious process over undirected graphs by deleting edges. We focus on the bootstrap percolation contagious process (Definition 8) where there is a set of initially infected vertices and noninfected vertices are infected if they have at least $r \geq 2$ neighbors and consider two edge-removal problems: *Stopping Contagion* and *Minimizing Contagion*. Informally, in stopping contagion we are given a subset of infected nodes A and seek to remove a minimal number of edges to ensure a "protected" subset of vertices B (disjoint from A) are not infected from A. In minimizing contagion we wish to ensure at most m additional vertices are infected from A for a target value m by deleting a minimal number of edges. Such edge removal problems might arise, among other applications [20, 21], in railways and air routes, where the goal might be to prevent spread while also minimizing interference to transportation. In this context, edge deletion may correspond to removing a transportation link altogether or introducing special requirements (such as costly checks) to people between the the endpoints. Edge removal can be also viewed as a *social distancing* measure to control an epidemic outbreak [5]. One can also study the problem of removing *vertices* to control the spread of an epidemic which is related to vaccinations: making nodes immune to infection and removing them from the network [49].

We design algorithms for stopping and minimizing contagion for random graphs and noisy trees. Note that our algorithms do not achieve polynomial time, even for k that is poly-logarithmic in n; whether there exists a polynomial time algorithm for minimizing contagion and stopping contagion in $G(n,p)$ for every value of k is an open question. Nonetheless, the dependency of our algorithm on k is better (assuming $k \leq n^{\epsilon}$ for an appropriate constant $\epsilon > 0$) than the dependency of k in the running time of the best known algorithms for minimizing contagion[2] in the worst case [14]. Please see Subsection 2.3 for details.

Our algorithms are based on the following three observations:

1. The local treewidth of binomial random graphs and noisy trees is sublinear in k.
2. There exist fast algorithms for minimizing and stopping contagion in graphs of bounded treewidth.
3. The set of seeds A has what we call the *bounded spread* property: w.h.p. at most $c|A|$ additional vertices are infected from A for some constant[3] c. Bounded spread allows us to solve minimizing contagion and stopping contagion on subgraphs that have small (sublinear in k) treewidth.

For the sake of brevity and readability we focus on *edge* deletion problems. We note that our algorithms can be easily adapted for the analogous problems of minimizing and stopping contagion by deleting *vertices* rather than edges. The reason is that our algorithms for minimizing/stopping contagion on bounded treewidth graphs work (with the same asymptotic running time guarantees) for vertex deletion problems. Combining algorithms for bounded treewidth with the bounded spread property as well the upper bound on the local treewidth yields algorithms for the vertex deletion versions of minimizing and stopping contagion.

[2] We are not aware of previous algorithms for the stopping contagion problem.
[3] For $G(n, d/n)$, our constant $c := c(d)$ is a function of d. When d is a constant independent of n so is c.

Our main contribution is studying the concept of local treewidth for random graphs and connecting it to algorithmic problems involving stopping contagion in networks. Our calculations are standard and the contribution is conceptual rather than introducing a new technique.

2 Our results

2.1 Local Treewidth Bounds

Recall we define the local treewidth of a graph G, denoted $t_k(G)$, to be the greatest treewidth among along subgraphs of size k. Trivially, for any graph with at least one edge and $k \leq n$, $1 \leq t_k(G) \leq k$.

Consider as an illustrative example the random graph $G = G(n, 1/2)$: with high probability, $t_k(G) = \Omega(k)$ for all values of k. For $k \leq 1.9 \log n$ this follows as there is a clique of size k in G w.h.p. For $k > 1.9 \log n$ this follows as a randomly chosen subset of size k has, with high probability, minimum degree $\Omega(k)$, and a graph with treewidth r has a vertex of degree at most r.

We can now state our bounds for t_k in the random graph models we consider. From here onward, $\epsilon > 0$ is taken to be a positive constant in $(0, 1)$. We give somewhat compressed statements; reference to the full Theorems are provided throughout this section.

▶ **Theorem 5.** *Let $G = G(n, p)$ with $p = d/n$ and $k \leq n^{1-\epsilon}$. Then, with high probability:*

$$t_k(G) \leq 3 + O\left(\frac{k \log d}{\log n}\right).$$

Since we always know $t_k(G) \leq k$, the upper bound in the Theorem above becomes trivial if $d \geq n^{\Omega(1)}$. Also observe that the Theorem does not hold for arbitrary $k \leq n$, as for $k = n, t_k(G) = \Omega(n)$ w.h.p. In terms of lower bounds, we have the following:

▶ **Theorem 6.** *Suppose $p = d/n$ and $d > 1 + \delta$ where $\delta > 0$ is a constant (not depending on n). Suppose $k \leq O(n/\log n)$; then, w.h.p.*

$$t_k(G) \geq \Omega\left(\frac{k}{\log n}\right).$$

More details can be found in Section 3. Our upper and lower bounds for the local treewidth of $G(n, d/n)$ also extend to the random d-regular graph $G(n, d)$–details can be found in Subsection 3.3.

For noisy trees, we have the following results.

▶ **Theorem 7.** *Let T be an n-vertex tree with maximum degree Δ. Let T' be a noisy tree obtained from T. Then w.h.p.*

$$t_k(T') \leq 3 + O\left(\frac{k(\log k + \log \Delta)}{\log n}\right).$$

Observe that the upper bound in the Theorem is trivial if k, Δ are $n^{\Omega(1)}$. As a result, in our proofs we will assume $k, \Delta \leq n^{\epsilon}$, for sufficiently small $\epsilon > 0$. Our results can be extended to the case where each non-edge is added with probability c/n for $c > 1$. Similar ideas (which are omitted) yield the upper bound:

$$t_k(T') \leq 3 + O\left(\frac{k(\log k + \log \Delta + \log c)}{\log n}\right).$$

We also provide a lower bound, showing that up to the $\log k, \log \Delta$ terms, the upper bound above is tight. Namely, the noisy path has w.h.p. local treewidth of order $\Omega(k/\log n)$. For more details on the lower and upper bounds please see Section 4.

2.2 Contagious Process and Edge Deletion problems

The local treewidth results outlined above prove useful in the context of two edge deletion problems we study. These problems arise when considering the evolution of a contagious processes over an undirected graph.

We focus on the r-neighbor bootstrap percolation model [11].

▶ **Definition 8.** *In r-neighbor bootstrap percolation we are given an undirected graph $G = (V, E)$ and an integer* threshold *$r \geq 1$. Every vertex is either* active *(we also use the term infected) or* inactive*; a set of vertices composed entirely of active vertices is called active. Initially, a set of vertices called* seeds*, A_0, is activated. A contagious process evolves in discrete steps, where for integral $i > 0$,*

$$A_i = A_{i-1} \cup \{v \in V : |N(v) \cap A_{i-1}| \geq r\}.$$

Here, $N(v)$ is the set of neighbors of v. In words, a vertex becomes active in a given step if it has at least r active neighbors. An active vertex remains active throughout the process and cannot become inactive. Set

$$\langle A_0 \rangle = \bigcup_i A_i.$$

The set $\langle A_0 \rangle$ is the set of nodes that eventually get infected from A_0 in G. Clearly, $\langle A_0 \rangle$ depends on the graph G, so we sometimes write $\langle A_0 \rangle_G$ to call attention to the underlying graph. We say a vertex $v \in V$ gets activated *or* infected *from a set of seeds A_0 if $v \in \langle A_0 \rangle$.*

It is straightforward to extend this definition to the case where every vertex v has its own threshold $t(v)$ and a vertex is infected only if it has at least $t(v)$ active neighbors at some point. As is customary in bootstrap percolation models, we usually assume that all thresholds are larger than 1. Now, given a network with an evolving contagious process, we introduce the stopping contagion problem:

▶ **Definition 9** (Stopping Contagion)**.** *In the stopping contagion problem, we are given as input a graph $G = (V, E)$ along with two disjoints sets of vertices, $A, B \subseteq V$. Given that the seed set is A, the goal is to compute the minimum number of edge deletions necessary to ensure that no vertices from B are infected. In other words, we want to make sure $\langle A \rangle_{G'} \cap B = \phi$, where G' is the graph obtained from G after edge deletions. Given an additional target parameter, ℓ, the corresponding decision problem asks whether it is possible to ensure no vertices from B are infected by deleting at most ℓ edges.*

Next we consider the setting where given a set of infected nodes we want to remove the minimal number of edges to ensure no more than k additional vertices are infected.

▶ **Definition 10.** *In the minimizing contagion problem, we are given a graph $G = (V, E)$, a subset of vertices $A \subseteq V$ and a parameter s. Given that the seed set is A, we want to compute the minimum number of edge deletions required to ensure at most s vertices in $V \setminus A$ are infected. If G' is the graph obtained from G by edge deletions, then this condition is equivalent to requiring $|\langle A \rangle_{G'}| \leq |A| + s$. In the decision problem, we want to decide if it is possible to ensure $|\langle A \rangle_{G'}| \leq |A| + s$ with at most ℓ edge deletions.*

Both stopping contagion and minimizing contagion are NP-complete, and stopping contagion remains NP-hard even if $|A| = 2$ and $|B| = 1$. For complete proofs, please refer to the Full version of this paper [39].

2.3 Algorithmic Results

For minimizing contagion, current algorithmic ideas [14] can be used to prove that if $|A|$ and the optimal solution are of size $O(k)$ the problem can be solved in time $2^{O(k)}\,\mathrm{poly}(n)$ on n-vertex graphs. No such algorithm, parameterized by $|A|$ and the size of the optimal solution, is known for stopping contagion. Using our upper bounds for local treewidth, however, we can prove:

▶ **Theorem 11.** *Let ϵ be a constant in $(0, 1)$. Suppose that $k \leq n^{1-\epsilon}$ and that every vertex has threshold greater than 1. Let $G := G(n, p)$ where $p = d/n$. Assuming d is a constant, we have that w.h.p. both minimizing contagion and stopping contagion can be solved in G in time $2^{o(k)}\,\mathrm{poly}(n)$.*

▶ **Theorem 12.** *Suppose that $k \leq n^{\epsilon}$ for sufficiently small $\epsilon \in (0, 1)$ and that every vertex has a threshold greater than 1. Let T' be a noisy tree where the base tree T has maximum degree $\Delta = O(1)$. Then w.h.p. both minimizing contagion and stopping contagion can be solved in T' in time $2^{o(k)}\,\mathrm{poly}(n)$.*

We stress that set A of seeds can be chosen in arbitrary way. In particular, an adversary can pick A *after* the random edges in our graph models have been chosen.

The dependence of the running time on n, k, d and Δ can be made explicit: for precise statements, please see Section 6. Algorithms for grids and planar graphs are presented in Section 6 as well.

For our purpose, to translate local treewidth bounds to algorithmic results, we need an algorithm for solving stopping contagion and minimizing contagion on graphs of low treewidth. We provide such an algorithm that runs in exponential time in the treewidth, assuming the maximum degree is constant, using ideas from [14]. More details can be found in Section 5.

2.4 Our Techniques

Our upper bounds for the local treewidth build on a simple "edge excess principle": A k-vertex connected graph with $k + r$ edges has treewidth at most $r + 1$. As the treewidth of a set of connected components is the maximum treewidth of a component, it suffices to analyze the number of edges in connected subgraphs of the random graphs we study. For $G(n, p)$ this is straightforward, but for noisy trees it is somewhat more involved. We find it easier to first analyze the edge excess of connected subgraphs, before considering connecting edges that allow us bound the excess of arbitrary subgraphs.

A key component in our lower bound is the simple fact that if H is a minor of G then $\mathrm{tw}(G) \geq \mathrm{tw}(H)$. Therefore it suffices to prove the existence of large treewidth subgraphs that are minors w.h.p. of random graphs and noisy trees. Recall that an n-vertex graph is called an *α-expander* if there exists $\alpha \in (0, 1)$ such that every subset S of vertices with at most $n/2$ vertices has at least $\alpha|S|$ neighbors not in S. We use the fact [35] that for any graph H with k vertices and edges, assuming $k = O(n/\log n)$ an n-vertex expander has an embedding[4] of

[4] See Subsection 2.7 for further details on minor-theoretic concepts we use.

H as a minor in G. Furthermore, every connected subgraph of G corresponding to a vertex in H is of size $O(\log n)$. The lower bound then follows as it is known [34, 35] that $G(n, \frac{1+\delta}{n})$ contains with high probability a subgraph with $\Omega(n)$ vertices that is an α-expander for an appropriate choice α. Similar ideas are used to prove the existence of large minors with linear treewidth in the noisy trees (e.g., the noisy path).

Our algorithms for minimizing contagion and stopping contagion in graphs of bounded treewidth build on techniques designed to exploit the tree-like nature of low treewidth graphs, sharing similarities to algorithms for target set selection in [8], where target set selection is the problem of finding a minimal set that infects an entire graph under the bootstrap percolation model. More directly, our problem resembles the Influence Diffusion Minimization (IDM) studied in [14], where the goal is to minimize the spread of the r-neighbor bootstrap percolation process by preventing spread through vertices. After subdividing edges, minimizing contagion essentially reduces to IDM, albeit with additional restrictions on the vertices we can immunize (only vertices that belong to the "middle" of a subdivided edge can be deleted); we therefore solve a generalization of the IDM problem and use this to provide efficient algorithms for the minimizing and stopping contagion.

At a high-level, our algorithm works by solving the stopping contagion recursively on subgraphs and then combining these solutions via dynamic-programming until we have a solution for the whole graph. To combine subproblems successfully, at each step we explicitly compute solutions for all possible states of vertices in a bag. While this could take exponential time in general, this approach provides an efficient algorithm in graphs with bounded treewidth.

Our proof of bounded spread in noisy trees builds works by proving that small subsets of such trees contain few edges [13, 25]. Since every non seed vertex needs at least two vertices to get infected, small contagious sets require small subsets that contain too many edges. Therefore, one can prove that small sets of seeds cannot infect too many vertices; the proof of small trees' local sparsity is similar to the proof that w.h.p. such noisy trees have small local treewidth.

2.5 Related Work

While the idea to remove edges or vertices to contain an epidemic has been studied before [47, 10, 3], most of these works focus using edge or vertex deletions that break the graph to connected components of sublinear (or even constant) size [20, 47, 10]. Recently approximation algorithms for edge deletion problems that arise in controlling epidemics has been studied in [5] for the SIR epidemic model. In particular, [5] studies the problem of deleting a set of edges of weight at most B that minimizes the set of infected nodes after edges deletions. All these works consider a different contagion model from the $r \geq 2$ bootstrap percolation model studied here.

Bootstrap percolation was first introduced by statistical physicists [11] and has been studied on a variety of graphs [6, 41, 25, 2, 50, 19, 48].

The fixed parameter tractability of minimizing contagion with respect to *vertex* deletions, as opposed to edge deletions, has been thoroughly investigated with respect to various parameters such as the maximum degree, treewidth, and the size of the seed set k in [14]. The authors of [14] present efficient algorithms for minimizing contagion for graphs of bounded maximum degree and treewidth. With respect to k, using ideas from FPT algorithms for cut problems [26], they give a $2^{k+\ell}\,\mathrm{poly}(n)$ algorithm for the case where the set of seeds is of size k and there is a solution of size ℓ to the problem. Their algorithm can be easily adapted to the case of edge deletions: see Theorem 24. We are not aware of the stopping contagion

problem studied before, nor are we aware of previous studies of the minimizing contagion problem in random graphs. In order to deal with both stopping contagion and minimizing contagion for graphs of bounded treewidth, we build on algorithmic ideas from [8]. The NP-hardness of minimizing contagion with respect to vertex deletion is proved in [14] – our proof for the NP-hardness of the edge deletion version of minimizing contagion was found concurrently and independently; the proof is different from the proof appearing in [14].

There are two regimes of interest for the study of treewidth in sparse random graphs. For the subcritical regime $p \leq d/n$ with $d < 1$, $G(n,p)$ has w.h.p. unicyclic connected components of size $O(\log n)$ [23] and hence has treewidth at most 2. For the supercritical regime with $p \geq d/n$ and $d > 1$, $G(n,p)$ has w.h.p. a giant component of size $\Omega(n)$ [23] and determining the treewidth is more complicated. Kloks [32] proved that the treewidth of $G(n,d/n)$ is $\Omega(n)$ w.h.p. for $d \geq 2.36$. His result was improved by Gao [28] who showed that for $d \geq 2.16$, the treewidth of $G(n,d/n)$ is $\Omega(n)$ with high probability. Gao asked if his result can be strengthened to prove that $G(n,d/n)$ has treewidth linear in n w.h.p. for any $d > 1$; this was later shown in in [38]. A different and somewhat simplified proof establishing that the treewidth of $G(n,d/n)$ is $\Omega(n)$ w.h.p. was given in [46]. Finally, the fine-grained behavior of treewidth of $G(n,(1+\epsilon)/n)$ was studied in [17] where it was shown that for sufficiently small ϵ, the treewidth of $G(n,(1+\epsilon)/n)$ is w.h.p.

$$\Omega\left(\frac{\epsilon^3}{\log 1/\epsilon}\right) n.$$

The first lower bound for the treewidth of random regular graphs appears to be from [46]: the authors prove that for every constant $d > d_0$ where d_0 is a sufficiently large constant, the treewidth of the random regular graph $G(n,d)$ is $\Omega(n)$ w.h.p. In [24] it was also shown that random graphs with a given degree sequence (with bounded maximum degree) that ensure the existence of a giant component w.h.p. (namely a degree sequence satisfying the Molloy-Reed criterion [40]) have linear treewidth as well, which implies, using a different argument than in [46], that $G(n,d)$ for $d > 2$ has linear treewidth w.h.p. A different proof for the linear lower bound of the treewidth of $G(n,d)$ for $d > 2$ is given in [17].

Several papers have examined notions of local treewidth in devising algorithms for algorithmic problems such as subgraph isomorphism [22, 30, 29, 27]. For example, Grohe [29] defines a graph family $\mathcal{C}$ of having bounded local treewidth if there exists a function $f : \mathbb{N} \to \mathbb{N}$ such that for every graph $G = (V,E)$ in $\mathcal{C}$ and every integer r, for every vertex $v \in V$ the treewidth of the subgraph of G induced on all vertices of distance at most r from v is at most $f(r)$. These works primarily focus on planar graphs and graphs avoiding a fixed minor. The only work we are aware of that has examined the local treewidth of random graphs is that of [18]. Their main goal is to demonstrate that the treewidth of balls of radius r around a given vertex depends only on r, as opposed to analyzing the local treewidth as function of n, d and k as we do here. We employ a similar edge excess argument to the one in [18] although there are some differences in the analysis and the results: please see Section 3 for more details. We are not aware of previous work lower bounding the local treewidth of random graphs.

Embedding minors in expanders has received attention in combinatorics [37] and theoretical computer science, finding applications in proof complexity [4]. Kleinberg and Rubinfeld [31] proved that if $G = (V,E)$ is a α-vertex expander with maximum degree Δ, then every graph with $n/\log^{\kappa} n$ vertices and edges is a minor of G for a constant $\kappa > 1$ depending on Δ and α. Later it was stated [12] that $\kappa(\Delta,\alpha) = \Omega(\log^2(d)/\log^2(1/\alpha))$. Krivelevich [35] together with Nandov proved that if G is an α-vertex expander then it contains every graph with $cn/\log n$ edges and vertices for some universal constant $c > 0$.

The sparsity of random graphs as well as randomly perturbed trees was used in showing that these families have w.h.p. bounded expansion[5] [43, 15]. These results are incomparable with our treewidth results: it is known that graphs with bounded maximum degree have bounded expansion and that $G(n, d/n)$ has bounded expansion w.h.p. [43, 42] In contrast, there exist 3-regular graphs with linear treewidth and as previously mentioned the treewidth of $G(n, d/n)$ is $\Omega(n)$.

2.6 Future Directions

Our work raises several questions. We consider undirected unweighted graphs. However directed edges can be more accurate in modeling epidemic spread [1] and some edges might be more costly to move than others. Extending our algorithms to directed weighted graphs is an interesting direction for future research.

Our upper and lower bounds for the local treewidth of $G(n, p)$ (with $p = d/n$) currently differ by a multiplicative factor of order $\log d$. We believe that for $k \leq n^{1-\epsilon}$ the local treewdith of $G(n, p)$ is w.h.p. $\Omega(k \log d/ \log n)$. Whether this is indeed the case remains for future work. Our upper bounds on the local treewidth of noisy trees can be made independent of the maximum degree of the tree; namely, for arbitrary trees, the local treewidth should be upper bounded w.h.p. by $O(k/ \log n)$ assuming k is not too large. Proving or disproving this however remains open. Understanding how well one can approximate minimizing contagion and stopping contagion in general graphs, as well as graphs with certain structural properties (e.g. planar graphs) is a potential direction for future research as well. Finally, it could be of interest to study if our bounds for local treewidth coupled with sophisticated algorithms for graphs with bounded local treewidth [27, 29, 22] could lead to improved running time for additional algorithmic problems in random graphs.

2.7 Preliminaries

Throughout the paper log denotes the logarithm function with base 2; we omit floor and ceiling signs to improve readability. All graphs considered are undirected and have no parallel edges. Given a graph $G = (V, E)$ and two disjoint sets of vertices A, B we denote by $E(A, B)$ the set of edges connecting a vertex in A to a vertex in B. For A, B as above we denote by $N_G(A, B)$ the set of vertices in B with a neighbor in A. For a subset of vertices $A \subseteq V$ and an edge e we say that A *touches* e if at least one of the endpoints of e belongs to A. If both endpoints of e belong to A then we say that A *spans* e.

A graph H is a *minor* of G if H can be obtained from G by repeatedly doing one of three operations: deleting an edge, contracting an edge or deleting a vertex. We keep our graphs simple and remove any parallel edges that may form during contractions. It can be verified [42] that a graph H with k vertices is a minor of G if and only if there are k vertex disjoint connected subgraphs of $G, C_1 \dots C_k$ such that for every edge (v_i, v_j) of H, there is an edge connecting a vertex in C_i to a vertex of C_j. We refer to the map mapping every vertex of H, v_j to C_j as an *embedding* of H in G; the maximum vertex cardinality of $C_i, 1 \leq i \leq k$ is called the *width* of the embedding. We shall be relying on the well-known fact [42, 16] that if H is a minor of G than the treewidth of G is lower bounded by the treewidth of H.

We will also need the following definition of an edge expander:

[5] Bounded expansion should not be confused with the edge expansion of a graph. For a precise definition please see [43, 42].

▶ **Definition 13.** *Let $\alpha \in (0,1)$. A graph G is an α-expander if every subset of vertices S with $|S| \leq n/2$ satisfies*

$$|N_G(S, V \setminus S)| \geq \alpha |S|.$$

3 Local Treewidth of Random Graphs

In this section we prove both an upper and lower bound for $t_k(G(n,p))$ that with high probability. We assume $k \leq n^{1-\epsilon}$ for a constant $\epsilon > 0$.

3.1 Upper Bound

Our main idea in upper bounding $t_k(G)$ is to leverage the fact that $G(n,p)$ is locally sparse and that if a few edges are added on top of a tree, the treewidth of the resulting graph cannot grow too much.

▶ **Lemma 14.** *Let G be a connected graph with n vertices and $n - 2 + \ell$ edges. Then* $\mathrm{tw}(G) \leq \ell$.

Proof. Since G is connected, it must have a spanning tree T with n vertices and $n-1$ edges. The graph G has exactly $\ell - 1$ additional edges; since adding an edge can increase a graph's treewidth by at most 1, we immediately get the desired bound.

$$\mathrm{tw}(G) \leq \mathrm{tw}(T) + \ell - 1 = \ell$$ ◀

We can now prove:

▶ **Theorem 15.** *Suppose that $k \leq n^{1-\epsilon}$. Then for $G = G(n,p)$ we have that w.h.p. for every $m \leq k$:*

$$t_m(G) \leq 3 + O\left(\frac{m \log d}{\log n}\right).$$

Proof. Since the Theorem is obvious for $d = n^{\Omega(1)}$ we assume that $d \leq n^{\epsilon/2}$. We first prove the statement for $m = k$. Given a graph G with treewidth t, it is always possible to find a connected subgraph of G with identical treewidth to G. In that spirit, rather than bounding the probability there exists some k-vertex subgraph of G with treewidth exceeding some r, we bound the probability some subgraph on $s \leq k$ vertices is connected and has treewidth greater than r in G.

Fix some $S \subseteq V$ with exactly s vertices. Note there are s^{s-2} possible spanning trees which could connect the vertices in S, each requiring $s-1$ edges. While the resulting subgraph would be connected, its treewidth is only 1. Therefore, r additional edges would also be required to produce a subgraph with treewidth at least $r+1$. Accounting for the ways to choose these edges, the probability the subgraph induced on S is connected and has treewidth greater than r is at most

$$s^{s-2}\binom{\binom{s}{2}}{r}\left(\frac{d}{n}\right)^{r+s-1}.$$

This follows since each edge occurs independently with probability $p = d/n$. Now, we bound the probability that any such subset S with at most k vertices exists. To that end, we take a union bound over all $\binom{n}{s}$ possible subsets of s vertices, letting s range from 1 to k. Putting this together and using the inequality $\binom{a}{b} \leq (ea/b)^b$ yields

$$\sum_{s=1}^{k} \binom{n}{s} \times s^{s-2} \binom{\binom{s}{2}}{r} \left(\frac{d}{n}\right)^{r+s-1} \leq \frac{d^r}{n^{r-1}} \sum_{s=1}^{k} e^s \left(\frac{es^2}{2r}\right)^r d^s$$
$$\leq \frac{d^r}{n^{r-1}} k e^k \left(\frac{ek^2}{r}\right)^r d^k$$

To complete the proof, notice this probability can be made to be at most n^{-1} (using $k \leq n^{1-\epsilon}$ and $d \leq n^{\epsilon/2}$) when r is taken to be

$$2 + O\left(\frac{k \log d}{\log n}\right).$$

The Theorem now follows for $m = k$ from Lemma 14. Using the above proof along with a simple union bound over all $m \leq k \leq n^{1-\epsilon}$ implies the statement for all $m \leq k$. ◀

Notice the approach above yields a sharper bound than if we solely attempted to bound the treewidth by counting the number of excess edges above $k-1$. To explain, notice a k-vertex subgraph can have treewidth r only if it has at least $r+k-1$ edges. A simple union bound over all possible subsets of k vertices, upper bounds the probability we are interested in.

$$\binom{n}{k}\binom{\binom{k}{2}}{r+k-1}\left(\frac{d}{n}\right)^{r+k-1} \leq \frac{k^{2k}k^{2r}d^k d^r}{n^{r-1}}$$

This is implicitly used in [18] to bound the treewidth of balls of radius r in $G(n,p)$; as mentioned above, our method improves on this result. More concretely, since the upper bound now has a additional k^k factor in the numerator, using this in our application would yield the weaker upper bound

$$t_k(G) = 3 + O\left(\frac{k(\log k + \log d)}{\log n}\right).$$

3.2 Lower Bound

Throughout this section we assume that $d > 1 + \delta$ where $\delta > 0$.

First we need the following result from [35]:

▶ **Proposition 16.** *Consider the random graph $G := G(n, \frac{1+\delta}{n})$. Then there is a constant $c > 0$ depending on δ such that for every graph H with at most k vertices and edges, G contains an embedding H' of H. Furthermore the width of the embedding is $O(\log n)$.*

▶ **Proposition 17.** *There exist graphs with m vertices and m edges of treewidth $\Omega(m)$.*

Proof. As random 3-regular graphs have with high probability linear treewidth [17, 24] there are m-vertex graphs with m vertices and $3m/2$ edges and treewidth $\Omega(m)$. Adding to such a graph $m/2$ isolated vertices results with a graph with the desired property. ◀

Using our results we can lower bound the local treewidth of a random graph:

▶ **Theorem 18.** *Let $G := G(n, d/n)$ be a random graph with $d > 1 + \delta$. Assume $k \leq O(n/\log n)$. Then w.h.p. G contains a subgraph with $O(k)$ vertices whose treewidth is $\Omega(\frac{k}{\log n})$.*

Proof. We may assume that $k = \Omega(\log n)$, otherwise the lower bound in the Theorem is immediate. Let H be a graph with s vertices and edges of treewidth $\Omega(s)$. Let $s \leq \left(\frac{n}{\log n}\right)$. By Proposition 16 G contains an embedding of H, H' of width $O(\log n)$. It follows that H' has at most $O(s \log n)$ vertices and treewidth at least $\Omega(s)$ (as H is a minor of H') which is what we wanted to prove. ◀

3.3 Local Treewidth of Random Regular Graphs

Similar bounds on the local treewidth of random regular graphs $G(n, d)$ can be established via similar arguments to those used for $G(n, d/n)$. For the upper bound, one can use the fact [13] that for every $k < nd/4$ distinct unordered pairs of vertices, the probability they all occur simultaneously in $G(n, d)$ is at most $(2d/n)^k$ and then nearly identical arguments to those in Theorem 15. The lower bound follows easily from embedding results for expanders:

▶ **Theorem 19.** *Let $d > 2$ be a constant. Then with high probability a random d-regular graph G is minor universal: any graph H with at most $O(n/\log n)$ vertices and edges can embedded into G. Furthermore, the width of the embedding is $O(\log n)$.*

Proof. By a result of [35] if G is an α-expander with $\alpha > 0$ bounded away from zero then the claim in the Proposition hold. The result now follows as it is well known [9, 33] that with high probability the random d-regular graph is an α-expander for $\alpha > 0$. ◀

We summarize this with the following Theorem:

▶ **Theorem 20.** *Suppose that $2 < d$ is a constant and $k \leq n^{1-\epsilon}$ for some constant $\epsilon \in (0, 1)$. Then for $G = G(n, d)$ we have that w.h.p.:*

$$\Omega\left(\frac{k}{\log n}\right) \leq t_k(G) \leq 3 + O\left(\frac{k \log d}{\log n}\right).$$

4 Local treewidth of Noisy Graphs

We study the local treewidth of noisy graphs: Recall that in this model there is a base n-vertex graph G with maximum degree Δ. On top of this base graph every non edge of G is added independently with probability $1/n$. All proofs missing from this section can be found in [39]. Our main result is:

▶ **Theorem 21.** *Let G be an n-vertex connected graph of maximum degree Δ. Suppose that we add every non-edge of G to G with probability $1/n$ independently of all other random edges. Call the resulting graph G'. With high probability, then, $t_k(G') \leq O(t_k(G) + r)$, where*

$$r = 3 + O\left(\frac{k(\log k + \log \Delta)}{\log n}\right).$$

For a proof please see the full version [39].

The upper bound in Theorem 21 is nearly tight for certain noisy trees.

▶ **Theorem 22.** *Consider the n vertex path, P_n. Suppose we add every nonedge to P_n with probability ϵ/n where $\epsilon > 0$ is an arbitrary constant. Call the perturbed graph P'. Then with high probability for any $\Omega(\log n) \leq k \leq O(n/\log n)$, there exists a subgraph of P' with $O(k)$ vertices with treewidth $\Omega(k/\log n)$.*

Proof. Fix B to be a large enough constant. Chop P_n to n/B disjoint paths[6] $A_1 \dots A_{n/b}$ each of length B. Consider now the graph G whose vertex set is $A_1 \dots A_{n/B}$ and two vertices A_i and A_j are connected if there is an edge (in P') connecting A_i to A_j. The probability two vertices in G are connected is at least

$$1 - (1 - \epsilon/n)^{B^2} \geq \epsilon B^2/2n.$$

For a fixed graph H with s vertices and edges, it is known [35] that the supercritical random graph $G(m, \frac{1+\epsilon}{m})$ contains an embedding of H into G as long as $s = O(m/\log m)$. Furthermore the width of the embedding is $O(\log m)$. The probability that two vertices in G are connected is larger than $\frac{1+\epsilon}{n/B}$. Therefore we can embed H into a subgraph H' of G whose size is at most $s \log n$ such that H is a minor of H'. Furthermore as the vertices of G are paths of length B (in P_n), the embedding of H into G directly translates to an embedding of H into P' whose width is $O(B \log n) = O(\log n)$. Choosing H with s vertices and edges and treewidth $\Omega(s)$ concludes the proof. ◀

5 Algorithms for Graphs of Bounded Treewidth

In this section, we build on the results of [14] to provide polynomial time algorithms for bounded treewidth instances of minimizing contagion and stopping contagion. As we sketched in our introduction, we generalize the influence diffusion minimization problem introduced by the authors and use a similar dynamic-programming algorithm. Our main result is the following algorithm for graphs of bounded treewidth τ:

▶ **Theorem 23.** *Let G be an n vertex graph with maximum degree Δ, maximum threshold r and treewidth τ. Then both minimizing and stopping contagion can be solved in time $O\left(\tau 1296^{\tau} \min\{r, \max\{\Delta, 2\}\}^{4\tau} \operatorname{poly}(n)\right)$.*

For a proof, including a description of our algorithm and runtime analysis, please see the full version [39]. Note that to combine subproblems, we must effectively account for the effect of infected vertices elsewhere on each subgraph we consider. We therefore essentially solve minimizing contagion and stopping contagion in a more flexible infection model, where thresholds are allowed to differ between vertices but remain at most r; as a result, our theorem cleanly translates to this setting as well.

6 Algorithms for Minimizing and Stopping Contagion in Grids, Random Graphs and Noisy Trees

In this section we study how to solve minimizing contagion and stopping contagion when the set of seeds A is not too large and does not spread by too much. We use this along with local treewidth upper bounds to devise algorithms for minimizing and stopping contagion in random graphs. We also consider algorithms for grids and planar graphs. As usual all missing proofs appear in [39]..

Using similar ideas to [14] (who consider vertex deletions problems) we have the following result for the minimizing contagion problem whose proof can be found in [39].

▶ **Theorem 24.** *Let $G = (V, E)$ be an n-vertex graph. Suppose there are t edges whose removal ensures no more than r vertices are infected in G from the seed set $A \subseteq V$. Then minimizing contagion can be solved optimally in (randomized) $2^{r+t} \operatorname{poly}(n)$ time where n is the number of vertices.*

[6] To simplify the presentation we assume B divides n. Similar ideas work otherwise.

The algorithm above can become slow if r or t are very large. Additionally, we do not know how to get similar results (e.g., algorithms of running time $2^{|A|}\,\mathrm{poly}(n)$) for stopping contagion. Below we show that we can improve upon this algorithm for graphs that have some local sparsity conditions. A key property we use is that for both minimizing contagion and stopping contagion with a seed set A, we restrict our attention to the subgraph of G induced on $\langle A\rangle$.

6.1 Grids and Planar Graphs

Consider the $n \times n$ grid where all vertices have threshold at least 2 we have the following "bounded spread" result:

▶ **Lemma 25.** *In the $n \times n$ grid every set of size k infects no more than $O(k^2)$ vertices.*

Proof. Embed the $n\times n$ grid $G = \{1,\ldots,n\}\times\{1,\ldots,n\}$ in $H = \{0,\ldots,n+1\}\times\{0,\ldots,n+1\}$ in the natural way. Given a subset A of G, the *perimeter* of A is the set of all vertices not belonging to A having a neighbor in A. The crucial observation is that if A is a set of infected seeds, the perimeter of A can never increase during the contagion process [7]. As the perimeter of A is at most $4k$ the infected set has perimeter at most $4k$ as well. The result follows as every set $A \subseteq \{1,\ldots,n\} \times \{1,\ldots,n\}$ of size m has perimeter $\Omega(\sqrt{m})$. ◀

Using Theorem 24 we have that minimizing contagion on the n by n grid with $k = |A|$ can be solved in time $2^{O(k^2)}\,\mathrm{poly}(n)$. We simply apply the algorithm in Theorem 24 to $\langle A\rangle$. Alternatively we can use exhaustive search over all subsets of edges in the graph induced on $\langle A\rangle$ to solve[7] both minimizing or stopping contagion. We can do better using the following fact:

▶ **Lemma 26.** *Let G be a subgraph of an n by n grid with r vertices. Then G has treewidth $O(\sqrt{r})$.*

Proof. Every m-vertex planar graph has treewidth $O(\sqrt{m})$. ◀

▶ **Corollary 27.** *Let $G = (V, E)$ be the n by n grid. Suppose $H = (V, E')$ where $E' \subseteq E$ and every vertex has a threshold of at least 2. Let A be the seed set with $k = |A|$. Then stopping contagion and minimizing contagion can be solved in time $2^{O(k)}\,\mathrm{poly}(n)$.*

Proof. For solving either problems we only need to consider the subgraph of $G, \langle A\rangle$. The result now follows from Theorem 23. ◀

Similarly, for a planar graph where every vertex has threshold at least 2 and at most b and every subset A of size k infects at most $f(k)$ vertices, stopping contagion can be solved in time $b^{O(\sqrt{f(k)})}\,\mathrm{poly}(n)$.

6.2 Sparse Random Graphs

Consider the random graph $G(n, d/n)$ assuming all vertices have threshold larger than 1. Assuming $d \leq n^{1/2-\delta}$ for $\delta \in (0, 1/2)$, it is known [25] that with high probability every set of size $O(\frac{n}{d^2 \log d})$ does not infect more than $O(|A| \log d)$ vertices. Furthermore, it is known [25] that any set of size $O(n/d^2)$ has with high probability constant average degree. It follows that assuming $|A| = O(\frac{n}{d^2 \log d})$ the optimal solution to minimizing contagion is of size

[7] For minimizing contagion using the FPT algorithm may be preferable as it may run significantly faster if the optimal solution has cardinality $o(k^2)$.

$O(|A| \log d)$. Therefore in random graphs with $|A| \leq O(\frac{n}{d^2 \log d})$, minimizing contagion can be solved using Theorem 24 in time $O(2^{|A| \log d} \operatorname{poly}(n))$. As before, exhaustive search over all edges on the graph induced on $\langle A \rangle$ can solve both minimizing and stopping contagion in time $O(2^{|A| \log d} \operatorname{poly}(n))$ as well.

Using our local treewidth estimates, Theorem 23, the bounded spread property and the fact that w.h.p the maximum degree of G is $O(\log n / \log \log n)$ we have the following improvement for the running time:

▶ **Theorem 28.** *Let $G := G(n, d/n), \epsilon \in (0,1)$ and $\delta \in (0, 1/2)$. Denote by k to be the size of the seed set A. Suppose that $k \leq O(\min(n^{1-\epsilon}, \frac{n}{d^2 \log d}))$ and $d \leq n^{1/2-\delta}$, and that every vertex has threshold larger than 1. Then w.h.p both minimizing contagion and stopping contagion can be solved in time*

$$\exp\left(O\left(\frac{k \log^2 d \log \log n}{\log n}\right)\right) \operatorname{poly}(n).$$

Proof. As before we can solve either problem on $\langle A \rangle$ using the upper bound on the treewidth from Theorem 15, the fact that with high probability $|\langle A \rangle| \leq O(\log d |A|)$ and the algorithm for graphs of bounded treewidth for stopping or minimizing contagion. ◀

6.3 Noisy trees

We now devise an algorithm for stopping contagion and minimizing contagion for noisy trees. To achieve this we first prove that for forests every sets of seeds does not spread by much and furthermore this property is maintained after adding a "small" number of edges on top of the edges belonging to the forest. Then we use similar ideas to Theorem 21 and prove that noisy trees are locally sparse in the sense that every subsets of vertices of cardinality k spans w.h.p $k + o(k)$ edges assuming k is not too large. We use this property to prove that any subset A of k seeds infects w.h.p $O(k)$ vertices. Thereafter we can use the algorithms for bounded treewidth to solve either minimizing contagion or stopping contagion on $\langle A \rangle$. We assume throughout this section that $\epsilon \in (0,1)$ is a sufficiently small constant ($\epsilon < 1/100$ would suffice for our proofs to go through). Using these ideas we can prove the following Theorem whose complete proof can be found in [39].

▶ **Theorem 29.** *Let T be a tree and let T' be the noisy tree obtained from T. Assume $|A| = k, \Delta \leq n^{\epsilon}$ and that every vertex has threshold larger than 1. Let $m := \max(\log \log n, \log \Delta)$. Then both minimizing contagion and stopping contagion can be solved in T' in time*

$$\exp\left(O\left(\frac{k(\log k + \log \Delta)m}{\log n}\right)\right) \operatorname{poly}(n).$$

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