On the Estimation of Number of Routers in an Ad Hoc Network

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Abstract

The aim of this thesis is to give an estimated number of routers in an *ad hoc* network, assuming its graph model is provided. There are two approaches proposed, both utilising the notion of dominating set of nodes. Firstly it is concerned with theoretical derivation of a new lower bound for the expectation of domination number for random graphs with base graph being a Cartesian product of cycles. This bound is based on already proven cases of Vizing's conjecture. Evaluation of accuracy and comparison to another known lower bound (particularly the one based on the vertex degree counting) was realised by simulations. The proposed new lower bound is more precise than the other one in the interval of lower values of the probability parameter p.

The second objective was realisation of a heuristic algorithm for finding a minimum dominating set. We focused only on the graphs with power law degree distribution which present a good model of real world networks. Proposed algorithm is based on adding the vertices which have neighbours of minimum degree. On our test sample the worst case increase in dominating set size compared to the minimum one was 15.7% and when the reduction of unnecessary vertices was used, it was below 5%. But the execution time was by few orders shorter than it was in the case of `greedy` algorithm. This can make significant difference in the case of large graphs and allows for dominating set size estimation even when the use of other methods would be intractable.

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1. Introduction

Random graphs, as well as the problem of domination in graphs, are studied for several decades for their own sake. Some interesting results connecting both topics was presented by Wieland and Godbole in [1]. It considers one of the classical Erdős-Rényi models [12], namely $\mathcal{G}(n, p)$, where all possible edges on n vertices are chosen independently with equal probability p. Here we restrict the edges which may appear in a random graph by fixing the base graph to a cycle graph. Domination number for a Cartesian product of cycles (not random) was studied by Klavžar and Seifter in [2].

Present paper concentrates on developing lower bound on the expected domination number for random graphs, which have a Cartesian product of cycles as their base graph. For a finite cycle graph itself, it is possible to count all of its subgraphs of the same order. These are basically isolated vertices, paths or the original cycle. For all of these subgraphs it is easy to determine domination number and so it is for expected value of domination number of a random cycle. Furthermore, as Vizing's conjecture holds for all of these subgraphs, it gives us the lower bound for mean domination number also for random graphs which can be constructed from cycles by Cartesian product, i.e. tori. We have made simulations for 2 and 3 dimensional tori and compared the results with other bound known for random graphs with a regular base graph. Each of them performs better on some interval of probability parameter p. Thus combining the two lower bounds could give more precise results.

After some preliminaries are given in the first section, the section 2.1 contains formulae describing probability distribution of particular subgraphs which can arise from a random graph with the cycle base graph. Then follows the explicit expression for the exact value of mean domination number for such a random graph. Section 2.4 shows the lower bound of mean domination number for random graphs which have their base graph composed

from Cartesian product of cycles, which is the main result of the paper. Section 2.5 describes algorithm of an alternative approach. And finally, section 2.6 gives comparison of both lower bounds with simulation results.

1.1 Domination Number

Dominating set of a simple graph G is some subset $D \subseteq V$, such that each vertex $v \in V$ is either in D or is adjacent to some vertex from D [5]. Formally, $\forall v \in V - D, N(v) \cap D \neq \emptyset$, where $N(v)$ is an open neighbourhood of vertex v, $N(v) = \{u | uv \in E\}$. Cardinality of minimum dominating set (MDS) over all dominating sets of G is called domination number of G and is denoted $\gamma(G)$. We will denote relative dominating number $\gamma_r(G) = \gamma(G)/n$. Finding an arbitrary dominating set is not difficult – $V(G)$ is trivially the dominating set of G. But to find a minimum dominating set is, in general, a problem belonging to the NP-complete complexity class [5].

However, for some special class of graphs it may not be too difficult to determine $\gamma(G)$. It is easy to see, that for an infinite path or cycle $\gamma_r = 1/3$. In general, for each k-regular graph holds $\gamma_r \geq 1/(k+1)$, as each vertex covers itself and k neighbours.

1.2 Random Graphs

There are several models used to formalise the notion of random graph [12]. We are going to use the model $\mathcal{G}(G, p)$, which is the probability space over all graphs which can arise from an ordinary base graph G by independently removing its edges with probability $q = 1-p$, or keeping an edge with probability $0 < p < 1$. We call particular graphs H created in this way from a base graph G the realisations, or instances, of random graph and write $H \in \mathcal{G}(G, p)$. Clearly, we have $H \subseteq G$ and $V(G) = V(H)$. Probability of obtaining a graph H with $m = |E(H)|$ edges is $\mathbb{P}(H) = p^m q^{N-m}$, where N is the total number of all possible edges on n vertices, e.g. $N = \binom{n}{2}$ for complete graph K_n and $N = n$ for a cycle C_n. Often the probability parameter is assumed to depend on graph order (hence denoted p_n), but we consider its value to be set regardless of n.

One of the aims of this paper is to enumerate all possible realisations of random graph $\mathcal{G}(C_n, p)$, which we will call a random cycle. This readily provides the expression for exact value of mean MDS size, which in turn gives lower bound also for other graphs composed from the cycles.

2. Expected Domination Number of $\mathcal{G}(C_n, p)$

Each invariant of a graph, for instance the maximum vertex degree, becomes a random variable in random graph. It is clear that the domination number of a cycle is $\gamma_r(C) = 1/3$. But how does it look like for a random cycle? We are particularly interested in the probability distribution of domination number for a random cycle and its expected value, for which the explicit formulae are given here, as well as for the lower bound of MDS size for random torus graphs.

2.1 Probability Distribution

Possible realisations of a finite random cycle $\mathcal{G}(C_n, p)$ range from an empty graph on n vertices $\bar{K}$ (which we surely get when $p = 0$), to the original cycle base graph C_n (which must be obtained when $p = 1$). In all cases

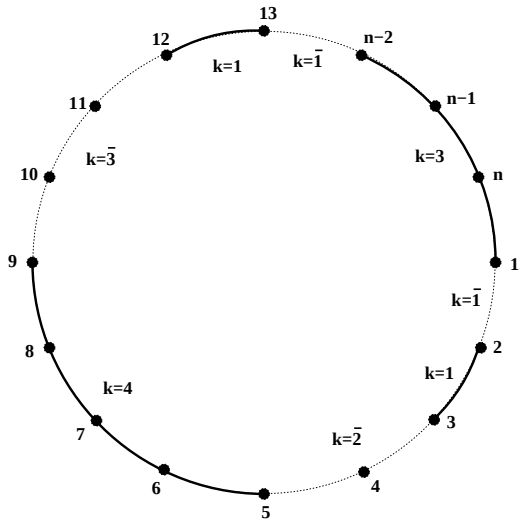


Figure 1: A realisation of random cycle with base graph C_{16}. It consists of alternating connected (solid black) and disconnected (dashed) edge sequences.

we can recognise some pattern in there, created by alternating sequences of connected and disconnected (isolated) vertices. In Fig. 1 we denote the length of each such sequence k, provided that white sequences (i.e. sequences of missing edges) are distinguished by a bar over the length number. As we can immediately determine the domination number of P_n and $\bar{K}_n$ and thus the domination number of any instance of random cycle, the main task here is to find out the distribution of particular realisations.

If we identify all edges that are present in a realisation of random cycle with black beads, and all missing edges with white beads, we get a so called bicolour necklace. Formally, these are equivalence classes of strings over two symbols under rotation [10, 11]. Only the lengths and order of black and white sequences is important. Number of different bicolour necklaces for a given size n has been studied already in 1950s. Result can be found for instance in [9]. But we turn our attention to the total number of paths of length k, which may arise in all possible realisations of random cycle $\mathcal{G}(C_n, p)$. We will denote its expected number as $D_{n,k}(p)$ and it can be expressed as

$$D_{n,k}(p) = \sum_{G | P_k \subseteq G} \mathbb{P}(G) \cdot m_k(G), \tag{1}$$

where the sum goes over all graphs G containing a path of length k as its subgraph. The $m_k(G)$ is number of such paths in G. Probability of getting G is according to the random graph model equal to $\mathbb{P}(G) = \binom{n}{k} p^k q^{n-k}$. There are two distinguished cases comprised in the above formula. Obviously it holds

$$D_{n,k}(p) = p^k q^{n-k}, k = 0, n, \tag{2}$$

and moreover we have

$$D_{n,k}(p) = np^k q^2, 1 \leq k < n-1 \tag{3}$$

$$D_{n,k}(p) = np^{n-1} q, k = n-1. \tag{4}$$

Assuming that removing of edges from base graph occurs independently of each other and with constant probability q, the equations (2) – (4) can be interpreted as an expected number of connected sequences of length k in

a realisation of random graph with C_n as its base graph $\mathcal{G}(C_n, p)$.

But occurrence of k edges missing in a row (sequence of white beads) is described by the same distribution, as we can change the probability of edge to be present to missing by swapping the values of p and q. In other words, it holds that $D_{n,k}(p) = D_{n,\bar{k}}(q)$, or equivalently $D_{n,\bar{k}}(p) = D_{n,k}(1-p)$, so we can use the same formulae to get number of parts with $\bar{k}$ missing edges, it means $k-1$ isolated vertices, in a row.

2.2 Expected Domination Number

In this section we show explicit formula for the mean value of the minimum dominating set size for a finite random cycle $\mathcal{G}(C_n, p)$ of order n with probability of edge to be present p. Further, mean of the relative size of MDS and its limit for an infinite cycle is given.

We can readily determine the domination number of any particular realisation of a random cycle, which always consists only of paths and isolated vertices. Each path P_k consisting of k edges can be covered by $\lceil \frac{k+1}{3} \rceil$ vertices (which must be added to dominating set). For the cycle C_n it changes to $\lceil \frac{n}{3} \rceil$. We can assign the expected number of occurrence to each case by $D_{n,k}(p)$.

Occurrence of $\bar{k}$ missing edges in a row, which happens $D_{n,\bar{k}}(p)$ times on average, generates $k-1$ isolated vertices. These must be all included in the dominating set. If there are no edges, then all n vertices must be added. Knowing domination number of each connected component G_i of a graph $G = \biguplus G_i$ (which is a disjoint union of its components) determines also its domination number as the sum $\gamma(G) = \sum \gamma(G_i)$, which also includes the number of isolated vertices as each forms a separate component ($\bar{K}_n$ forms always n components, not a single one).

We will denote a discrete random variable describing MDS size for a realisation of random cycle by $\Gamma(C_n, p)$. As explained above, its probability distribution is actually also connected to $D_{n,k}(p)$. In general, expected value of Γ is by definition $\mathbb{E}\{\Gamma(G,p)\} = \sum \mathbb{P}(G) \cdot \gamma(G)$. In our case we assume $\Gamma = \Gamma(C_n, p)$ and the sum runs for all possible realisations of $\mathcal{G}(C_n, p)$. Since the number of isolated vertices can be expressed as nq^2, after substituting for $D_{n,k}(p)$ and applying the formula for the sum of geometric series (or its derivative) we can simplify the mean value to

$$\mathbb{E}\{\Gamma\} = nq^2 + \sum_{i=1}^{n-1} \left\lceil \frac{i+1}{3} \right\rceil D_{n,i}(p) + \left\lceil \frac{n}{3} \right\rceil p^n \qquad (5)$$

Dividing (5) by n gives the relative mean value of minimum dominating set size.

$$\mathbb{E}\{\Gamma_r\} = q^2 \left\{ 1 + \frac{p^{n-1}}{q} + \sum_{i=1}^{n-2} \left\lceil \frac{i+1}{3} \right\rceil p^i \right\} + p^n \qquad (6)$$

Now taking the limit of (6) for $n \to \infty$ gives the average fraction of vertices which forms the minimum dominating set for a (possibly infinite) random cycle.

$$\lim_{n\to\infty} \frac{\mathbb{E}\{\Gamma(C_n,p)\}}{n} = \frac{1}{p^2+p+1} \qquad (7)$$

Previous equations (5) – (7) holds for $0 < p < 1$. This guarantees convergence of geometric series in p and vanishing powers of p in the limit. For the border values of p it is no longer a random graph. However, it is easy to see that for $p = 0$ the MDS must always include all of n vertices, so $\gamma = n$, and for $p = 1$ it is $\gamma(C_n) = \lceil n/3 \rceil$.

2.3 Using Vizing's Conjecture

Results from the previous section can be used to determine precisely the mean value of MDS for a random cycle. But in practice, the cycle has very simple topology with limited applications. On the other hand, meshes and tori were used in the past as models for transputer networks and are used today, for example, as models for sensor networks. Some attempts have already been made to set bounds for the mean of MDS size for regular graphs [13]. We use the Vizing's conjecture to get better lower bound of MDS size expectation for random tori.

Vizing's conjecture, which in its general form is still an open problem for half of century states, that the domination number of Cartesian product of two graphs is greater than or equal to the product of their domination numbers.

$$\gamma(G \square H) \geq \gamma(G) \cdot \gamma(H) \qquad (8)$$

The conjecture, or its variants, have been proved for several special classes of graphs. Details can be found, for instance, in [5] or in the survey [7].

To make use of Vizing's conjecture for the expectation of domination numbers instead of domination numbers itself, we must first ensure that it holds for each realisation of random graphs under consideration. As discussed above, from $\mathcal{G}(C_n, p)$ we can only get cycle, path, or a graph consisting of several paths and possibly isolated vertices. In 2007 Aharoni and Szabó proved the conjecture for all chordal graphs, i.e. for graphs which have an edge between each pair of non-adjacent vertices in a cycle of length greater than 3 [6, 7]. Graphs containing no cycle, like paths, are trivially chordal.

Furthermore, the cycle is known to satisfy so called B-G property (after Barcalkin and German) [5, 8]. Graphs with this property also meets the Vizing's conjecture. Proof can be found in [7]. Thus all realisations of random cycle are graphs for which Vizing's conjecture holds, and it can be used to set the lower bound on expected value of γ for some random torus $\mathcal{G}(T_{n,m}, p)$.

2.4 Vizing's Conjecture for the Mean

Let $\mathcal{G}(G,p)$ and $\mathcal{G}(H,p)$ be random graphs such that (8) holds for each pair of their realisations G and H respectively, $\mathcal{G}(G,p) \square \mathcal{G}(H,p)$ is their Cartesian product and Γ_G, Γ_H and $\Gamma_{G\square H}$ denotes random variables acquiring values of corresponding domination numbers of particular random graph realisations. Then using the fact that expectation of a positive quantity is also positive, the linearity of expectation and independence of realisations G and H it can be easily shown, that

$$\mathbb{E}[\Gamma_{G\square H}] - \mathbb{E}[\Gamma_G] \cdot \mathbb{E}[\Gamma_H] \geq 0. \qquad (9)$$

And from (9) we readily see desired result for the lower bound on mean domination number of a random $2d$ torus.

$$\mathbb{E}\left\{\Gamma(T_{m,n},p)\right\} \geq \mathbb{E}\left\{\Gamma(C_m,p)\right\} \cdot \mathbb{E}\left\{\Gamma(C_n,p)\right\} \qquad (10)$$

We can substitute to the right hand side for the expectation of MDS size of random cycle from either (5), (6) or

(7) to obtain a result of particular interest. For instance, we get

$$\mathbb{E}\{\Gamma_r(T,p)\} \geq \frac{1}{(p^2+p+1)^2} \tag{11}$$

for an infinite two dimensional torus base graph. We will refer to this lower bound as $LB1$.

2.5 Degree Counting

Here we describe an algorithm for computation of another lower bound. Bounds on expectation of MDS size for any random graphs with a k-regular base graph was introduced by Nehéz in [13]. The lower bound is based on counting vertices in descending order of their degree, until all of n vertices are covered. We compare this bound, denoted as $LB2$ hereafter, to the results obtained by Vizing's conjecture in the previous section.

Among other results on MDS size bounds based on vertex degree presented in [5], the theorem 2.12 states that if $(d_1, d_2, \ldots, d_n)$ is the degree sequence of graph G ordered in such a way that $d_i \geq d_{i+1}$, then

$$\gamma(G) \geq \min\{t | t + d_1 + d_2 + \cdots + d_t \geq n\}. \tag{12}$$

The dominating set must include at least so many vertices, that there is enough incident edges to connect all remaining vertices. To cover all of the n vertices in a graph we start adding those with highest degree and also add 1 for each vertex itself, until the sum is at least n. The smallest number t for which the sum reaches the number of vertices is a lower bound on MDS size of a graph G.

In case of a k-regular graph, the vertex degree d_i of all vertices is always the same. But if we consider a random graph based on a regular graph, in one instance we can get all degree values up to k. Probability that a randomly chosen vertex have the degree i follows binomial distribution [16]. Recalling that p is the probability of edge presence, we have $\mathbb{P}(d(v) = i) = B_{i,k}(p)$, where $B_{i,k}(p) = \binom{k}{i} \cdot p^i \cdot (1-p)^{k-i}$. Average number of vertices of degree i can be expressed as $n \cdot B_{i,k}(p)$. It is clear that number of isolated vertices must be $n \cdot (1-p)^k$ which is exactly $n \cdot B_{0,k}(p)$.

2.6 Results and Evaluation

In this section we compare our main results from section 2 based on Vizing's conjecture ($LB1$) to the approach based on degree counting ($LB2$) as describe in section 2.5. Both are related to the simulation results.

To evaluate results obtained above we performed simulation of random torus. For each value of probability parameter p some C realisations of random torus $\mathcal{G}(T_{400,400}, p)$ were generated. Then the minimum dominating set was determined. Searching for the MDS can be viewed as an optimisation problem, which can be solved by the integer linear programming method. To each graph vertex $v_i \in V$ we assign a boolean variable $x_i \in \{0, 1\}$ and write an inequality involving sum of the variables for all of the neighbouring nodes. The objective is to assign to all x_i minimum total number of 1's, such that all the inequalities are satisfied, i.e. each vertex is covered by at least one of its neighbours. Formally, the set of inequalities together with the objective forms following instance of linear programming optimisation problem

$$\texttt{minimise} \quad \sum_{i \in V} x_i \tag{13}$$

$$\texttt{subject to} \quad \forall i \in V : \sum_{j \in N(x_i)} x_j \geq 1. \tag{14}$$

For convenience we supposed $V = \{1, 2, \ldots, n\}$. The solution immediately gives the MDS as $D = \{i | x_i = 1, \forall i \in V\}$. For each graph the optimisation package `JuMP` for the `julia` language [3] was used to solve the problem instance. Though finding MDS is in general a demanding NP-complete problem, using linear programming solvers for this purpose appears to be quite efficient approach. Details can be found in [4].

2.7 Comparison of Lower Bounds

In the Fig. 2a we can see the plot of mean relative MDS size as resulted from the simulations together with two lower bounds for $\mathcal{G}(T_{400,400}, p)$. Step of the probability parameter was 0.025. The topmost curve plotted by solid line represents simulation results. Dash-dot line shows the lower bound $LB2$ according to [13] determined by degree counting. It meets experimental data in the end points. Dashed line represents lower bound $LB1$ for $\mathbb{E}\{\Gamma(T_{400,400}, p)\}$ computed from (9) and (6). Fig. 2b depicts the same for the random graph $\mathcal{G}(T_{216,216,216}, p)$ with 3-dimensional torus base graph. The probability step in this case was 0.01.

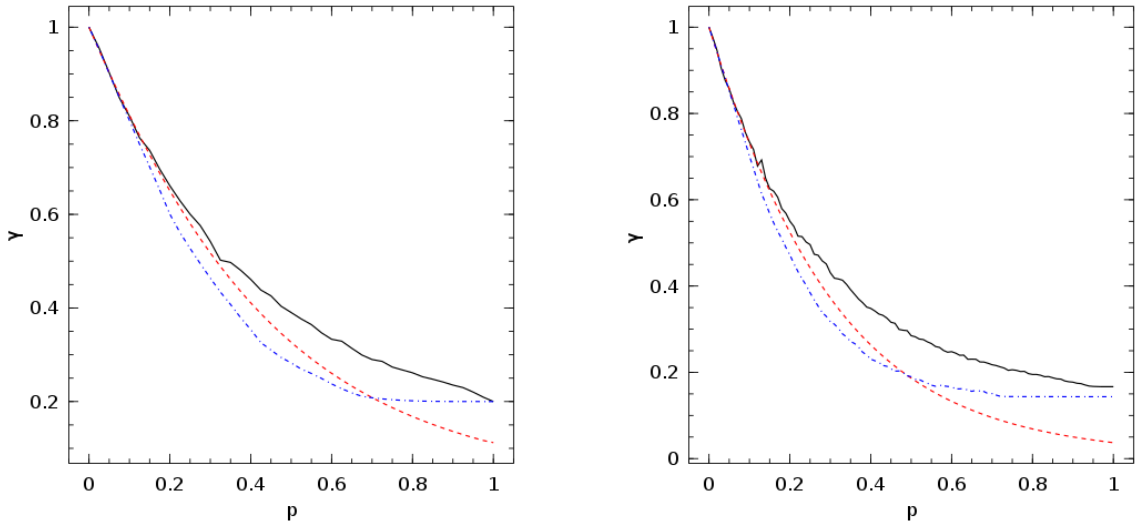
It is clear from the picture that our bound $LB1$ gives better results for lower values of parameter p, until it intersects with $LB2$. For higher values of p the bound $LB2$ performs better. Numerically determined intervals for intersection points are $p_2 \in \langle 0.701154, 0.701155 \rangle$ and $p_3 \in \langle 0.48387, 0.494286 \rangle$ for 2-dimensional and 3-dimensional case, respectively.

As we have $\mathbb{E}\{\Gamma_r(C,1)\} = \gamma_r(C) = 1/3$, according to (10) the value of $LB1$ in $p = 1$ for a d-dimensional torus will be $\left(\frac{1}{3}\right)^d$. But the exact value of relative domination number is $\gamma_r(C^d) = 1/(2d+1)$. Thus our lower bound for a torus C^d, derived from the exact mean value for a cycle C, will differ more and more from proper value with increasing dimension d. This mostly remains true also in finite cases, though the exact value of domination number for tori may slightly differ, $\gamma_r(C_n^d) \geq 1/(2d+1)$. For 2-dimensional finite grids $G_{n,m}$, which are in many aspects same as tori, the exact values can be found in [14].

To support the evaluation of lower bounds, Table 1 shows the sum of squares of differences between a bound and actual simulation results. The sum is taken over all values of parameter p for both bounds and both simulated graphs. The obvious way how to get better overall estimate of lower bound on expected MDS size is to combine the two bounds by taking the maximum of both. Sum of the squared differences for this case can be found in the table too.

Table 1: The Sum of Squared Differences

	$LB1$	$LB2$	max
$T_{400,400}$	0.174253	0.217199	0.096941
$T_{216,216,216}$	0.917025	0.606909	0.376002



(a) 2-d torus $\mathcal{G}(T_{400,400}, p)$ (b) 3-d torus $\mathcal{G}(T_{216,216,216}, p)$

Figure 2: Mean MDS size. Solid line represents simulation results for the expectation of relative MDS size (γ axis). Dash-dot line shows the lower bound $LB2$. Dashed line is $LB1$, computed as $\mathbb{E}\{\Gamma_r\}$.

3. Heuristic Algorithm for Finding MDS

In this section we describe a new algorithm for finding minimum dominating set approximation. The input is a graph file and output a dominating set. Because it is an approximation, the result may not be necessarily a minimal one. But the purpose and advantage of proposed algorithm is computation speed.

3.1 Node Selection Criterion

The algorithms from the class of approximation approaches based on *greedy* algorithm start with an empty set and successively add vertices according to some criterion until a domination set is created. In most simple case the criterion can be just a random (or blind) choice of node. This provides constant time complexity of the selection, but at the cost of poor precision because no information about the graph is used for making the chaise. Another possibility is to sort vertices by the degree and add them to the DS in descending order. In this case the sorting is made just once, at the beginning. This principle was used in upper bound from section 2.5. But usually by *greedy* algorithm is considered a version which in each step sorts the vertices by the number of their uncovered neighbours. Thus to the DS is always added the vertex which covers the most of the remaining nodes. As it is possible that there may be more vertices with equal number of uncovered neighbours, the result of the algorithm may be ambiguous.

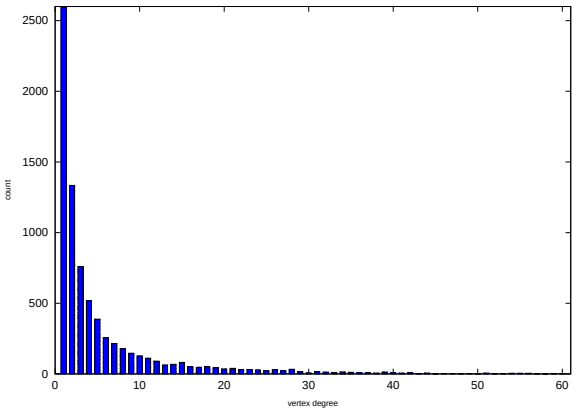
Our proposed algorithm is based on similar principle as the *greedy* algorithm. But the criterion for selecting a node to be added to DS is based on another property. It can be shown that good candidates are the nodes neighbouring to leaves of the graph, i.e. the neighbours of the nodes of degree 1. These nodes can be found in time $O(n)$ and they do not make DS larger compared to minimal one. But by this step all such nodes are covered (if there were some) and we must continue in different way. Thus in each step we find the minimum vertex degree and then add all neighbours of nodes with minimal degree. This generalised criterion covers the leaves in the first step. If there are some cliques with degree 2, they are covered in the second step. So at the early phases of the process the vertices added by our algorithm certainly belongs to MDS but during further steps the heuristics need not meet the exact solution.

At the end of each step we remove vertices which have been covered and count all vertices remaining uncovered. If its number is not zero and it is different from the previous step, we repeat whole procedure. Adding the nodes in the first iteration step is unambiguous, because each leave has only one neighbour. In following steps we add each vertex with a neighbour of minimal degree (if it does not has the minimal degree itself). Here is where further optimisation is possible. For example the vertex degree could be used as a secondary criterion if there are more neighbours. Here we will correct the result of our algorithm by removing unnecessary nodes (redundant in DS) at the last phase.

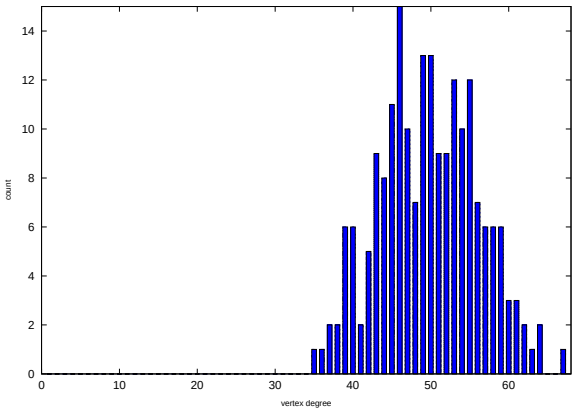
The above described criterion does not take into account isolated vertices, because they have no neighbours. All of them must be immediately added to DS. It may happen that isolated vertex is created in modified graph by removing vertices covered in the previous step. Such a node can be already covered in the original graph. In this case it is not added to DS. At the end, when iteration process does not bring new DS members, all remaining uncovered vertices are added.

3.2 Algorithm Properties

The algorithm always searches for the nodes with small degree and these are covered by adding their neighbours to DS. This is the reason why it is especially suitable for graphs with large number of vertices with small degree. Actually this is a very interesting and important class of graphs which includes many real world systems, whether biological, transport, social or communication networks [17], [18]. All of them are modelled by a scale-free graphs



(a) The PPI network of Drosophila Melanogaster ($\Delta = 1193$), a power law shape.



(b) An instance of random graph $\mathcal{G}(K_{200}, 0.25)$.

Figure 3: Histograms of degree distribution.

which are known to have power law distribution of vertex degree, i.e. the probability of a vertex having degree k is proportional to k^{-c}, where c is a parameter called critical exponent. For the proposed approximation algorithm it is important, that according to power law distribution there is majority of nodes with small degree and few nodes with some large degree. It is depicted in the figure 3a. This is the condition under which the algorithm performs well.

Making a time complexity guess of the algorithm we can assume that the operation of finding vertex neighbourhood can be executed in linear time. But actually it is bounded by maximum degree in the graph $\Delta(G)$, which can be considered to be a constant. If the neighbourhood of a subset of vertices must be found repeatedly, the time complexity is in the worst case quadratic (for a complete graph K_n). Because in each step vertices of particular degree are covered and working graph is reduced, number of iterations must have an upper bound $\Delta(G)$. Overall time complexity of approximation algorithm is thus $O(\Delta^2 \cdot n)$. Published bounds for the original greedy algorithm is of order $O(n^2)$. Another view on the time complexity can be provided by power law degree distribution in figure 3a. The algorithm proceeds from the left side covering in early steps majority of vertices.

The memory complexity is similar as for the `greedy` algorithm. It is mainly determined by the storage space for the input graph. This is possible within bounds $\Theta(n+e)$ (e.g. by using neighbourhood list representation of the graph). Auxiliary variables takes no more space than $O(n)$, which has no effect on overall estimate. This is an advantage compared to some optimisation procedures which could sometime provide exact results in reasonable time, but have exhausting memory demands.

3.3 Experimental Evaluation and Results

The algorithm have been implemented and tested on several real world network graphs, as well as generated random graphs. Performance was evaluated in the terms of precision and computation time. The precision was measured by an approximation ratio for the domination number given by our algorithm to the exact value provided by approach based on optimisation procedure using integer linear programming methods [4]. We used Cbc solver under `julia` language [3] for that purpose, as for the evaluation of theoretical results described in previous section. Though in general finding a graph domination number requires time exponential to the graph order or size, these technique appears in many practical cases as reasonably fast.

For the networks of real world systems, particularly the protein-protein interaction graphs which, are supposed to have a power law distribution of vertex degrees, like in Figure 3a, achieved results of approximation ratio was between 1.096 and 1.157. After applying the redundant vertex reduction it was in the range 1.008 to 1.029.

For the sake of completeness, we used for testing also synthetic random graphs. These do not obey the power law distribution of their vertex degrees, see Figure 3b. In this case the algorithm is not expected to perform well. Indeed, the approximation ratio reached values up to 3 or 5. This is in accordance with previously stated assumptions.

4. Conclusions

We showed how to compute the distribution of paths of length k, which may arise from random graph $\mathcal{G}(C_n, p)$ with the cycle base graph. Then the exact formula for expected value of MDS size was derived. Using Vizing's conjecture the results can be used to set lower bound of expected MDS size for other random graphs obtained by applying Cartesian product to cycles. We presented simulation results for random 2 and 3-dimensional torus. The comparison showed that combining previously known lower bound with present results improves the estimate of the mean MDS size of random graphs with regular base graphs. Further, a new algorithm for MDS approximation was presented. It is targeted to graphs with power law degree distribution. On real networks test data it achieved approximation ratio between 1.15 to 1.1 in a time shorter by few orders than other methods.

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