Network Optimization by Randomization

Excursion: Distributed Algorithms and Social Networks

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Introduction

In this part of the course, we attend to a crucial network design principle: *decentralization*. By decentralization we mean that the functionality or logic of the network is *distributed* across many network components, e.g., there is no single server responsible for the entire service. Thus, bottlenecks or single points of failures can be avoided. Decentralization often implies a better scalability: For example, the high number of participants in a decentralized peer-to-peer network such as BitTorrent or the Kad network is unproblematic, as more users also contribute more resources (e.g., total upload bandwidth). Another good example of a decentralized network is the Internet itself.

We will introduce some fundamental concepts of distributed computing, and focus on two classic and exemplary problems: *vertex coloring* and *maximal independent sets*. Vertex coloring is the problem of how to assign colors to nodes in a network, such that no two adjacent nodes have the same color. Colorings are for example important in wireless networks: nodes which are close to each other should use different frequency bands (i.e., colors) in order to avoid interference and minimize retransmissions. And the computation of independent sets is not only an evergreen of theoretical computer science, but also plays a role in networking, e.g., for the distributed computation of backbones. As we will see, the two problems are closely related, and solutions for one problem can be used for the other.

Finally, if time permits, we take a look at an important class of networks which are often modeled using randomization, namely *social networks*. Interestingly, today we still do not know much about the structure and dynamics of these networks, and research is very active in this field. Moreover, due to the nice properties of these networks, researchers have proposed to build computer networks similarly to social networks.

Have fun!

Chapter 1

Vertex Coloring

1.1 Introduction

Vertex coloring is an infamous graph theory problem. It is also a useful toy example to see the style of this course already in the first lecture. Vertex coloring does have quite a few practical applications, for example in the area of wireless networks where coloring is the foundation of so-called TDMA MAC protocols. Generally speaking, vertex coloring is used as a means to break symmetries, one of the main themes in distributed computing. In this chapter we will not really talk about vertex coloring applications but treat the problem abstractly. At the end of the class you probably learned the fastest (but not constant!) algorithm ever! Let us start with some simple definitions and observations.

Problem 1.1 (Vertex Coloring)**.** *Given an undirected graph $G = (V, E)$, assign a color c_u to each vertex $u \in V$ such that the following holds: $e = (v, w) \in E \Rightarrow c_v \neq c_w$.*

Remarks:

- Throughout this course, we use the terms *vertex* and *node* interchangeably.
- The application often asks us to use few colors! In a TDMA MAC protocol, for example, less colors immediately imply higher throughput. However, in distributed computing we are often happy with a solution which is sub-optimal. There is a tradeoff between the optimality of a solution (efficacy), and the work/time needed to compute the solution (efficiency).

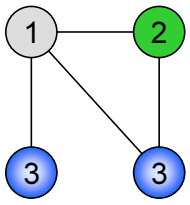

Figure 1.1: 3-colorable graph with a valid coloring.

Assumption 1.2 (Node Identifiers)**.** *Each node has a unique identifier, e.g., its IP address. We usually assume that each identifier consists of only* $\log n$ *bits if the system has* n *nodes.*

Remarks:

- Sometimes we might even assume that the nodes exactly have identifiers $1, \ldots, n$.
- It is easy to see that node identifiers (as defined in Assumption 1.2) solve the coloring problem 1.1, but not very well (essentially requiring n colors). How many colors are needed at least is a well-studied problem.

Definition 1.3 (Chromatic Number)**.** *Given an undirected Graph* $G = (V, E)$*, the* chromatic number $\chi(G)$ *is the minimum number of colors to solve Problem 1.1.*

To get a better understanding of the vertex coloring problem, let us first look at a simple non-distributed ("centralized") vertex coloring algorithm:

Algorithm 1 Greedy Sequential

1: **while** $\exists$ uncolored vertex v **do**
2: color v with the minimal color (number) that does not conflict with the already colored neighbors
3: **end while**

Definition 1.4 (Degree)**.** *The number of neighbors of a vertex* v*, denoted by* $\delta(v)$*, is called the* degree *of* v*. The maximum degree vertex in a graph* G *defines the graph degree* $\Delta(G) = \Delta$*.*

Theorem 1.5 (Analysis of Algorithm 1)**.** *The algorithm is correct and terminates in* n *"steps". The algorithm uses* $\Delta + 1$ *colors.*

Proof: Correctness and termination are straightforward. Since each node has at most Δ neighbors, there is always at least one color free in the range $\{1, \ldots, \Delta + 1\}$.

Remarks:

- In Definition 1.7 we will see what is meant by "step".
- For many graphs coloring can be done with much less than $\Delta + 1$ colors.
- This algorithm is not distributed at all; only one processor is active at a time. Still, maybe we can use the simple idea of Algorithm 1 to define a distributed coloring subroutine that may come in handy later.

Now we are ready to study distributed algorithms for this problem. The following procedure can be executed by every vertex v in a distributed coloring algorithm. The goal of this subroutine is to improve a given initial coloring.

Procedure 2 First Free

Require: Node Coloring {e.g., node IDs as defined in Assumption 1.2}
Give v the smallest admissible color {i.e., the smallest node color not used by any neighbor}

Remarks:

- With this subroutine we have to make sure that two adjacent vertices are not colored at the same time. Otherwise, the neighbors may at the same time conclude that some small color c is still available in their neighborhood, and then at the same time decide to choose this color c.

Definition 1.6 (Synchronous Distributed Algorithm)**.** *In a synchronous algorithm, nodes operate in synchronous rounds. In each round, each processor executes the following steps:*

1. *Do some local computation (of reasonable complexity).*
2. *Send messages to neighbors in graph (of reasonable size).*
3. *Receive messages (that were sent by neighbors in step 2 of the same round).*

Remarks:

- Any other step ordering is fine.

Algorithm 3 Reduce

1: Assume that initially all nodes have ID's (Assumption 1.2)
2: **Each node** v executes the following code
3: node v sends its ID to all neighbors
4: node v receives IDs of neighbors
5: **while** node v has an uncolored neighbor with higher ID **do**
6: node v sends "undecided" to all neighbors
7: node v receives new decisions from neighbors
8: **end while**
9: node v chooses a free color using subroutine **First Free** (Procedure 2)
10: node v informs all its neighbors about its choice

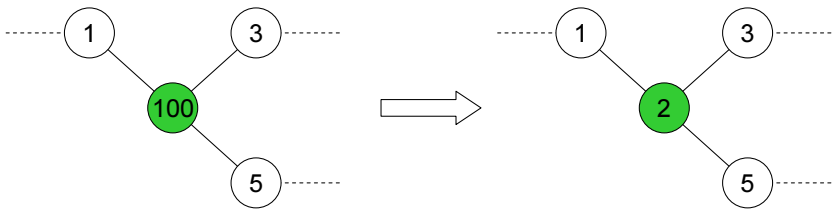

Figure 1.2: Vertex 100 receives the lowest possible color.

Definition 1.7 (Time Complexity)**.** *For synchronous algorithms (as defined in 1.6) the* time complexity *is the number of rounds until the algorithm terminates.*

Remarks:

- The algorithm terminates when the last processor has decided to terminate.
- To guarantee correctness the procedure requires a legal input (i.e., pairwise different node IDs).

Theorem 1.8 (Analysis of Algorithm 3)**.** *Algorithm 3 is correct and has time complexity n. The algorithm uses $\Delta + 1$ colors.*

Remarks:

- Quite trivial, but also quite slow.
- However, it seems difficult to come up with a fast algorithm.
- Maybe it's better to first study a simple special case, a tree, and then go from there.

1.2 Coloring Trees

Lemma 1.9. $\chi(Tree) \leq 2$

Constructive Proof: If the distance of a node to the root is odd (even), color it 1 (0). An odd node has only even neighbors and vice versa. If we assume that each node knows its parent (root has no parent) and children in a tree, this constructive proof gives a very simple algorithm:

Algorithm 4 Slow Tree Coloring

```
1: Color the root 0, root sends 0 to its children
2: Each node v concurrently executes the following code:
3: if node v receives a message x (from parent) then
4:    node v chooses color c_v = 1 − x
5:    node v sends c_v to its children (all neighbors except parent)
6: end if
```

Remarks:

- With the proof of Lemma 1.9, Algorithm 4 is correct.
- How can we determine a root in a tree if it is not already given? We will figure that out later.
- The time complexity of the algorithm is the height of the tree.
- If the root was chosen unfortunately, and the tree has a degenerated topology, the time complexity may be up to n, the number of nodes.
- Also, this algorithm does not need to be synchronous . . . !

Definition 1.10 (Asynchronous Distributed Algorithm)**.** *In the asynchronous model, algorithms are event driven ("upon receiving message . . . , do . . . "). Processors cannot access a global clock. A message sent from one processor to another will arrive in finite but unbounded time.*

Remarks:

- The asynchronous model and the synchronous model (Definition 1.6) are the cornerstone models in distributed computing. As they do not necessarily reflect reality there are several models in between synchronous and asynchronous. However, from a theoretical point of view the synchronous and the asynchronous model are the most interesting ones (because every other model is in between these extremes).
- Note that in the asynchronous model, messages that take a longer path may arrive earlier.

Definition 1.11 (Time Complexity)**.** *For asynchronous algorithms (as defined in 1.6) the* time complexity *is the number of time units from the start of the execution to its completion in the worst case (every legal input, every execution scenario), assuming that each message has a delay of at most one time unit.*

Remarks:

- You cannot use the maximum delay in the algorithm design. In other words, the algorithm has to be correct even if there is no such delay upper bound.

Definition 1.12 (Message Complexity)**.** *The* message complexity *of a synchronous or asynchronous algorithm is determined by the number of messages exchanged (again every legal input, every execution scenario).*

Theorem 1.13 (Analysis of Algorithm 4)**.** *Algorithm 4 is correct. If each node knows its parent and its children, the (asynchronous) time complexity is the tree height which is bounded by the diameter of the tree; the message complexity is* $n - 1$ *in a tree with* n *nodes.*

Remarks:

- In this case the asynchronous time complexity is the same as the synchronous time complexity.
- Nice trees, e.g. balanced binary trees, have logarithmic height, that is we have a logarithmic time complexity.
- This algorithm is not very exciting. Can we do better than logarithmic?!?

The following algorithm terminates in $\log^* n$ time. Log-Star?! That's the number of logarithms (to the base 2) you need to take to get down to at least 2, starting with n:

Definition 1.14 (Log-Star)**.**
$\forall x \leq 2 : \ \log^* x := 1 \quad \forall x > 2 : \ \log^* x := 1 + \log^*(\log x)$

Remarks:

- Log-star is an amazingly slowly growing function. Log-star of all the atoms in the observable universe (estimated to be 10^{80}) is 5! There are functions which grow even more slowly, such as the inverse Ackermann function, however, the inverse Ackermann function of all the atoms is 4. So log-star increases indeed very slowly!

Here is the idea of the algorithm: We start with color labels that have $\log n$ bits. In each synchronous round we compute a new label with exponentially smaller size than the previous label, still guaranteeing to have a valid vertex coloring! But how are we going to do that?

Algorithm 5 "6-Color"

1: Assume that initially the vertices are legally colored. Using Assumption 1.2 each label only has $\log n$ bits
2: The root assigns itself the label 0.
3: **Each** other **node** v executes the following code (synchronously in parallel)
4: send c_v to all children
5: **repeat**
6: receive c_p from parent
7: interpret c_v and c_p as little-endian bit-strings: $c(k), \ldots, c(1), c(0)$
8: let i be the smallest index where c_v and c_p differ
9: the new label is i (as bitstring) followed by the bit $c_v(i)$ itself
10: send c_v to all children
11: **until** $c_w \in \{0, \ldots, 5\}$ for all nodes w

Example:

Algorithm 5 executed on the following part of a tree:

Grand-parent	0010110000	$\rightarrow$	10010	$\rightarrow$	...
Parent	1010010000	$\rightarrow$	01010	$\rightarrow$	111
Child	0110010000	$\rightarrow$	10001	$\rightarrow$	001

Theorem 1.15 (Analysis of Algorithm 5)**.** *Algorithm 5 terminates in* $\log^* n$ *time.*

Proof: A detailed proof is, e.g., in [Peleg 7.3]. In class we do a sketch of the proof.

Remarks:

- Colors $11*$ (in binary notation, i.e., 6 or 7 in decimal notation) will not be chosen, because the node will then do another round. This gives a total of 6 colors (i.e., colors 0,..., 5).
- Can one reduce the number of colors in only constant steps? Note that algorithm 3 does not work (since the degree of a node can be much higher than 6)! For fewer colors we need to have siblings monochromatic!
- Before we explore this problem we should probably have a second look at the end game of the algorithm, the UNTIL statement. Is this algorithm truly local?! Let's discuss!

Algorithm 6 Shift Down

1: Root chooses a new (different) color from $\{0, 1, 2\}$
2: **Each** other **node** v concurrently executes the following code:
3: Recolor v with the color of parent

Lemma 1.16 (Analysis of Algorithm 6)**.** *Algorithm 6 preserves coloring legality; also siblings are monochromatic.*

Now Algorithm 3 (Reduce) can be used to reduce the number of used colors from six to three.

Algorithm 7 Six-2-Three

1: **Each node** v concurrently executes the following code:
2: Run Algorithm 5 for $\log^* n$ rounds.
3: **for** $x = 5, 4, 3$ **do**
4: Perform subroutine Shift down (Algorithm 6)
5: **if** $c_v = x$ **then**
6: choose new color $c_v \in \{0, 1, 2\}$ using subroutine **First Free** (Algorithm 2)
7: **end if**
8: **end for**

Theorem 1.17 (Analysis of Algorithm 7)**.** *Algorithm 7 colors a tree with three colors in time* $O(\log^* n)$.

Remarks:

- The term $O()$ used in Theorem 1.15 is called "big O" and is often used in distributed computing. Roughly speaking, $O(f)$ means "in the order of f, ignoring constant factors and smaller additive terms." More formally, for two functions f and g, it holds that $f \in O(g)$ if there are constants x_0 and c so that $|f(x)| \leq c|g(x)|$ for all $x \geq x_0$. For an elaborate discussion on the big O notation we refer to other introductory math or computer science classes.

- As one can easily prove, a fast tree-coloring with only 2 colors is more than exponentially more expensive than coloring with 3 colors. In a tree degenerated to a list, nodes far away need to figure out whether they are an even or odd number of hops away from each other in order to get a 2-coloring. To do that one has to send a message to these nodes. This costs time linear in the number of nodes.

- Also other lower bounds have been proved, e.g., any algorithm for 2-coloring the d-regular tree of radius r which runs in time at most $2r/3$ requires at least $\Omega(\sqrt{d})$ colors.

- The idea of this algorithm can be generalized, e.g., to a ring topology. Also a general graph with constant degree Δ can be colored with $\Delta + 1$ colors in $O(\log^* n)$ time. The idea is as follows: In each step, a node compares its label to each of its neighbors, constructing a logarithmic difference-tag

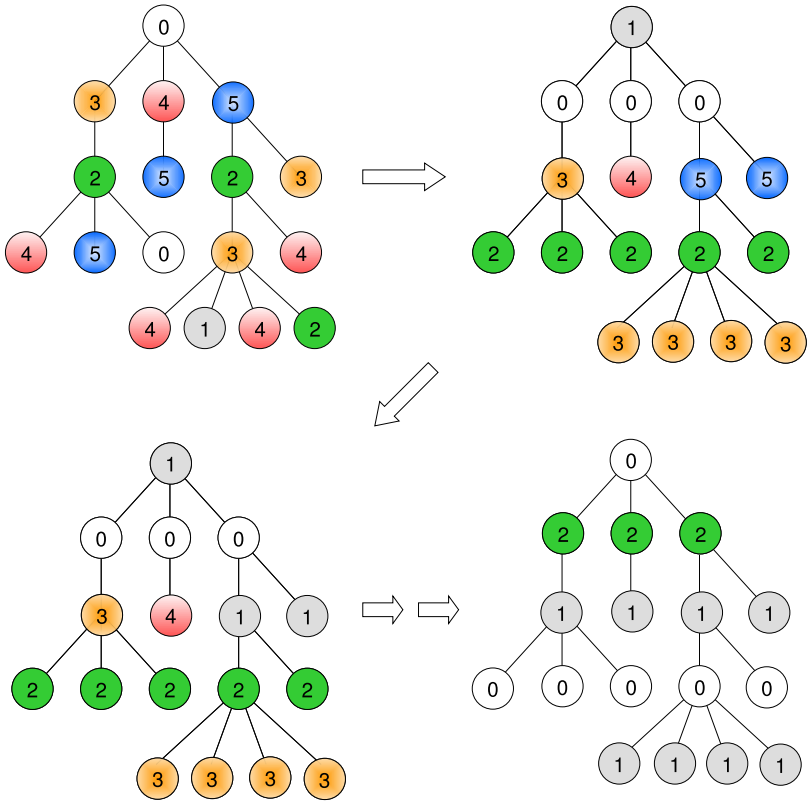

Figure 1.3: Possible execution of Algorithm 7.

as in 6-color (Algorithm 5). Then the new label is the concatenation of all the difference-tags. For constant degree Δ, this gives a 3Δ-label in $O(\log^* n)$ steps. Algorithm 3 then reduces the number of colors to $\Delta + 1$ in $2^{3\Delta}$ (this is still a constant for constant Δ!) steps.

- Recently, researchers have proposed other methods to break down long ID's for log-star algorithms. With these new techniques, one is able to solve other problems, e.g., a maximal independent set in bounded growth graphs in $O(\log^* n)$ time. These techniques go beyond the scope of this course.

- Unfortunately, coloring a general graph is not yet possible with this technique. We will see another technique for that in Chapter 2. With this technique it is possible to color a general graph with $\Delta + 1$ colors in $O(\log n)$ time.

- A lower bound by Linial shows that many of these log-star algorithms are asymptotically (up to constant factors) optimal. This lower bound uses an interesting technique. However, because of the one-topic-per-class policy we cannot look at it today.

Chapter 2

Maximal Independent Set

In this chapter we present a highlight of this course, a fast maximal independent set (MIS) algorithm. The algorithm is the first randomized algorithm that we study in this class. In distributed computing, randomization is a powerful and therefore omnipresent concept, as it allows for relatively simple yet efficient algorithms. As such the studied algorithm is archetypal.

A MIS is a basic building block in distributed computing, some other problems pretty much follow directly from the MIS problem. At the end of this chapter, we will give two examples: matching and vertex coloring (see Chapter 1).

2.1 MIS

Definition 2.1 (Independent Set)**.** *Given an undirected Graph $G = (V, E)$ an* independent set *is a subset of nodes $U \subseteq V$, such that no two nodes in U are adjacent. An independent set is* maximal *if no node can be added without violating independence. An independent set of* maximum *cardinality is called maximum.*

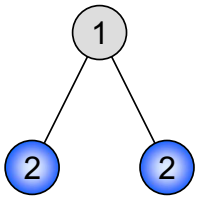

Figure 2.1: Example graph with 1) a maximal independent set (MIS) and 2) a maximum independent set (MaxIS).

Remarks:

- Computing a maximum independent set (MaxIS) is a notoriously difficult problem. It is equivalent to maximum clique on the complementary graph. Both problems are NP-hard, in fact not approximable within $n^{\frac{1}{2}-\epsilon}$.
- In this course we concentrate on the maximal independent set (MIS) problem. Please note that MIS and MaxIS can be quite different, indeed e.g. on a star graph the MIS is $\Theta(n)$ smaller than the MaxIS (cf. Figure 2.1).
- Computing a MIS sequentially is trivial: Scan the nodes in arbitrary order. If a node u does not violate independence, add u to the MIS. If u violates independence, discard u. So the only question is how to compute a MIS in a distributed way.

Algorithm 8 Slow MIS

Require: Node IDs

Every node v executes the following code:

1: **if** all neighbors of v with larger identifiers have decided not to join the MIS **then**
2: v decides to join the MIS
3: **end if**

Remarks:

- Not surprisingly the slow algorithm is not better than the sequential algorithm in the worst case, because there might be one single point of activity at any time. Formally:

Theorem 2.2 (Analysis of Algorithm 8)**.** *Algorithm 8 features a time complexity of $O(n)$ and a message complexity of $O(m)$.*

Remarks:

- This is not very exciting.
- There is a relation between independent sets and node coloring (Chapter 1), since each color class is an independent set, however, not necessarily a MIS. Still, starting with a coloring, one can easily derive a MIS algorithm: We first choose all nodes of the first color. Then, for each additional color we add "in parallel" (without conflict) as many nodes as possible. Thus the following corollary holds:

Corollary 2.3. *Given a coloring algorithm that needs C colors and runs in time T, we can construct a MIS in time $C + T$.*

Remarks:

- Using Theorem 1.17 and Corollary 2.3 we get a distributed deterministic MIS algorithm for trees (and for bounded degree graphs) with time complexity $O(\log^* n)$.

- With a lower bound argument one can show that this deterministic MIS algorithm for rings is asymptotically optimal.
- There have been attempts to extend Algorithm 5 to more general graphs, however, so far without much success. Below we present a radically different approach that uses randomization. Please note that the algorithm and the analysis below is not identical with the algorithm in Peleg's book.

2.2 Fast MIS from 1986

Algorithm 9 Fast MIS

The algorithm operates in synchronous rounds, grouped into phases.
A single phase is as follows:
1) Each node v marks itself with probability $\frac{1}{2d(v)}$, where $d(v)$ is the current degree of v.
2) If no higher degree neighbor of v is also marked, node v joins the MIS. If a higher degree neighbor of v is marked, node v unmarks itself again. (If the neighbors have the same degree, ties are broken arbitrarily, e.g., by identifier).
3) Delete all nodes that joined the MIS and their neighbors, as they cannot join the MIS anymore.

Remarks:

- Correctness in the sense that the algorithm produces an independent set is relatively simple: Steps 1 and 2 make sure that if a node v joins the MIS, then v's neighbors do not join the MIS at the same time. Step 3 makes sure that v's neighbors will never join the MIS.
- Likewise the algorithm eventually produces a MIS, because the node with the highest degree will mark itself at some point in Step 1.
- So the only remaining question is how fast the algorithm terminates. To understand this, we need to dig a bit deeper.

Lemma 2.4 (Joining MIS)**.** *A node v joins the MIS in step 2 with probability $p \geq \frac{1}{4d(v)}$.*

Proof: Let M be the set of marked nodes in step 1. Let $H(v)$ be the set of neighbors of v with higher degree, or same degree and higher identifier. Using independence of the random choices of v and nodes in $H(v)$ in Step 1 we get

$$\begin{aligned} P[v \notin \text{MIS} | v \in M] &= P[\exists w \in H(v), w \in M | v \in M] \\ &= P[\exists w \in H(v), w \in M] \\ &\leq \sum_{w \in H(v)} P[w \in M] = \sum_{w \in H(v)} \frac{1}{2d(w)} \\ &\leq \sum_{w \in H(v)} \frac{1}{2d(v)} \leq \frac{d(v)}{2d(v)} = \frac{1}{2}. \end{aligned}$$

Then

$$P[v \in \text{MIS}] = P[v \in \text{MIS} | v \in M] \cdot P[v \in M] \geq \frac{1}{2} \cdot \frac{1}{2d(v)}.$$

□

Lemma 2.5 (Good Nodes)**.** *A node v is called* good *if*

$$\sum_{w \in N(v)} \frac{1}{2d(w)} \geq \frac{1}{6}.$$

Otherwise we call v a bad *node. A good node will be removed in Step 3 with probability $p \geq \frac{1}{36}$.*

Proof: Let node v be good. Intuitively, good nodes have lots of low-degree neighbors, thus chances are high that one of them goes into the independent set, in which case v will be removed in step 3 of the algorithm.

If there is a neighbor $w \in N(v)$ with degree at most 2 we are done: With Lemma 2.4 the probability that node w joins the MIS is at least $\frac{1}{8}$, and our good node will be removed in Step 3.

So all we need to worry about is that all neighbors have at least degree 3: For any neighbor w of v we have $\frac{1}{2d(w)} \leq \frac{1}{6}$. Since $\sum_{w \in N(v)} \frac{1}{2d(w)} \geq \frac{1}{6}$ there is a subset of neighbors $S \subseteq N(v)$ such that $\frac{1}{6} \leq \sum_{w \in S} \frac{1}{2d(w)} \leq \frac{1}{3}$

We can now bound the probability that node v will be removed. Let therefore R be the event of v being removed. Again, if a neighbor of v joins the MIS in Step 2, node v will be removed in Step 3. We have

$$\begin{aligned} P[R] &\geq P[\exists u \in S, u \in \text{MIS}] \\ &\geq \sum_{u \in S} P[u \in \text{MIS}] - \sum_{u,w \in S; u \neq w} P[u \in \text{MIS } \textbf{and } w \in \text{MIS}]. \end{aligned}$$

For the last inequality we used the inclusion-exclusion principle truncated after the second order terms. Let M again be the set of marked nodes after Step 1. Using $P[u \in M] \geq P[u \in \text{MIS}]$ we get

$$\begin{aligned} P[R] &\geq \sum_{u \in S} P[u \in \text{MIS}] - \sum_{u,w \in S; u \neq w} P[u \in M \textbf{ and } w \in M] \\ &\geq \sum_{u \in S} P[u \in \text{MIS}] - \sum_{u \in S} \sum_{w \in S} P[u \in M] \cdot P[w \in M] \\ &\geq \sum_{u \in S} \frac{1}{4d(u)} - \sum_{u \in S} \sum_{w \in S} \frac{1}{2d(u)} \frac{1}{2d(w)} \\ &\geq \sum_{u \in S} \frac{1}{2d(u)} \left(\frac{1}{2} - \sum_{w \in S} \frac{1}{2d(w)} \right) \geq \frac{1}{6} \left(\frac{1}{2} - \frac{1}{3} \right) = \frac{1}{36}. \end{aligned}$$

□

Remarks:

- We would be almost finished if we could prove that many nodes are good in each phase. Unfortunately this is not the case: In a star-graph, for instance, only a single node is good! We need to find a work-around.

Lemma 2.6 (Good Edges)**.** *An edge $e = (u, v)$ is called* bad *if both u and v are bad; else the edge is called* good*. The following holds: At any time at least half of the edges are good.*

Proof: For the proof we construct a directed auxiliary graph: Direct each edge towards the higher degree node (if both nodes have the same degree direct it towards the higher identifier). Now we need a little helper lemma before we can continue with the proof.

Lemma 2.7. *A bad node has outdegree at least twice its indegree.*

Proof: For the sake of contradiction, assume that a bad node v does not have outdegree at least twice its indegree. In other words, at least one third of the neighbor nodes (let's call them S) have degree at most $d(v)$. But then

$$\sum_{w \in N(v)} \frac{1}{2d(w)} \geq \sum_{w \in S} \frac{1}{2d(w)} \geq \sum_{w \in S} \frac{1}{2d(v)} \geq \frac{d(v)}{3} \frac{1}{2d(v)} = \frac{1}{6}$$

which means v is good, a contradiction. □

Continuing the proof of Lemma 2.6: According to Lemma 2.7 the number of edges directed into bad nodes is at most half the number of edges directed out of bad nodes. Thus, the number of edges directed into bad nodes is at most half the number of edges. Thus, at least half of the edges are directed into good nodes. Since these edges are not bad, they must be good.

Theorem 2.8 (Analysis of Algorithm 9)**.** *Algorithm 9 terminates in expected time $O(\log n)$.*

Proof: With Lemma 2.5 a good node (and therefore a good edge!) will be deleted with constant probability. Since at least half of the edges are good (Lemma 2.6) a constant fraction of edges will be deleted in each phase.

More formally: With Lemmas 2.5 and 2.6 we know that at least half of the edges will be removed with probability at least $1/36$. Let R be the number of edges to be removed. Using linearity of expectation we know that $\mathbb{E}[R] \geq m/72$, m being the total number of edges at the start of a phase. Now let $p := P[R \leq \mathbb{E}[R]/2]$. Bounding the expectation yields

$$\mathbb{E}[R] = \sum_r P[R = r] \cdot r \leq p \cdot \mathbb{E}[R]/2 + (1 - p) \cdot m.$$

Solving for p we get

$$p \leq \frac{m - \mathbb{E}[R]}{m - \mathbb{E}[R]/2} < \frac{m - \mathbb{E}[R]/2}{m} \leq 1 - 1/144.$$

In other words, with probability at least $1/144$ at least $m/144$ edges are removed in a phase. After expected $O(\log m)$ phases all edges are deleted. Since $m \leq n^2$ and thus $O(\log m) = O(\log n)$ the Theorem follows. □

Remarks:

- With a bit of more math one can even show that Algorithm 9 terminates in time $O(\log n)$ "with high probability".
- The presented algorithm is a simplified version of an algorithm by Michael Luby, published 1986 in the SIAM Journal of Computing. Around the same time there have been a number of other papers dealing with the same or related problems, for instance by Alon, Babai, and Itai, or by Israeli and Itai. The analysis presented here takes elements of all these papers, and from other papers on distributed weighted matching. The analysis in the book by David Peleg is different, and only achieves $O(\log^2 n)$ time.
- Though not as incredibly fast as the $\log^*$-coloring algorithm for trees, this algorithm is very general. It works on any graph, needs no identifiers, and can easily be made asynchronous.
- Surprisingly, much later, there have been half a dozen more papers published, with much worse results!! In 2002, for instance, there was a paper with linear running time, improving on a 1994 paper with cubic running time, restricted to trees!
- In 2009, Métivier, Robson, Saheb-Djahromi and Zemmari found a slightly different (and simpler) way to compute a MIS in the same logarithmic time:

2.3 Fast MIS from 2009

Algorithm 10 Fast MIS 2

The algorithm operates in synchronous rounds, grouped into phases.
A single phase is as follows:
1) Each node v chooses a random value $r(v) \in [0, 1]$ and sends it to its neighbors.
2) If $r(v) < r(w)$ for all neighbors $w \in N(v)$, node v enters the MIS and informs its neighbors.
3) If v or a neighbor of v entered the MIS, v terminates (v and all edges adjacent to v are removed from the graph), otherwise v enters the next phase.

Remarks:

- Correctness in the sense that the algorithm produces an independent set is simple: Steps 1 and 2 make sure that if a node v joins the MIS, then v's neighbors do not join the MIS at the same time. Step 3 makes sure that v's neighbors will never join the MIS.
- Likewise the algorithm eventually produces a MIS, because the node with the globally smallest value will always join the MIS, hence there is progress.
- So the only remaining question is how fast the algorithm terminates. To understand this, we need to dig a bit deeper.

- Our proof will rest on a simple, yet powerful observation about expected values of random variables that *may not be independent*:

Theorem 2.9 (Linearity of Expectation)**.** *Let X_i, $i = 1, \ldots, k$ denote random variables, then*

$$\mathbb{E}\left[\sum_i X_i\right] = \sum_i \mathbb{E}\left[X_i\right].$$

Proof. It is sufficient to prove $\mathbb{E}[X+Y] = \mathbb{E}[X]+\mathbb{E}[Y]$ for two random variables X and Y, because then the statement follows by induction. Since

$$\begin{aligned} P[(X,Y)=(x,y)] &= P[X=x]\cdot P[Y=y|X=x] \\ &= P[Y=y]\cdot P[X=x|Y=y] \end{aligned}$$

we get that

$$\begin{aligned} \mathbb{E}[X+Y] &= \sum_{(X,Y)=(x,y)} P[(X,Y)=(x,y)]\cdot(x+y) \\ &= \sum_{X=x}\sum_{Y=y} P[X=x]\cdot P[Y=y|X=x]\cdot x \\ &+ \sum_{Y=y}\sum_{X=x} P[Y=y]\cdot P[X=x|Y=y]\cdot y \\ &= \sum_{X=x} P[X=x]\cdot x + \sum_{Y=y} P[Y=y]\cdot y \\ &= \mathbb{E}[X]+\mathbb{E}[Y]. \end{aligned}$$

Remarks:

- How can we prove that the algorithm only needs $O(\log n)$ phases in expectation? It would be great if this algorithm managed to remove a constant fraction of nodes in each phase. Unfortunately, it does not.
- Instead we will prove that the number of *edges* decreases quickly. Again, it would be great if any single edge was removed with constant probability in Step 3. But again, unfortunately, this is not the case.
- Maybe we can argue about the expected number of edges to be removed in one single phase? Let's see: A node v enters the MIS with probability $1/(d(v)+1)$, where $d(v)$ is the degree of node v. By doing so, not only are v's edges removed, but indeed all the edges of v's neighbors as well – generally these are much more than $d(v)$ edges. So there is hope, but we need to be careful: If we do this the most naive way, we will count the same edge many times.
- How can we fix this? The nice observation is that it is enough to count just some of the removed edges. Given a new MIS node v and a neighbor $w \in N(v)$, we count the edges only if $r(v) < r(x)$ for all $x \in N(w)$. This looks promising. In a star graph, for instance, only the smallest random value can be accounted for removing all the edges of the star.

Lemma 2.10 (Edge Removal)**.** *In a single phase, we remove at least half of the edges in expectation.*

Proof: To simplify the notation, at the start of our phase, the graph is simply $G = (V, E)$. Suppose that a node v joins the MIS in this phase, i.e., $r(v) < r(w)$ for all neighbors $w \in N(v)$. If in addition we have $r(v) < r(x)$ for all neighbors x of a neighbor w of v, we call this event $(v \to w)$. The probability of event $(v \to w)$ is at least $1/(d(v) + d(w))$, since $d(v) + d(w)$ is the maximum number of nodes adjacent to v or w (or both). As v joins the MIS, all edges (w, x) will be removed; there are $d(w)$ of these edges.

In order to count the removed edges, we need to weigh events properly.

Whether we remove the edges adjacent to w because of event $(v \to w)$ is a random variable $X_{(v\to w)}$. If event $(v \to w)$ occurs, $X_{(v\to w)}$ has the value $d(w)$, if not it has the value 0. For each edge $\{v, w\}$ we have two such variables, the event $X_{(v\to w)}$ and $X_{(w\to v)}$. Due to Theorem 2.9, the expected value of the sum X of all these random variables is at least

$$\begin{aligned}
\mathbb{E}[X] &= \sum_{\{v,w\}\in E} \mathbb{E}[X_{(v\to w)}] + \mathbb{E}[X_{(w\to v)}] \\
&= \sum_{\{v,w\}\in E} P[\text{Event } (v \to w)] \cdot d(w) + P[\text{Event } (w \to v)] \cdot d(v) \\
&\geq \sum_{\{v,w\}\in E} \frac{d(w)}{d(v) + d(w)} + \frac{d(v)}{d(w) + d(v)} \\
&= \sum_{\{v,w\}\in E} 1 = |E|.
\end{aligned}$$

In other words, in expectation all edges are removed in a single phase?!? Probably not. This means that we still counted some edges more than once. Indeed, for an edge $\{v, w\} \in E$ our random variable X includes the edge if the event $(u \to v)$ happens, but X also includes the edge if the event $(x \to w)$ happens. So we may have counted the edge $\{v, w\}$ twice. Fortunately however, not more than twice, because at most one event $(\cdot \to v)$ and at most one event $(\cdot \to w)$ can happen. If $(u \to v)$ happens, we know that $r(u) < r(w)$ for all $w \in N(v)$; hence another $(u' \to v)$ cannot happen because $r(u') > r(u) \in N(v)$. Therefore the random variable X must be divided by 2. In other words, in expectation at least half of the edges are removed.

Remarks:

- This enables us to follow a bound on the expected running time of Algorithm 10 quite easily.

Theorem 2.11 (Expected running time of Algorithm 10)**.** *Algorithm 10 terminates after at most* $3 \log_{4/3} m + 1 \in O(\log n)$ *phases in expectation.*

Proof: The probability that in a single phase at least a quarter of all edges are removed is at least 1/3. For the sake of contradiction, assume not. Then with probability less than 1/3 we may be lucky and many (potentially all) edges are removed. With probability more than 2/3 less than 1/4 of the edges are removed. Hence the expected fraction of removed edges is strictly less than $1/3 \cdot 1 + 2/3 \cdot 1/4 = 1/2$. This contradicts Lemma 2.10.

Hence, at least every third phase is "good" and removes at least a quarter of the edges. To get rid of all but two edges we need $\log_{4/3} m$ good phases in expectation. The last two edges will certainly be removed in the next phase. Hence a total of $3\log_{4/3} m + 1$ phases are enough in expectation.

Remarks:

- Sometimes one expects a bit more of an algorithm: Not only should the expected time to terminate be good, but the algorithm should *always* terminate quickly. As this is impossible in randomized algorithms (after all, the random choices may be "unlucky" all the time!), researchers often settle for a compromise, and just demand that the probability that the algorithm does not terminate in the specified time can be made absurdly small. For our algorithm, this can be deduced from Lemma 2.10 and another standard tool, namely Chernoff's Bound.

Definition 2.12 (W.h.p.)**.** *We say that an algorithm terminates* w.h.p. *(with high probability) within $O(t)$ time if it does so with probability at least $1 - 1/n^c$ for any choice of $c \geq 1$. Here c may affect the constants in the Big-O notation because it is considered a "tunable constant" and usually kept small.*

Definition 2.13 (Chernoff's Bound)**.** *Let $X = \sum_{i=1}^{k} X_i$ be the sum of k independent $0-1$ random variables. Then* Chernoff's bound *states that w.h.p.*

$$|X - \mathbb{E}[X]| \in O\left(\log n + \sqrt{\mathbb{E}[X] \log n}\right).$$

Corollary 2.14 (Running Time of Algorithm 10)**.** *Algorithm 10 terminates w.h.p. in $O(\log n)$ time.*

Proof: In Theorem 2.11 we used that *independently* of everything that happened before, in each phase we have a constant probability p that a quarter of the edges are removed. Call such a phase *good*. For some constants C_1 and C_2, let us check after $C_1 \log n + C_2 \in O(\log n)$ phases, in how many phases at least a quarter of the edges have been removed. In expectation, these are at least $p(C_1 \log n + C_2)$ many. Now we look at the random variable $X = \sum_{i=1}^{C_1 \log n + C_2} X_i$, where the X_i are independent $0-1$ variables being one with exactly probability p. Certainly, if X is at least x with some probability, then the probability that we have x good phases can only be larger (if no edges are left, certainly "all" of the remaining edges are removed). To X we can apply Chernoff's bound. If C_1 and C_2 are chosen large enough, they will overcome the constants in the Big-O from Chernoff's bound, i.e., w.h.p. it holds that $|X - \mathbb{E}[X]| \leq \mathbb{E}[X]/2$, implying $X \geq \mathbb{E}[X]/2$. Choosing C_1 large enough, we will have w.h.p. sufficiently many good phases, i.e., the algorithm terminates w.h.p. in $O(\log n)$ phases.

Remarks:

- The algorithm can be improved a bit more even. Drawing random real numbers in each phase for instance is not necessary. One can achieve the same by sending only a total of $O(\log n)$ random (and as many non-random) bits over each edge.

- One of the main open problems in distributed computing is whether one can beat this logarithmic time, or at least achieve it with a deterministic algorithm.

- Let's turn our attention to applications of MIS next.

2.4 Applications

Definition 2.15 (Matching)**.** *Given a graph $G = (V, E)$ a* matching *is a subset of edges $M \subseteq E$, such that no two edges in M are adjacent (i.e., where no node is adjacent to two edges in the matching). A matching is* maximal *if no edge can be added without violating the above constraint. A matching of maximum cardinality is called* maximum*. A matching is called* perfect *if each node is adjacent to an edge in the matching.*

Remarks:

- In contrast to MaxIS, a maximum matching can be found in polynomial time (Blossom algorithm by Jack Edmonds), and is also easy to approximate (in fact, already any maximal matching is a 2-approximation).
- An independent set algorithm is also a matching algorithm: Let $G = (V, E)$ be the graph for which we want to construct the matching. The auxiliary graph G' is defined as follows: for every edge in G there is a node in G'; two nodes in G' are connected by an edge if their respective edges in G are adjacent. A (maximal) independent set in G' is a (maximal) matching in G, and vice versa. Using Algorithm 10 directly produces a $O(\log n)$ bound for maximal matching.
- More importantly, our MIS algorithm can also be used for vertex coloring (Problem 1.1):

Algorithm 11 General Graph Coloring

1: Given a graph $G = (V, E)$ we virtually build a graph $G' = (V', E')$ as follows:
2: Every node $v \in V$ clones itself $d(v)+1$ times $(v_0, \ldots, v_{d(v)} \in V')$, $d(v)$ being the degree of v in G.
3: The edge set E' of G' is as follows:
4: First all clones are in a clique: $(v_i, v_j) \in E'$, for all $v \in V$ and all $0 \leq i < j \leq d(v)$
5: Second all i^{th} clones of neighbors in the original graph G are connected: $(u_i, v_i) \in E'$, for all $(u, v) \in E$ and all $0 \leq i \leq \min(d(u), d(v))$.
6: Now we simply run (simulate) the fast MIS Algorithm 10 on G'.
7: If node v_i is in the MIS in G', then node v gets color i.

Theorem 2.16 (Analysis of Algorithm 11)**.** *Algorithm 11 $(\Delta + 1)$-colors an arbitrary graph in $O(\log n)$ time, with high probability, Δ being the largest degree in the graph.*

Proof: Thanks to the clique among the clones at most one clone is in the MIS. And because of the $d(v)+1$ clones of node v every node will get a free color! The running time remains logarithmic since G' has $O\left(n^2\right)$ nodes and the exponent becomes a constant factor when applying the logarithm.

Remarks:

- This solves our open problem from Chapter 1.1!
- Together with Corollary 2.3 we get quite close ties between (Δ+1)-coloring and the MIS problem.
- However, in general Algorithm 11 is not the best distributed algorithm for $O(\Delta)$-coloring. For fast distributed vertex coloring please check Kothapalli, Onus, Scheideler, Schindelhauer, IPDPS 2006. This algorithm is based on a $O(\log\log n)$ time *edge* coloring algorithm by Grable and Panconesi, 1997.
- Computing a MIS also solves another graph problem on graphs of bounded independence.

Definition 2.17 (Bounded Independence)**.** $G = (V, E)$ *is of* bounded independence*, if each neighborhood contains at most a constant number of independent (i.e., mutually non-adjacent) nodes.*

Definition 2.18 ((Minimum) Dominating Sets)**.** *A* dominating set *is a subset of the nodes such that each node is in the set or adjacent to a node in the set. A* minimum dominating set *is a dominating set containing the least possible number of nodes.*

Remarks:

- In general, finding a dominating set less than factor $\log n$ larger than an minimum dominating set is NP-hard.
- Any MIS is a dominating set: if a node was not covered, it could join the independent set.
- In general a MIS and a minimum dominating sets have not much in common (think of a star). For graphs of bounded independence, this is different.

Corollary 2.19. *On graphs of bounded independence, a constant-factor approximation to a minimum dominating set can be found in time $O(\log n)$ w.h.p.*

Proof: Denote by M a minimum dominating set and by I a MIS. Since M is a dominating set, each node from I is in M or adjacent to a node in M. Since the graph is of bounded independence, no node in M is adjacent to more than constantly many nodes from I. Thus, $|I| \in O(|M|)$. Therefore, we can compute a MIS with Algorithm 10 and output it as the dominating set, which takes $O(\log n)$ rounds w.h.p.

Chapter 3

Social Networks

Distributed computing is applicable in various contexts. This lecture exemplarily studies one of these contexts, social networks, an area of study whose origins date back a century. To give you a first impression, consider Figure 3.1.

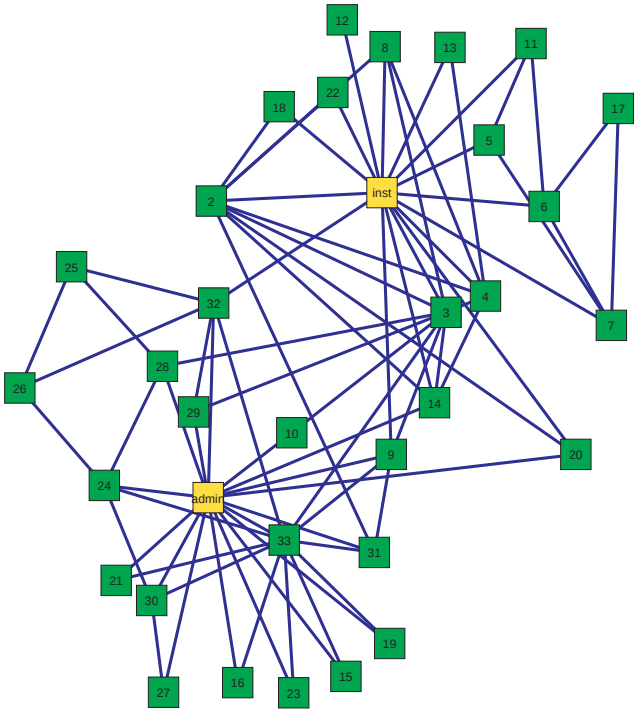

Figure 3.1: This graph shows the social relations between the members of a karate club, studied by anthropologist Wayne Zachary in the 1970s. Two people (nodes) stand out, the instructor and the administrator of the club, both happen to have many friends among club members. At some point, a dispute caused the club to split into two. Can you predict how the club partitioned? (If not, just search the Internet for Zachary and Karate.)

3.1 Small-World Networks

Back in 1929, Frigyes Karinthy published a volume of short stories that postulated that the world was "shrinking" because human beings were connected more and more. Some claim that he was inspired by radio network pioneer Guglielmo Marconi's 1909 Nobel Prize speech. Despite physical distance, the growing density of human "networks" renders the actual social distance smaller and smaller. As a result, it is believed that any two individuals can be connected through at most five (or so) acquaintances, i.e., within six hops.

- The topic was hot in the 1960s. For instance, in 1964, Marshall McLuhan coined the metaphor "Global Village". He wrote: "As electrically contracted, the globe is no more than a village". He argues that due to the almost instantaneous reaction times of new ("electric") technologies, each individual inevitably feels the consequences of his actions and thus automatically deeply participates in the global society. McLuhan understood what we now can directly observe – real and virtual world are moving together. He realized that the transmission medium, rather than the transmitted information is at the core of change, as expressed by his famous phrase "the medium is the message".

- This idea has been followed ardently in the 1960s by several sociologists, first by Michael Gurevich, later by Stanley Milgram. Milgram wanted to know the average path length between two "random" humans, by using various experiments, generally using randomly chosen individuals from the US Midwest as starting points, and a stockbroker living in a suburb of Boston as target. The starting points were given name, address, occupation, plus some personal information about the target. They were asked to send a letter to the target. However, they were not allowed to *directly* send the letter, rather, they had to pass it to somebody they knew on first-name basis and that they thought to have a higher probability to know the target person. This process was repeated, until somebody knew the target person, and could deliver the letter. Shortly after starting the experiment, letters have been received. Most letters were lost during the process, but if they arrived, the average path length was about 5.5. The observation that the entire population is connected by short acquaintance chains got later popularized by the terms "six degrees of separation" and "small world".

- Statisticians tried to explain Milgram's experiments, by essentially giving network models that allowed for short diameters, i.e., each node is connected to each other node by only a few hops. Until today there is a thriving research community in statistical physics that tries to understand network properties that allow for "small world" effects.

- One of the keywords in this area are power-law graphs, networks were node degrees are distributed according to a power-law distribution, i.e. the number of nodes with degree δ is proportional to $\delta^{-\alpha}$, for some $\alpha > 1$. Such power-law graphs have been witnessed in many application areas, apart from social networks also in the web, or in Biology or Physics.

- Obviously, two power-law graphs might look and behave completely differently, even if α and the number of edges is exactly the same.

One well-known model towards this end is the Watts-Strogatz model. Watts and Strogatz argued that social networks should be modeled by a combination of two networks: As the basis we take a network that has a large cluster coefficient ...

Definition 3.1. *The cluster coefficient of a network is defined by the probability that two friends of a node are likely to be friends as well, summing up over all the nodes.*

..., then we augment such a graph with random links, every node for instance points to a constant number of other nodes, chosen uniformly at random. This augmentation represents acquaintances that connect nodes to parts of the network that would otherwise be far away.

Remarks:

- Without further information, knowing the cluster coefficient is of questionable value: Assume we arrange the nodes in a grid. Technically, if we connect each node to its four closest neighbors, the graph has cluster coefficient 0, since there are no triangles; if we instead connect each node with its eight closest neighbors, the cluster coefficient is 3/7. The cluster coefficient is quite different, even though both networks have similar characteristics.

This is interesting, but not enough to really understand what is going on. For Milgram's experiments to work, it is not sufficient to connect the nodes in a certain way. In addition, the nodes *themselves* need to know how to forward a message to one of their neighbors, even though they cannot know whether that neighbor is really closer to the target. In other words, nodes are not just following physical laws, but they make decisions themselves. In contrast to those mathematicians that worked on the problem earlier, Jon Kleinberg understood that Milgram's experiment essentially shows that social networks are "navigable", and that one can only explain it in terms of a *greedy routing*.

In particular, Kleinberg set up an artificial network with nodes on a grid topology, plus some additional random links per node. In a quantitative study he showed that the random links need a specific distance distribution to allow for efficient greedy routing. This distribution marks the sweet spot for any navigable network.

Definition 3.2 (Augmented Grid)**.** *We take $n = m^2$ nodes $(i, j) \in V = \{1, \dots, m\}^2$ that are identified with the lattice points on an $m \times m$ grid. We define the distance between two nodes (i, j) and (k, ℓ) as $d\big((i, j), (k, \ell)\big) = |k - i| + |\ell - j|$ as the distance between them on the $m \times m$ lattice. The network is modeled using a parameter $\alpha \geq 0$. Each node u has a directed edge to every lattice neighbor. These are the* local contacts *of a node. In addition, each node also has an additional random link (the* long-range contact*). For all u and v, the long-range contact of u points to node v with probability proportional to $d(u, v)^{-\alpha}$, i.e., with probability $d(u, v)^{-\alpha} / \sum_{w \in V \setminus \{u\}} d(u, w)^{-\alpha}$. Figure 3.2 illustrates the model.*

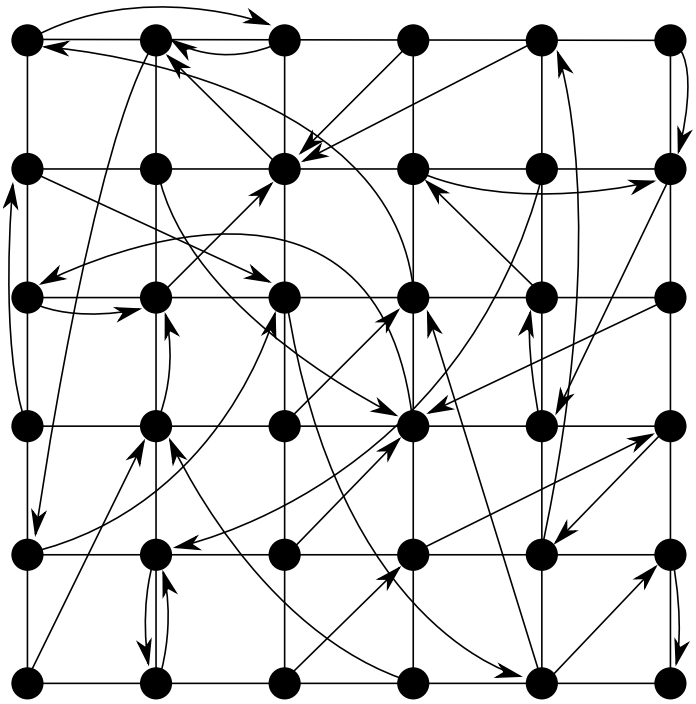

Figure 3.2: Augmented grid with $m = 6$

Remarks:

- The network model has the following geographic interpretation: nodes (individuals) live on a grid and know their neighbors on the grid. Further, each node has some additional acquaintances throughout the network.
- The parameter α controls how the additional neighbors are distributed across the grid. If $\alpha = 0$, long-range contacts are chosen uniformly at random (as in the Watts-Strogatz model). As α increases, long-range contacts become shorter on average. In the extreme case, if $\alpha \to \infty$, all long-range contacts are to immediate neighbors on the grid.
- It can be shown that as long as $\alpha \leq 2$, the diameter of the resulting graph is polylogarithmic in n (polynomial in $\log n$) with high probability. In particular, if the long-range contacts are chosen uniformly at random ($\alpha = 0$), the diameter is $O(\log n)$.

Since the augmented grid contains random links, we do not know anything for sure about how the random links are distributed. In theory, all links could point to the same node! However, this is almost certainly not the case. Formally this is captured by the term *with high probability*.

Definition 3.3 (With High Probability)**.** *Some probabilistic event is said to occur* with high probability (w.h.p.)*, if it happens with a probability $p \geq 1 - 1/n^c$, where c is a constant. The constant c may be chosen arbitrarily, but it is considered constant with respect to Big-O notation.*

Remarks:

- For instance, a running time bound of $c \log n$ or $e^{c!} \log n + 5000c$ with probability at least $1 - 1/n^c$ would be $O(\log n)$ w.h.p., but a running time of n^c would not be $O(n)$ w.h.p. since c might also be 50.
- This definition is very powerful, as any polynomial (in n) number of statements that hold w.h.p. also holds w.h.p. at the same time, regardless of any dependencies between random variables!

Theorem 3.4. *The diameter of the augmented grid with $\alpha = 0$ is $O(\log n)$ with high probability.*

Proof Sketch. For simplicity, we will only show that we can reach a node w starting from some node v. However, it can be shown that (essentially) each of the intermediate claims holds with high probability, which then by means of the union bound yields that *all* of the claims hold simultaneously with high probability for *all* pairs of nodes.

Let N_g be the $\lceil \log n \rceil$-hop neighborhood of v on the grid, containing $\Omega(\log^2 n)$ nodes. Each of the nodes in N_g has a random link, probably leading to distant parts of the graph. As long as we have reached only $o(n)$ nodes, any new random link will with probability $1 - o(1)$ lead to a node for which none of its grid neighbors has been visited yet. Thus, in expectation we find almost $|N_g|$ new nodes whose neighbors are "fresh". Using their grid links, we will reach $(4 - o(1))|N_g|$ more nodes within one more hop. If bad luck strikes, it could still happen that many of these links lead to a few nodes, already visited nodes, or nodes that are very close to each other. But that is very unlikely, as we have lots of random choices! Indeed, it can be shown that not only in expectation, but with high probability $(5 - o(1))|N_g|$ many nodes are reached this way.

Because all these shiny new nodes have (so far unused) random links, we can repeat this reasoning inductively, implying that the number of nodes grows by (at least) a constant factor for every two hops. Thus, after $O(\log n)$ hops, we will have reached $n/\log n$ nodes (which is still small compared to n). Finally, consider the expected number of links from these nodes that enter the $(\log n)$-neighborhood of some target node w with respect to the grid. Since this neighborhood consists of $\Omega(\log^2 n)$ nodes, in expectation $\Omega(\log n)$ links come close enough to w. This is large enough to almost guarantee that this happens. Summing everything up, we still used merely $O(\log n)$ hops in total to get from v to w.

□

This shows that for $\alpha = 0$ (and in fact for all $\alpha \leq 2$), the resulting network has a small diameter. Recall however that we also wanted the network to be navigable. For this, we consider a simple greedy routing strategy (Algorithm 12).

Algorithm 12 Greedy Routing

1: **while** not at destination **do**
2: go to a neighbor which is closest to destination (considering grid distance only)
3: **end while**

Lemma 3.5. *In the augmented grid, Algorithm 12 finds a routing path of length at most* $2(m-1) \in O(\sqrt{n})$.

Proof. Because of the grid links, there is always a neighbor which is closer to the destination. Since with each hop we reduce the distance to the target at least by one in one of the two grid dimensions, we will reach the destination within $2(m-1)$ steps. □

This is not really what Milgram's experiment promises. We want to know how much the additional random links speed up the process. To this end, we first need to understand how likely it is that two nodes u and v are connected by a random link in terms of n and their distance $d(u,v)$.

Lemma 3.6. *Node u's random link leads to a node v with probability*

- $\Theta(1/(d(u,v)^\alpha m^{2-\alpha}))$ *if* $\alpha < 2$.
- $\Theta(1/(d(u,v)^2 \log n))$ *if* $\alpha = 2$,
- $\Theta(1/d(u,v)^\alpha)$ *if* $\alpha > 2$.

Moreover, if $\alpha > 2$, *the probability to see a link of length at least* d *is in* $\Theta(1/d^{\alpha-2})$.

Proof. For $\alpha \neq 2$, we have that

$$\sum_{w \in V \setminus \{u\}} \frac{1}{d(u,w)^\alpha} \in \sum_{r=1}^{m} \frac{\Theta(r)}{r^\alpha} = \Theta\left(\int_{r=1}^{m} \frac{1}{r^{\alpha-1}}\, dr\right) = \Theta\left(\left[\frac{r^{2-\alpha}}{2-\alpha}\right]_1^m\right).$$

If $\alpha < 2$, this gives $\Theta(m^{2-\alpha})$, if $\alpha > 2$, it is in $\Theta(1)$. If $\alpha = 2$, we get

$$\sum_{w \in V \setminus \{u\}} \frac{1}{d(u,w)^\alpha} \in \sum_{r=1}^{m} \frac{\Theta(r)}{r^2} = \Theta(1) \cdot \sum_{r=1}^{m} \frac{1}{r} = \Theta(\log m) = \Theta(\log n).$$

Multiplying with $d(u,v)^\alpha$ yields the first three bounds.

For the last statement, compute

$$\sum_{\substack{w \in V \\ d(u,v) \geq d}} \Theta(1/d(u,v)^\alpha) = \Theta\left(\int_{r=d}^{m} \frac{r}{r^\alpha}\, dr\right) = \Theta\left(\left[\frac{r^{2-\alpha}}{2-\alpha}\right]_d^m\right) = \Theta(1/d^{\alpha-2}).$$

□

Remarks:

- For $\alpha \neq 2$, this is bad news for the greedy routing algorithm, as it will take $n^{\Omega(1)} = m^{\Omega(1)}$ expected steps to reach the destination. This is disappointing, we were hoping for something polylogarithmic.
- If $\alpha < 2$, in distance $m^{(2-\alpha)/3}$ to the target are $m^{2(2-\alpha)/3}$ many nodes. Thus it takes $\Theta(m^{(2-\alpha)/3})$ links in expectation to find a link that comes that close to the destination. Without finding such a link, we have to go at least this far using grid links only.

- If $\alpha > 2$, it takes $\Theta(m^{(\alpha-2)/(\alpha-1)})$ steps until we see a link of length at least $m^{1/(\alpha-1)}$ in expectation. Without such links, it takes at least $m/m^{1/(\alpha-1)} = m^{(\alpha-2)/(\alpha-1)}$ steps to travel a distance of m.
- Any algorithm that uses only the information on long-range contacts that it can collect at the so far visited nodes cannot be faster.
- However, the case $\alpha = 2$ looks more promising.

Definition 3.7 (Phase)**.** *Consider routing from a node u to a node v and assume that we are at some intermediate node w. We say that we are in phase j at node w if the lattice distance $d(w, v)$ to the target node v is between $2^j < d(w, v) \leq 2^{j+1}$.*

Remarks:

- Enumerating the phases in decreasing order is useful, as notation becomes less cumbersome.
- There are $\lceil \log m \rceil \in O(\log n)$ phases.

Lemma 3.8. *Assume that we are in phase j at node w when routing from u to v. The probability for getting to phase $j-1$ in one step is at least $\Omega(1/\log n)$.*

Proof. Let B_j be the set of nodes x with $d(x, v) \leq 2^j$. We get from phase j to phase $j-1$ if the long-range contact of node w points to some node in B_j. Note that we always make progress while following the greedy routing path. Therefore, we have not seen node w before and the long-range contact of w points to a random node that is independent of anything seen on the path from u to w.

For all nodes $x \in B_j$, we have $d(w, x) \leq d(w, v) + d(x, v) \leq 2^{j+1} + 2^j < 2^{j+2}$. Hence, for each node $x \in B_j$, the probability that the long-range contact of w points to x is $\Omega(1/2^{2j+4} \log n)$. Further, the number of nodes in B_j is at least $(2^j)^2/2 = 2^{2j-1}$. Hence, the probability that some node in B_j is the long range contact of w is at least

$$\Omega\left(|B_j| \cdot \frac{1}{2^{2j+4} \log n}\right) = \Omega\left(\frac{2^{2j-1}}{2^{2j+4} \log n}\right) = \Omega\left(\frac{1}{\log n}\right). \qquad \square$$

Theorem 3.9. *Consider the greedy routing path from a node u to a node v on an augmented grid with parameter $\alpha = 2$. The expected length of the path is $O(\log^2 n)$.*

Proof. We already observed that the total number of phases is $O(\log n)$ (the distance to the target is halved when we go from phase j to phase $j-1$). At each point during the routing process, the probability of proceeding to the next phase is at least $\Omega(1/\log n)$. Let X_j be the number of steps in phase j. Because the probability for ending the phase is $\Omega(1/\log n)$ in each step, in expectation we need $O(\log n)$ steps to proceed to the next phase, i.e., $\mathbb{E}[X_j] \in O(\log n)$. Let $X = \sum_j X_j$ be the total number of steps of the routing process. By linearity of expectation, we have

$$\mathbb{E}[X] = \sum_j \mathbb{E}[X_j] \in O(\log^2 n). \qquad \square$$

3.2 Propagation Studies

In networks, nodes may influence each other's behavior and decisions. There are many applications where nodes influence their neighbors, e.g. they may impact their opinions, or they may bias what products they buy, or they may pass on a disease.

On a beach (modeled as a line segment), it is best to place an ice cream stand right in the middle of the segment, because you will be able to "control" the beach most easily. What about the second stand, where should it settle? The answer generally depends on the model, but assuming that people will buy ice cream from the stand that is closer, it should go right next to the first stand.

Rumors can spread astoundingly fast through social networks. Traditionally this happens by word of mouth, but with the emergence of the Internet and its possibilities new ways of rumor propagation are available. People write email, use instant messengers or publish their thoughts in a blog. Many factors influence the dissemination of rumors. It is especially important where in a network a rumor is initiated and how convincing it is. Furthermore the underlying network structure decides how fast the information can spread and how many people are reached. More generally, we can speak of diffusion of information in networks. The analysis of these diffusion processes can be useful for viral marketing, e.g. to target a few influential people to initiate marketing campaigns. A company may wish to distribute the rumor of a new product via the most influential individuals in popular social networks such as Facebook. A second company might want to introduce a competing product and has hence to select where to seed the information to be disseminated. Rumor spreading is quite similar to our ice cream stand problem.

More formally, we may study propagation problems in graphs. Given a graph, and two players. Let the first player choose a seed node u_1; afterwards let the second player choose a seed node u_2, with $u_2 \neq u_1$. The goal of the game is to maximize the number of nodes that are closer to one's own seed node.

In many graphs it is an advantage to choose first. In a star graph for instance the first player can choose the center node of the star, controlling all but one node. In some other graphs, the second player can at least score even. But is there a graph where the second player has an advantage?

Theorem 3.10. *In a two player rumor game where both players select one node to initiate their rumor in the graph, the first player does not always win.*

Proof. See Figure 3.3 for an example where the second player will always win, regardless of the decision the first player. If the first player chooses the node x_0 in the center, the second player can select x_1. Choice x_1 will be outwitted by x_2, and x_2 itself can be answered by z_1. All other strategies are either symmetric, or even less promising for the first player. □

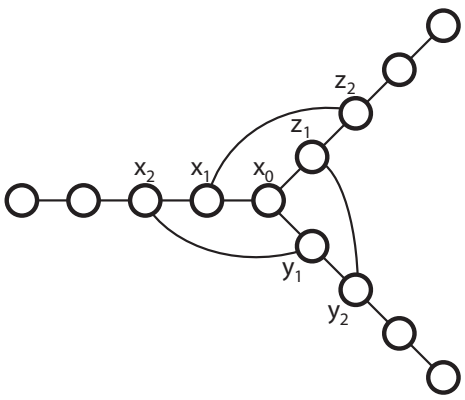

Figure 3.3: Counter example.