Distributed team formation in multi-agent systems: stability and approximation

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Abstract

We consider a scenario in which leaders are required to recruit teams of followers. Each leader cannot recruit all followers, but interaction is constrained according to a bipartite network. The objective for each leader is to reach a state of *local stability* in which it controls a team whose size is equal to a given constraint. We focus on distributed strategies, in which agents have only local information of the network topology and propose a distributed algorithm in which leaders and followers act according to simple local rules. The performance of the algorithm is analyzed with respect to the convergence to a *stable solution*.

Our results are as follows. For any network, the proposed algorithm is shown to converge to an *approximate* stable solution in polynomial time, namely the leaders quickly form teams in which the total number of additional followers required to satisfy all team size constraints is an arbitrarily small fraction of the entire population. In contrast, for general graphs there can be an exponential time gap between convergence to an approximate solution and to a stable solution.

I. INTRODUCTION

A multi-agent system (MAS) is composed of many interacting intelligent agents. Agents can be software, robots, or humans, and the system is highly distributed, as agents do not have a global view of the state and act autonomously of each other. These systems can be used to collectively solve problems that are difficult to solve by a single entity. Their application ranges from robotics, to disaster response, social structures, crowd-sourcing etc. A main feature of MAS is that they can manifest self-organization as well as other complex control paradigms

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even when the individual strategies of the agents are very simple. In short, simple local interaction can conspire to determine complex global behaviors. Examples of such emerging behaviors are in economics and game theory, where local preferences translate into global equilbria [35], in social sciences, where local exposure governs the spread of innovation [41], and in control, where local decision rules determine whether and how rapidly consensus is reached [4], [28], [29], [30], [36], [37].

From a practical perspective, the performance of a MAS often depends on how quickly convergence to a global, possibly approximate, solution is reached and it is in general influenced by the network structure. For example, in the context of information diffusion in social networks, the rate of convergence of the system's dynamics is affected by the underlaying network and the local interaction rules [21], [26].

One of the critical issues in multi-agent systems is coordination. Due to the autonomous behavior of the agents and to the absence of a central controller, coordination must be distributed. In the case of human agents, it is also important that the distributed control algorithm is simple enough to be suitable to model basic principles of human behavior [8]. Two prominent problems related to consensus and coordination in multi-agent systems are leader election and group formation. In the former case, multiple agents elect a leader that can then assign tasks [24], while in the latter they divide themselves into teams in such a way that each agent knows to what team it belongs [11]. In both cases agents are all equal and coordination occurs among agents of a single class.

We consider a scenario in which there are agents of two classes, *leaders* and *followers*. Each leader must recruit a team of followers whose size is equal to a given constraint, by sending requests to the followers. Followers can only accept or reject incoming leaders' requests. While multiple followers can be part of a leader's team, each follower can be part of a single team at any time, but is allowed to change team over time. Moreover, a leader cannot recruit *all* followers, but can only recruit the followers it is in direct communication with. The communication structure between leaders and followers is captured by an arbitrary bipartite network, and we assume that each agent has knowledge of and can interact with its neighbors only. That is, agents only have local knowledge of the underlying network. In general, the communication constraints of the population (and therefore the structure of the bipartite network) can be dictated by physical constraints (as for example antenna visibility range or signal to noise ratio threshold), social

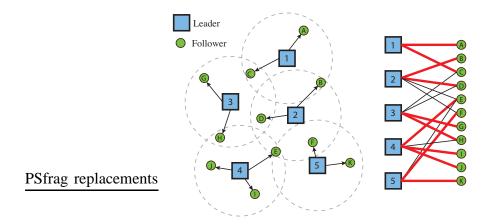


Fig. 1. Example of a bipartite network between leaders and followers determined by physical constraints. Left: each leader can only recruit the followers in its visibility range (dotted circle), arrows represent team membership, and the set of arrows defines a partition of the followers into teams.

Right: the resulting bipartite network. An edge between leader ℓ and follower f exists if and only if f is in ℓ 's visibility range. Matching edges define team membership and are highlighted.

context, and so on. A pictorial representation of a bipartite network arising from physical constraints is given in Figure 1.

We consider a notion of stability in which each agent controls a team of adequate size. Each leader has an incentive to reach *local* stability (that is, to build a team of followers of the right size) by dynamically interacting with its neighbors. The question we aim to answer is: can simple local rules lead to stable, or *close* to stable, team formation in reasonable time? By "close to stable" we mean that the total number of additional followers required to satisfy all team size constraints is an arbitrary small fraction of the entire population. We propose a simple, distributed, memoryless algorithm in which leaders do not communicate between each other, and we show that, in any network of size n, any constant approximation of a stable outcome (or of a suitably defined *best* outcome if a stable one does not exist) is reached in time polynomial in n with high probability. In contrast, for general graphs we show through a counterexample that there can be an exponential gap between the time needed to reach stability and that needed to reach approximate stability, that is, to find the *best* solution compared to a *good* solution. We remark that, in its simplicity, the proposed algorithm is suitable to model human agents, it can be programmed on simple robots with limited computation abilities, and it is amenable to

analysis.

The rest of the paper is organized as follows. After discussing how our work relates to the existing literature, in Section II we formally define the problem and the notions of stability and approximate stability, in Section III we present the distributed algorithm for leaders and followers, in Sections IV and V we present our technical results on the algorithm's performance, and in Section VI we further discuss the algorithm's performance by showing some simulations' results. To prove our result on the convergence to approximate stability, we derive a technical lemma (Lemma 1) that relates the quality of a matching to the existence of particular paths (that we call *deficit-decreasing* paths) of given length. The lemma extends a known combinatorial result by Hopcroft and Karp [15] to the setup of many-to-one matching, and can be considered to be of independent interest.

A. Related work

The problem of team formation that we consider is an example of distributed many-toone matching in bipartite networks [2], [14], [34]. The one-to-one case has been previously studied in the context of theoretical computer science [23] [32]. In the control literature, our work is related to the distributed assignment problem and to group formation in MAS. In this framework, Moore and Passino [27] proposed a variant of the distributed auction algorithm for the assignment of mobile agents to tasks. Cenedese et al. [6] proposed a variant of the Stable Marriage algorithm [12] to solve the distributed task assignment problem. Abdallah and Lesser [1] proposed an "almost" distributed algorithm for coalition formation, allowing for a special agent with the role of "manager". Gatson and den Jardins [13] studied a scenario of group formation where agents can adapt to the network structure. Tosic and Agha [39] proposed an algorithm for group formation based on the distributed computation of maximal cliques in the underlying network. Further work studied team formation in multi-robot systems [40], in the case where communication between agents is not allowed [3]. Other authors considered MAS composed by leaders and followers. To cite a few, Tanner [38] derived a necessary and sufficient condition for a group of interconnected agents to be controllable by one of them acting as a leader; Rahmani et al. [33] studied the controlled agreement problem in networks in which certain agents have leader roles, translating graph-theoretic properties into control-theoretic properties; Pasqualetti et al. [31] analyzed the problem of driving a group of mobile agents, represented by a network of leaders and followers, in which follower act according to a simple consensus rule.

We distinguish ourselves from all mentioned papers, as we propose a fully distributed algorithm for group formation on arbitrary networks in which agents act according to simple local rules and perform very limited computation, and we derive performance guarantees in the form of theorems. For an exhaustive overview on distributed algorithms in multi-agent systems, the interested reader is referred to the books by Lynch [24] and by Bullo et al. [5] and the references therein, while the survey by Horling and Lesser [16] offers an overview on three decades of research on organizational paradigms as team and coalition formation.

A more recent line of research aims to study how humans connected over a network solve tasks in a distributed fashion [8], [10], [17], [19], [20], [25]. In the work of Kearns et al. [20], human subjects positioned at the vertices of a virtual network were shown to be able to collectively reach a coloring of the network, given only local information about their neighbors. Similar papers further investigated human coordination in the case of coloring [10], [17], [25] and consensus [17], [19], with the main goal of characterizing how performance is affected by the network's structure. Using experimental data of maximum matching games performed by human subjects in a laboratory setting, Coviello et al. [8] proposed a simple algorithmic model of human coordination that allows complexity analysis and prediction.

Finally, related to our work is also the research on social exchange networks [7], [22], that considers a networked scenario in which each edge is associated to an economic value, nodes have to come to an agreement on how to share these values, and each agent can only finalize a single mutual exchange with a single neighbor. Recently, Kanoria et al. [18] proposed a distributed algorithm that reaches approximate stability in linear time. However, we consider a different setup since we allow leaders to build teams of multiple followers.

II. PROBLEM FORMULATION

We consider a population composed of agents of two different classes: leaders and followers. Each leader is required to recruit a team of followers whose size is equal to a given constraint, by sending requests to the followers. Followers can only accept or reject leaders' requests. While multiple followers can be in a leader's team, each follower can be part of a single team at a time, but is allowed to change team over time. A leader is not allowed to recruit *all* followers, but can only recruit the followers it is in direct communication with. The communication constraints of the population are captured by a bipartite network $G = (L \cup F, E)$ whose nodes' partition is given by the set *L* of leaders and the set *F* of followers, and where there exists an edge $(f, \ell) \in E$ between follower *f* and leader ℓ if and only if *f* and ℓ can communicate between each other (see Figure 1). Let $N_{\ell} = \{f \in F : (f, \ell) \in E\}$ be the neighborhood of $\ell \in L$. For each $\ell \in L$, leader ℓ is required to recruit a team of c_{ℓ} followers, where $c_{\ell} \ge 1$.

Definition 1 (Matching): A subset $M \subseteq E$ is a matching of G if for each $f \in F$ there exists at most a single $\ell \in L$ such that $(\ell, f) \in M$.

The definition of matching is consistent with the fact that multiple followers can be part of a leader's team. There is a one-to-one correspondence between matchings M of G and tuples of teams $\{T_{\ell}(M) : \ell \in L\}$, where $T_{\ell}(M)$ denotes the team of leader ℓ under the matching M. We have that $T_{\ell}(M) = \{f \in F : (\ell, f) \in M\} \subseteq N_{\ell}$ for every matching M. We consider the following notion of stability.

Definition 2 (Stable matching): Given constraints c_{ℓ} for each $\ell \in L$, a matching M of G is stable if and only if $|T_{\ell}(M)| = c_{\ell}$ for all $\ell \in L$.

Depending on the constraints c_{ℓ} , a network G might not admit a stable matching. Nonetheless, given a matching of G, we are interested in assessing its *quality*. Our main result builds on the following definitions of *deficit* of a leader and deficit of a matching.

Definition 3 (Deficit of a leader): Let ℓ be a leader with constraint $c_{\ell} \ge 1$, and M be a matching of G. The deficit of ℓ under the matching M is

$$d_{\ell}(M) = c_{\ell} - |T_{\ell}(M)|.$$

Definition 4 (Deficit of a matching): Given constraints $c_{\ell} \ge 1$ for each $\ell \in L$, the deficit of a matching *M* of *G* is

$$d(M) = \sum_{\ell \in L} d_\ell(M) = \sum_{\ell \in L} \left(c_\ell - |T_\ell(M)| \right).$$

In words, $d_{\ell}(M)$ is the number of additional followers leader ℓ needs to satisfy its size constraint. Similarly, d(M) sums the numbers of additional followers each leader needs to satisfy its size constraint. Given a matching M, we say that a leader ℓ is *poor* if $d_{\ell}(M) > 0$ (that is, $|T_{\ell}(M)| < c_{\ell}$) and *stable* if $|T_{\ell}(M)| = c_{\ell}$. In this work, we do not consider the case of $|T_{\ell}(M)| > c_{\ell}$ since we assume that each leader ℓ never recruits more than c_{ℓ} followers simultaneously. This can be justified by the fact that recruiting additional followers might be costly.

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Given G, two matchings of G can be compared with respect to their deficit, and the best matching of G can be defined as one minimizing the deficit.

Definition 5 (Best matching): A matching M of G is a best matching of G if $d(M) \le d(M')$ for every matching M' of G.

Observe that a stable matching is also a best matching. Moreover, if G admits a stable matching, d(M) quantifies how much M differs from a stable matching of G. In general, if M^* is a best matching of G with $d(M^*) = d^*$, then, $d(M) - d^*$ tells how much M differs from a best matching of G. Given a matching M of G, the following definition provides a measure of how well M approximates a best matching of G.

Definition 6 (Approximate best matching): Fix $\varepsilon \in [0, 1]$, and let m be the number of followers in G. Let M^* be a best matching of G. Then, a matching M is a $(1-\varepsilon)$ -approximate best matching of G if $d(M) - d(M^*) < \varepsilon m$.

When G admits a stable matching, we are interested in the notion of approximate stable matching.

Definition 7 (Approximate stable matching): Let G admit a stable matching. Fix $\varepsilon \in [0, 1]$, and let m be the number of followers in G. Then, a matching M is a $(1 - \varepsilon)$ -approximate stable matching of G if $d(M) < \varepsilon m$.

III. The algorithm

We now present a distributed algorithm for team formation. Time is divided into rounds, and each round is composed by two stages. In the first stage, each leader acts according to the algorithm in Table 1, and in the second stage each follower acts according to the algorithm in Table 2.

First consider a leader ℓ , and let M be the matching at the beginning of a given round. If ℓ is poor (that is, $|T_{\ell}(M)| < c_{\ell}$) and $|T_{\ell}(M)| < |N_{\ell}|$ (that is, ℓ is not already matched with all followers in N_{ℓ}) then, with probability p (where $p \in (0, 1]$ is a fixed constant), ℓ attempts to recruit an additional follower, chosen as explained below, by sending a matching request. An unmatched follower in N_{ℓ} , if any, is chosen uniformly at random; otherwise, a follower in $N_{\ell} \setminus T_{\ell}(M)$ is chosen uniformly at random. In other words, leaders always prefer to recruit followers that are currently unmatched over matched ones. Note that a leader tries to recruit an additional follower after checking if *local stability* holds (that is, after checking if its team size is equal to c_{ℓ}).

Consider now a follower f. During each round, if f has incoming requests then each request is rejected independently of the others with probability 1 - q (where $q \in (0, 1]$ is a fixed constant). If all incoming requests are rejected, then f does not change team (if currently matched) or it remains unmatched (if currently unmatched). Otherwise, one among the active requests is chosen uniformly at random, f joins the corresponding leader, and all the other requests are discarded. For ease of presentation, we assume that a follower is equally likely to join a team when unmatched and to change team when currently matched, but all our results hold if we consider different values of q for matched and unmatched followers (and even if we consider a different value of q for each follower, as long as each value is a constant).

Table 1 Algorithm for leader $\ell \in L$
if $ T_{\ell}(M) < \min\{c_{\ell}, N_{\ell} \}$ then
with probability p do the following
if \exists unmatched $f \in N_{\ell}$ then
choose an unmatched follower $f' \in N_{\ell}$ u.a.r.
else
choose a follower $f' \in N_{\ell} \setminus T_{\ell}(M)$ u.a.r.
end if
send a matching request to f'
end if

The proposed algorithm enjoys several properties. It is memoryless, the actions of each agent only depend on local information, and the leaders do not communicate between each other. Also, it is *self-stabilizing*, that is, once a stable matching is reached, leaders stop recruiting followers. Moreover, it is a single-stage algorithm, that is, agents never change their behavior until stability is reached. Finally, observe that the exchanged messages can be represented by a single bit.

IV. CONVERGENCE TO APPROXIMATE STABLE MATCHINGS

In this section, we only consider networks admitting stable matchings, and we show that, given any network and any constant $\varepsilon \in (0, 1)$, a $(1 - \varepsilon)$ -approximate stable matching is reached in a

Table 2 Algorithm for follower $f \in F$
if f has incoming requests then
for each leader ℓ requesting f do
with probability $1 - q$ reject ℓ 's request
end for
if there are active requests then
select one u.a.r. and join the corresponding team
reject all other requests
end if
end if

number of rounds that is polynomial in the network size with high probability. The assumption that a stable matching exists is for ease of presentation, and all our results also hold for reaching approximate best matchings, by replacing d(M) with $d(M) - d(M^*)$, where M^* is a best matching of *G*.

Given a network G, for every $t \ge 0$, let M(t) be the matching of G at the beginning of round t, with deficit d(M(t)). The next property follows from the fact that leaders do not voluntarily disengage from the followers in their teams (and therefore the deficit of a leader increases of a unit only if the deficit of another leader decreases by one unit).

Property 1: For $t \ge 0$, d(M(t)) is non-increasing in t.

The next property follows from the assumption $c_{\ell} \ge 1, \forall \ell$.

Property 2: If G admits a stable matching, then $d(M(t)) \le m$ for every $t \ge 0$.

We are now ready to state our main result.

Theorem 1: Let G be a network with m followers and which admits a stable matching. Let $\Delta = \max_{\ell \in L} |N_{\ell}|$ be the maximum degree of the leaders. Fix $0 < \varepsilon < 1$, and let $c \ge 1 + \frac{1}{m(1-\varepsilon)}$. Then, a $(1 - \varepsilon)$ -approximate stable matching of G is reached within $c \lfloor 1/\varepsilon \rfloor (\Delta/pq)^{\lfloor 1/\varepsilon \rfloor} m$ rounds of the algorithm with probability at least $1 - e^{-cm\varepsilon^2/2}$.

Example 1: If Δ is constant in the network size, then one can choose $\varepsilon = 1/\log m$, and Theorem 1 implies that a $(1 - 1/\log m)$ -approximate stable matching is reached in at most $O(m^2 \log m)$ rounds with probability that goes to one as $m \to \infty$.

To prove Theorem 1, we introduce the notion of *deficit-decreasing* path, that in our setup

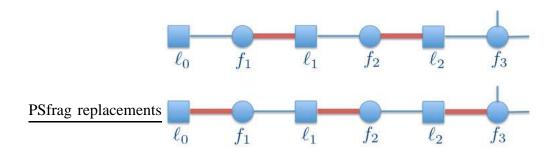


Fig. 2. A deficit-decreasing path of length 5 is represented at the top of the figure: ℓ_0 is a poor leader, f_3 is an unmatched follower, and matching edges are highlighted. The path is "solved" by turning each matched edge into an unmatched edge and vice versa, as show at the bottom of the figure: ℓ_0 obtains an additional follower (and therefore its deficit decreases by a unit) and both ℓ_1 and ℓ_2 do not change their numbers of followers.

plays the same role as the augmenting path in the context of one-to-one matching [9]. Since we consider bipartite networks, a path alternates leaders and followers.

Definition 8 (Deficit-decreasing path): Given a matching M of G, a cycle-free path $P = \ell_0, f_1, \ell_1, \ldots, f_k$ (of odd length 2k-1) is a deficit-decreasing path relative to M if $(\ell_i, f_i) \in M$ for all $1 \le i \le k - 1$, ℓ_0 is a poor leader, and f_k is an unmatched follower.

In words, a deficit-decreasing path starts at a poor leader with an edge not in M, ends at a follower that is not matched, and alternates edges in M and edges not in M. To justify the nomenclature, observe that, if d(M) > 0 and P is a deficit-decreasing path relative to M, a new matching M' such that d(M') = d(M) - 1 can be obtained by flipping each unmatched edge of P into a matched edge, and vice versa. This is depicted in Fig. 2.

The proof of Theorem 1 builds on a technical lemma that, given a matching M with $d(M) \ge \varepsilon m$, guarantees the existence of a deficit-decreasing path of length at most $2\lfloor 1/\varepsilon \rfloor$. The existence of such a path allows us to bound the number of rounds needed for a one-unit reduction of the deficit. Our technical lemma extends a known result by Hopcroft and Karp [15, Theorem 1] given in the context of one-to-one matching, but our proof is more subtle because leaders can be matched to multiple followers and can have different size constraints c_ℓ . The symmetric difference of two sets A and B is defined as $A \oplus B = (A \setminus B) \cup (B \setminus A)$. Two paths are *follower-disjoint* if they do not share any follower (even though they might share some leader).

Lemma 1: Let G admit a stable matching N. Let M be a matching of G with deficit d(M) > 0. Then, in $M \oplus N$ there are at least d(M) follower-disjoint deficit-decreasing paths relative to M. Proof: See Appendix A.

We make use of Lemma 1 through the following corollary.

Corollary 1: Let G be a network with m followers, admitting a stable matching N. Let M be a matching of G with deficit $d(M) \ge \varepsilon m$, for some $\varepsilon > 0$. Then, in $M \oplus N$ there exists a deficit-decreasing path relative to M of length at most $2\lfloor 1/\varepsilon \rfloor - 1$.

Proof: By Lemma 1, if $d(M) \ge \varepsilon m$ and N is a stable matching of G, then in $M \oplus N$ we can choose εm follower-disjoint deficit-decreasing paths relative to M, whose cumulative length is at most 2m (since they do not share followers and G is bipartite). Necessarily, one of them has length at most $2\lfloor 1/\varepsilon \rfloor - 1$ (note that a deficit-decreasing path has odd length).

We are now ready to present the proof of Theorem 1.

A. Proof of Theorem 1

Let *G* be a network with *m* followers and which admits a stable matching. Fix $0 < \varepsilon < 1$. For $t \ge 0$, M(t) denotes the matching at the beginning of round *t*. For every $0 < x \le 1$, let

$$\tau(x) = \min\left\{t \ge 0 : d(M(t)) < xm\right\}$$

be the first round at whose beginning the deficit is strictly smaller than *xm*. We are interested in bounding $\tau(\varepsilon)$.

Consider any round $t \ge 0$. By Property 2, $d(M(t)) \le m$, and therefore there exists $0 < \varepsilon' \le 1$ such that $d(M(t)) = \varepsilon'm$ (we assume $\varepsilon' > 0$, since the case of $\varepsilon' = 0$ is trivial). The following lemma bounds the number of rounds $\tau(\varepsilon') - t$ needed for a one-unit reduction of the deficit. Let $\Delta = \max_{\ell \in L} |N_{\ell}|$ be the maximum degree of the leaders in *G*.

Lemma 2: Let $d(M(t)) = \varepsilon' m$ for some $0 < \varepsilon' \le 1$. Then

$$\Pr\left(\tau(\varepsilon') - t \le \lfloor 1/\varepsilon' \rfloor\right) \ge \left(\frac{pq}{\Delta}\right)^{\lfloor 1/\varepsilon' \rfloor}.$$

Proof: Let $h(t) \ge 1$ be the odd length of the shortest deficit-decreasing path relative to M(t). By Corollary 1, $h(t) \le 2\lfloor 1/\varepsilon' \rfloor - 1$. We distinguish the cases of h(t) = 1 and $h(t) \ge 3$.

First consider h(t) = 1. With probability at least pq/Δ the deficit decreases by at least one unit during the next round of the algorithm. Too see this, consider a deficit-decreasing path ℓ , f. With probability at least p/Δ , ℓ attempts to recruit f and, conditional on this event, f considers ℓ 's proposal with probability q, resulting in the lower bound pq/Δ .

Now consider $h(t) \ge 3$, and let P be a shortest deficit-decreasing path of length h(t) ending at an unmatched follower f. By the same argument as above, the length of P decreases by one during the next round with probability at least pq/Δ (observe that, as long as h(t) > 1, f remains unmatched during round t since P is a deficit decreasing path of shortest length).

By independence of successive rounds of the algorithm and the bound $h(t) \le 2\lfloor 1/\varepsilon' \rfloor - 1$, with probability at least $(pq/\Delta)^{\lfloor 1/\varepsilon' \rfloor}$, a sequence of $\lfloor 1/\varepsilon' \rfloor - 1$ rounds reduces the length of *P* to 1 and then in one additional round *P* gets "solved" and the deficit decreases by one unit.

Consider consecutive phases of $\lfloor 1/\varepsilon \rfloor$ rounds each. For phases i = 0, 1, 2, ..., let X_i be *iid* Bernoulli random variables with $Pr(X_i = 1) = (pq/\Delta)^{\lfloor 1/\varepsilon \rfloor}$. By Lemma 2, after *T* phases (i.e., at the beginning of round $t^* = T\lfloor 1/\varepsilon \rfloor$), the deficit of the matching is upper bounded by

$$d(M(t^*)) < \max\left\{\varepsilon m, m+1 - \sum_{i=1}^T X_i\right\},\,$$

since by Property 2 the matching at the beginning of round 0 has deficit $d(M(0)) \le m$. By independence of the phases, a Chernoff bound implies that for any $0 < \delta \le 1$

$$\Pr\Big(\sum_{i=1}^{T} X_i < (1-\delta)T(pq/\Delta)^{\lfloor 1/\varepsilon \rfloor}\Big) < e^{-T(pq/\Delta)^{\lfloor 1/\varepsilon \rfloor}\delta^2/2}.$$

Setting $\delta = \varepsilon$ and $T = cm(\Delta/pq)^{\lfloor 1/\varepsilon \rfloor}$ (where *c* is a constant to be specified later), the deficit of the matching at the beginning of round $t^* = \lfloor 1/\varepsilon \rfloor cm(\Delta/pq)^{\lfloor 1/\varepsilon \rfloor}$ is upper bounded by

$$d(M(t^*)) < \max \{\varepsilon m, m+1 - (1-\varepsilon)cm\}$$

with probability at least $1 - e^{-cm\varepsilon^2/2}$. To conclude the proof of the theorem we need that $\varepsilon m \ge m + 1 - (1 - \varepsilon)cm$, which is true for any $c \ge 1 + \frac{1}{m(1-\varepsilon)}$.

V. EXPONENTIAL CONVERGENCE

Theorem 1 gives a polynomial bound for reaching a $(1 - \varepsilon)$ -approximate stable matching for any constant $0 < \epsilon < 1$ and any network. However, a similar guarantee cannot be derived for the case of a stable matching, as shown in this section through a counterexample. In particular, we define a sequence of networks of increasing size and maximum degree that diverges with the network size, and show that the number of rounds required to converge from an approximate matching *M* with d(M) = 1 to the stable matching (that is, to reduce the deficit of a single unit) is exponentially large in the network's size with high probability from an overwhelming fraction of the approximate matchings M such that d(M) = 1.

For $n \ge 1$, let $G_n = (L_n \cup F_n, E_n)$ be the network with *n* leaders and *n* followers (i.e., $L_n = \{\ell_1, \ldots, \ell_n\}$ and $F_n = \{f_1, \ldots, f_n\}$), with edges $E_n = \{(\ell_i, f_j) : 1 \le i \le n, j \le i\}$, and team size constraints $c_\ell = 1$ for all $\ell \in L_n$, see Figure 3. G_n has maximum degree *n* and a unique stable matching given by $M_n^* = \{(\ell_i, f_i) : 1 \le i \le n\}$.



Fig. 3. The network G_n for n = 6. The matching M'_n is highlighted.

Theorem 2: For any matching M of G_n , let $\tau^*(M)$ denote the number of rounds to converge to the perfect matching when starting from M. Then, for any fixed constant $0 < \gamma < 1$, $\tau^*(M)$ is exponentially large in γn with high probability for a $1 - O(n2^{-(1-\gamma)n})$ fraction of all the matchings M such that d(M) = 1.

Here we only provide a sketch of the proof, whose details are presented in Appendix B. To get an understanding of the algorithm's dynamics, consider the matching

$$M'_{n} = \{ (\ell_{i}, f_{i-1}) : 2 \le i \le n \},\$$

highlighted in Figure 3 for the case of n = 6. Observe that $d(M'_n) = 1$ and, under M'_n , ℓ_1 is poor, and the remaining leaders are stable. According to the algorithm, ℓ_1 attempts to recruit f_1 (currently in ℓ_2 's team). If f_1 accepts, then ℓ_1 becomes stable and ℓ_2 becomes poor (and can in turn attempt to recruit either f_1 or f_2). After each round, there exists a unique poor leader until the stable matching is reached. The stable matching is reached when ℓ_{n-1} (ℓ_5 in Figure 3) becomes poor and then successfully recruits f_{n-1} (f_5 in Figure 3), and finally ℓ_n successfully recruits f_n (recall that leaders prefer unmatched followers). In general, fix any matching M of G_n such that d(M) = 1. In M, there is a single poor leader ℓ_{i_0} and a single unmatched follower f_{i_K} . M is associated to a unique deficit-decreasing path $\ell_{i_0}, f_{i_0}, \ldots, \ell_{i_{K-1}}, f_{i_{K-1}}, \ell_{i_K}, f_{i_K}$. We define the *height* h(M) of M as follows. If $K \ge 1$ then $h(M) = i_{K-1}$, if K = 0 then h(M) = 0.

Starting from *M*, for every $t < \tau(M)$, the matching M(t) at the beginning of round *t* has deficit d(M(t)) = 1 (by Property 1), a single poor leader denoted by $\ell_{i(t)}$, the single unmatched follower f_{i_K} and height $h(M(t)) = h(M) = i_{K-1}$. The stochastic process $\{i(t)\}$ tracking the position of the poor leader $\ell_{i(t)}$ is not a classical random walk on $\{\ell_1, \ldots, \ell_{i_K}\}$ and its transition probabilities at each round depend on the current matching. The time to reach stability is upper bounded by $\min\{t : i(t) = h(M)\}$, that is, the first round in which $\ell_{h(M)}$ becomes poor (since $\ell_{h(M)}$ can then match with $f_{h(M)}$ leaving ℓ_{i_K} poor, who would in turn match with the unmatched follower f_{i_K} , thus reaching the stable matching).

We prove a one-to-one correspondence between the matchings M(t) reachable from M in which $i(t) \le h(M)$ (note that d(M(t)) = 1 for each of them) and the nodes of a tree whose size is exponentially large in the height h(M). In particular, we can show that the process $\{M(t) : t \ge 0, M(0) = M\}$ is equivalent to a classical random walk on the nodes of the tree, and that reaching the matching with i(t) = h(M) corresponds to reaching the root of the tree. A random walk starting at any node of the tree visits the root after a number of steps that is exponentially large in the height h(M) with high probability. Finally, the proof of Theorem 2 is completed by arguing that, for any constant $0 < \gamma < 1$, a $1 - O(n2^{-(1-\gamma)n})$ fraction of all matchings M of G_n such that d(M) = 1 have height $h(M) \ge \gamma n$.

VI. SIMULATIONS

In this section, the performance of our algorithm is further evaluated through simulation. In Figure 4, the algorithm's average convergence time on the sequence of networks G_n defined in Section V is shown (in logarithmic scale). On the one hand, the thick solid line suggests that the average number of rounds to reach a 0.9-approximate stable matching is upper bounded by a polynomial of small degree, consistently with Theorem 1. On the other hand, convergence to the stable matching requires an average number of rounds that grows exponentially in n (thin solid line), as predicted by Theorem 2. Moreover, the dotted line represents the average time after which all followers become matched, that grows slowly with n.

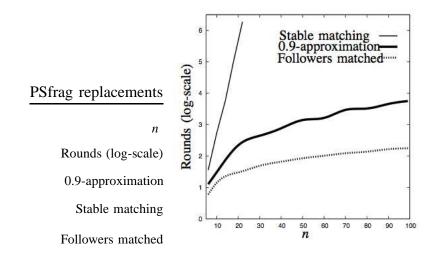


Fig. 4. Algorithm's convergence time on the sequence of networks G_n .

Figure 5 shows the algorithm's performance in reaching successively finer approximations of the best matching on random networks $G(n, m, \rho)$. Here, $G(n, m, \rho)$ refers to a random bipartite network with *n* leaders and *m* followers, in which each edge exists independently of the others with probability ρ (we fixed $\rho = 0.04$), and with constraint $c_{\ell} = \min\{m/n, |N_{\ell}|\}$ for each leader ℓ . For each of the (n, m) pairs that we considered, 20 random $G(n, m, \rho)$ were generated, and the algorithm was run 20 times on each. We observe that, consistently with Theorem 1, $\tau(\varepsilon)$ increases both when ε decreases (i.e., when a finer approximation is desired) and when the number *m* of followers increases. The plot visually suggests that a good solution is reached quickly, while most of the time is spent in the attempt of improving it to the best solution.

VII. DISCUSSION

The distributed algorithm we proposed, in which leaders and followers act according to simple local rules, is computationally tractable and allows us to derive performance guarantees in the form of theorems. Despite its simplicity, the algorithm is shown to reach an arbitrarily close approximation of a stable matching (or of a best matching) in polynomial time in any network. However, in general there can be an exponential gap between reaching an approximate solution and a stable solution.

In the proposed algorithm, leaders do not communicate between each other, and only act in response to their own status and the status of their neighborhoods. The only collaboration between

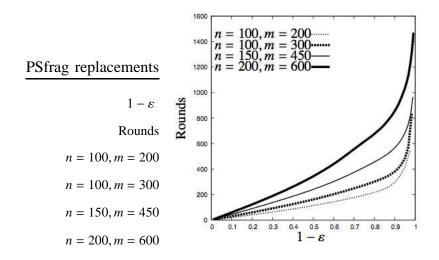


Fig. 5. Algorithm's average time to reach a $(1 - \varepsilon)$ -approximate best matching on random bipartite networks $G(n, m, \rho)$, for $\rho = 0.04$.

them consists in the fact that the leaders whose size constraints are satisfied do not attempt to recruit additional matched followers, and this is justified since recruiting more followers might be costly. How communication between leaders affects performance is an open question, as well as determining what amounts of communication and complexity are necessary to remove the exponential gap in the case of unbounded degree networks.

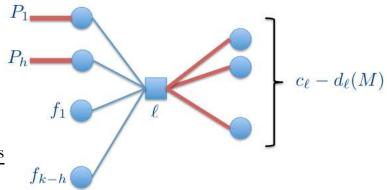
Finally, in Section V, we defined a sequence of networks in which the maximum degree of the leaders scales linearly with the network size. It would be interesting to understand whether a counterexample in which the maximum degree scales more slowly (e.g., logarithmically in the network size) could be derived.

Appendix

A. Proof of Lemma 1

Given the matching *M* and the stable matching *N*, for brevity we write deficit-decreasing path instead of deficit-decreasing path in $M \oplus N$ relative to *M*. Similarly, by telling that leader ℓ and follower *f* are matched we mean that $(\ell, f) \in M$, unless otherwise specified.

We prove a stronger claim than the one stated in the lemma, proceeding as follows. First, we show that for each leader ℓ with deficit $d_{\ell}(M) > 0$ there are at least $d_{\ell}(M)$ follower-disjoint deficit-



PSfrag replacements

Fig. 6. A leader ℓ with constraint c_{ℓ} , degree $|N_{\ell}| \ge c_{\ell}$ and deficit $d_{\ell}(M)$. Matched edges are highlighted. ℓ is matched to exactly $c_{\ell} - d_{\ell}(M)$ followers (depicted on the right). Among the other $k \ge d_{\ell}(M)$ followers in N_{ℓ} , h < k of them are the first followers on h follower-disjoint deficit-decreasing paths starting at ℓ (these paths are denoted by P_1, \ldots, P_h), and none of the remaining k - h (denoted by f_1, \ldots, f_{k-h}) is the first follower of a deficit-decreasing paths starting at ℓ .

decreasing paths starting at ℓ . Then, we argue that d(M) follower-disjoint deficit-decreasing paths can be chosen, $d_{\ell}(M)$ of which start at each leader ℓ with deficit $d_{\ell}(M) > 0$.

Consider a leader ℓ with $d_{\ell}(M) > 0$. Assume by contradiction that there are strictly less then $d_{\ell}(M)$ follower-disjoint deficit-decreasing paths starting at ℓ , and refer to Fig. 6 for a schematic representation.

Since ℓ has a team size constraint $c_{\ell} > 0$, there are exactly $c_{\ell} - d_{\ell}(M)$ followers that are matched to ℓ . Observe that no follower matched to ℓ can be the first follower of a deficit-decreasing path starting at ℓ , since a deficit-decreasing path starts with an edge in $N \setminus M$.

Since *G* admits a stable matching, the neighborhood N_{ℓ} of ℓ has size $|N_{\ell}| \ge c_{\ell}$. Therefore, there are are $k \ge d_{\ell}(M)$ followers in N_{ℓ} that are not matched to ℓ . Assume that $h < d_{\ell}(M)$ of the followers in N_{ℓ} are the first followers of *h* follower-disjoint deficit-decreasing paths starting at ℓ (these paths are denoted by P_1, \ldots, P_h in Figure 6). Denote the remaining k - h > 0 followers by f_1, \ldots, f_{k-h} , and assume by contradiction that none among them is the first follower of a deficit-decreasing path starting at ℓ (this is equivalent to assuming that there are strictly less than $d_{\ell}(M)$ follower-disjoint deficit-decreasing paths starting at ℓ).

Observe that, in order to become stable, ℓ needs to match with at least one additional follower among $\{f_1, \ldots, f_{k-h}\}$. We show that, under the assumption above, a one-unit reduction in the deficit of ℓ would eventually result in a one-unit increase of the deficit of another leader, implying that

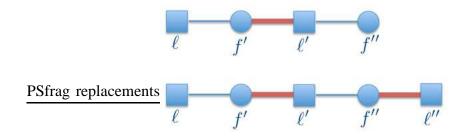


Fig. 7. If f'' is not matched then ℓ, f', ℓ', f'' would be a deficit-decreasing path (shown at the top of the figure, in which matching edges are highlighted), contradicting the assumption that no follower in $\{f_1, \ldots, f_{k-h}\}$ can be the first follower of a deficit-decreasing path starting at ℓ . Therefore, f'' is matched to a leader ℓ'' (the bottom of the figure represents the case of $\ell \neq \ell''$).

G does not admit a stable matching, generating a contradiction.

Consider any follower $f' \in \{f_1, \ldots, f_{k-h}\}$, and observe that f' is matched in M since otherwise $\ell f'$ would be a deficit-decreasing path starting at ℓ . Let ℓ' be the leader such that $(\ell', f') \in M$, and observe that if ℓ' is matched to all followers in $N_{\ell'}$ then ℓ cannot match to f' without causing a one-unit increase of the deficit of ℓ' . Therefore assume that in $N_{\ell'}$ there is a follower f'' such that $(\ell'', f'') \in M$ for some leader $\ell'' \neq \ell'$ (f'' is matched in M since otherwise ℓ, f', ℓ', f'' would be a deficit-decreasing path starting at ℓ , see Fig. 7). In the following two cases ℓ cannot match to f' without eventually increasing the deficit of another leader.

- (i) ℓ" = ℓ. In this case ℓ, f', ℓ', f", ℓ is a cycle, and if ℓ matches to f' then the deficit of a leader in the cycle must increase of one unit.
- (ii) $\ell'' \neq \ell$ and ℓ'' is matched to all followers in $N_{\ell''}$ other than f'. In this case if ℓ matches to f' then the deficit of a leader on the path $\ell, f', \ell', f'', \ell''$ must eventually increase by a unit.

Therefore assume that in $N_{\ell''}$ there is a follower f''' such that $(\ell''', f''') \in M$ for some leader $\ell''' \neq \ell''$ (again, f''' is matched in M since otherwise $\ell, f', \ell', f'', \ell'', f'''$ would be a deficitdecreasing path). Again, ℓ cannot match to f' without eventually increasing the deficit of another leader if either $\ell''' = \ell$ or $\ell''' = \ell'$ (each similar to the case (i) above), or if ℓ''' is matched to all followers in $N_{\ell''}$ other than f', f'' (similar to the case (ii) above).

By iteration, it follows that ℓ cannot match to any follower $f' \in \{f_1, \ldots, f_{k-h}\}$ without eventually increasing the deficit of another leader, in contradiction with the existence of the stable matching *N*. Hence, there are at least $d_{\ell}(M)$ follower-disjoint deficit-decreasing paths starting at ℓ .

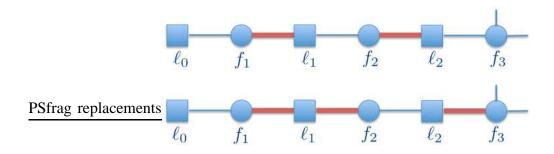


Fig. 8. Given the matching at the top of the figure (matching edges are highlighted), assume that both ℓ_0 and ℓ_1 are poor, and that f_3 is unmatched. The deficit-decreasing paths $P = \ell_0, f_1, \ell_1, f_2, \ell_2, f_3$ and $P' = \ell_0, f_1, \ell_1, f_2$ are not follower-disjoint. If P' is solved (shown at the bottom of the figure), then P is not solved, and vice versa.

To complete the proof of the lemma, we show that we can choose d(M) follower-disjoint deficit-decreasing paths, $d_{\ell}(M)$ of which start at each leader ℓ with $d_{\ell}(M) > 0$.

We proceed by contradiction, and make the following assumption. Let \mathcal{P} be any set of d(M) deficit-decreasing paths, $d_{\ell}(M)$ of which start at each leader ℓ with $d_{\ell}(M) > 0$ (denote by \mathcal{P}_{ℓ} the elements of \mathcal{P} starting at ℓ); then, there are two leaders ℓ , ℓ' such that two paths $P \in \mathcal{P}_{\ell}$, $P' \in \mathcal{P}_{\ell'}$ are not follower-disjoint. In order to reach the stable matching N starting from M, a set of d(M) deficit-decreasing paths must be solved. However, if P is solved (by "flipping" matched edges into unmatched edges, and vice versa) then P' is not solved, and if P' is solved then P is not solved (see Figures 8 and 9 for a schematic representation). If follows that N cannot be reached from M by solving the d(M) deficit-decreasing paths in \mathcal{P} .

The last argument holds for any choice of \mathcal{P} , and this generates a contradiction on the reachability of *N* starting from *M* (observe that *N* can be reached from *M* in finite time, e.g. by a cat-and-mouse argument on the space of all the matchings of *G*). Hence, we can choose d(M) follower-disjoint deficit-decreasing paths, $d_{\ell}(M)$ of which start at each leader ℓ with $d_{\ell}(M) > 0$, and the lemma is proven.

B. Proof of Theorem 2

Let \mathcal{M}_n be the set of all the matchings of G_n such that d(M) = 1. We proceed as follows. First, we show that each $M \in \mathcal{M}_n$ is uniquely identified by the set of the leaders that are not matched with "horizontal" edges (that is, leaders ℓ_i such that $(\ell_i, f_i) \notin M$). Second, we define trees T_m^* , $m \ge 1$ such that a random walk on T_m^* starting at any node different than the root hits the root

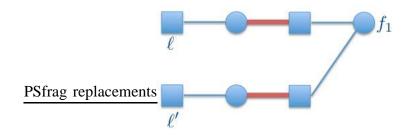


Fig. 9. If, under the matching highlighted in the figure, both ℓ and ℓ' are poor and f_1 is unmatched then there are two deficit-decreasing paths that are not follower-disjoint (one starting at ℓ ad ending at f_1 , the other starting at ℓ' ad ending at f_1). If one of them is solved then the other is not solved, and vice versa.

after a number of steps that is exponentially large in *m* with high probability. Third, for each matching $M \in \mathcal{M}_n$ we define a quantity h(M) that we call the *height* of *M* and we argue that, when initialized at *M*, the algorithm's dynamics is equivalent to a random walk on the tree $T^*_{h(M)}$ and reaching the stable matching of G_n corresponds to reaching the root of $T^*_{h(M)}$ (and therefore it requires a number of rounds that is exponentially large in h(M) with high probability). Finally, by a counting argument, we show that for any constant $0 < \gamma < 1$ a $1 - O(n2^{-(1-\gamma)n})$ fraction of all the matchings in \mathcal{M}_n have height at least γn , completing the proof of the theorem.

A. Properties of the matchings in \mathcal{M}_n .

Matchings in \mathcal{M}_n enjoy the following structural properties.

Lemma 3: Let $M \in \mathcal{M}_n$. The following properties hold.

- (1) There are a single poor leader $\ell_{i^*(M)}$ and a single unmatched follower $\ell_{j^*(M)}$ in M.
- (2) $1 \le i^*(M) \le j^*(M) \le n$.
- (3) $(\ell_k, f_k) \in M$ for all $k < i^*(M)$ and all $k > j^*(M)$.
- (4) Let $\mathcal{I}(M) = \{j_0, j_1, \dots, j_K\}$ be the sorted set of indexes j such that $(\ell_j, f_j) \notin M$. Then
 - (a) $j_1 = i^*(M)$ and $j_K = j^*(M)$.
 - (b) $(\ell_{j_{k+1}}, f_{j_k}) \in M$ for all $k \in \{0, \dots, K-1\}$.

Proof: Property (1). Since $d(M) = \sum_{\ell \in L} d_{\ell}(M) = 1$, there is a single poor leader $\ell_{i^*(M)}$ in M. Since $c_{\ell} = 1$ for all $\ell \in L$, each leader $\ell \neq \ell_{i^*(M)}$ is matched to a single follower. It follows that there is a unique unmatched follower $f_{i^*(M)}$. Property (2). Suppose by contradiction that $i^*(M) > j^*(M)$. Since $N_{\ell_{j^*(M)}} = \{f_1, \ldots, f_{j^*(M)}\}$ and $f_{j^*(M)}$ is unmatched, leader $\ell_{j^*(M)}$ is matched to one of the followers in $\{f_1, \ldots, f_{j^*(M)-1}\}$. Hence, the $j^*(M)-1$ leaders $\ell_1, \ldots, \ell_{j^*(M)-1}$ are matched to at most $j^*(M)-2$ out of the $j^*(M)-1$ followers $f_1, \ldots, f_{j^*(M)-1}$, and one of them is necessarily poor, contradicting Property (1). Therefore, $i^*(M) \le j^*(M)$.

Property (3). We proceed by induction. If $i^*(M) > 1$, then $(\ell_1, f_1) \in M$ since $N_{\ell_1} = \{f_1\}$ and ℓ_1 is matched with a follower. Assume that if $i^*(M) > j$ then $(\ell_k, f_k) \in M$ for all $k \leq j$. If $i^*(M) > j+1$, then, by the inductive assumption, ℓ_{j+1} can only be matched to f_{j+1} since $N_{\ell_{j+1}} = \{f_1, \ldots, f_{j+1}\}$. This shows that $(\ell_k, f_k) \in M$ for all $k < i^*(M)$. If $j^*(M) < n$ then $(\ell_n, f_n) \in M$ since f_n is matched and ℓ_n is the only leader connected to f_n . Assume by induction that if $j^*(M) < j$ then $(\ell_k, f_k) \in M$ for all $k \geq j$. If $j^*(M) < j - 1$, then, by the inductive assumption, f_{j-1} can only be matched to ℓ_{j-1} since f_{j-1} is adjacent to $\ell_{j-1}, \ldots, \ell_n$. This shows that $(\ell_k, f_k) \in M$ for all $k > j^*(M)$.

Property (4). If K = 0 then $M = \{(\ell_i, f_i) : i \neq i^*(M)\}, j^*(M) = i^*(M)$, and properties (4a) and (4b) trivially hold. Now consider $K \ge 1$. Let $\mathcal{I}(M) = \{j_0, j_1, \dots, j_K\}$ be the sorted set of indexes *j* such that $(\ell_j, f_j) \notin M$. By property (3), we have that $j_0 = i^*(M)$ and $j_K = j^*(M)$, therefore property (4a) follows. Hence, $(\ell_{j_2}, f_{j_1}) \in M$ since $(\ell_k, f_k) \in M$ for all $k \in \{j_1 + 1, \dots, j_2 - 1\}$ by definition of $\mathcal{I}(M)$, and $N_{\ell_{j_2}} = \{f_1, \dots, f_{j_2}\}$. Property (4b) follows by induction.

Lemma 3 states that non-horizontal matching edges do not intersect. In particular, given a matching $M \in \mathcal{M}_n$, the set $\mathcal{I}(M)$ represents the set of (the sorted indexes of) the leaders that are not matched with horizontal edges (see Figure 10 for an example), $\ell_{i^*(M)}$ for $i^*(M) = \min \mathcal{I}(M)$ is the unique unmatched leader, and $\ell_{j^*(M)}$ for $j^*(M) = \max \mathcal{I}(M)$ is the unique unmatched follower. Recall that $M_n^* = \{(\ell_k, f_k) : 1 \le k \le n\}$ is the unique stable matching of G_n , and let $\mathcal{I}(M_n^*) = \emptyset$. Lemma 3 implies that every matching $M \in \mathcal{M}_n \cup \{M^*n\}$ is uniquely identified by the set $\mathcal{I}(M)$. In particular, the following result holds.

Lemma 4: Consider the mapping $\mathcal{I}(\cdot)$ from $\mathcal{M}_n \cup \{M_n^*\}$ to $\mathcal{S} = \{A : A \subseteq \{1, \ldots, n\}\}$ defined by $M \mapsto \mathcal{I}(M)$. Then $\mathcal{I}(\cdot)$ is a bijection.

Proof: The stable matching M_n^* is associated to $I(M_n^*) = \emptyset$. The mapping $I(\cdot)$ is injective since if $M, M' \in \mathcal{M}_n$ and $M \neq M'$ then $I(M) \neq I(M')$. To see that $I(\cdot)$ is surjective, fix $K \leq n-1$ and $A = \{i_0, i_1, \ldots, i_K\} \in S$ such that $1 \leq i_0 < i_1 < \ldots < i_K \leq n$. The matching $M \in \mathcal{M}_n$ such that



Fig. 10. An example of a matching M of G_6 with d(M) = 1. M is uniquely determined by the set $I(M) = \{2, 4, 6\}$, that encodes the following: ℓ_2 is not matched, ℓ_4 is matched with f_2 , ℓ_6 is matched with f_4 , f_6 is not matched. Also note that $P(M) = \ell_2, f_2, \ell_4, f_4, \ell_6, f_6$ is the unique deficit-decreasing path relative to M.

I(M) = A is given by

$$M = \{(\ell_{i_{k+1}}, f_{i_k}) : 0 \le k \le K - 1\} \cup \{(\ell_k, f_k) : k \notin A\} \in \mathcal{M}_n.$$

Remark 1: Lemma 3 and Lemma 4 imply that every matching $M \in \mathcal{M}_n$, $I(M) = \{i_0, \ldots, i_K\}$, is associated to a unique deficit-decreasing path in $M \oplus M_n^*$ relative to M, given by

$$P(M) = \ell_{i_0}, f_{i_0}, \ell_{i_1}, f_{i_1}, \dots, \ell_{i_K}, f_{i_K}.$$

Too see this, observe that $M \setminus M_n^*$ is given by the non-horizontal edges in M, while $M_n^* \setminus M$ is given by the horizontal edges that are not in M. Therefore, by Lemma 3,

$$M \setminus M_n^* = \{ (\ell_{i_1}, f_{i_0}), (\ell_{i_2}, f_{i_1}), \dots, (\ell_{i_K}, f_{i_{K-1}}) \},$$
$$M_n^* \setminus M = \{ (\ell_{i_0}, f_{i_0}), (\ell_{i_1}, f_{i_1}), \dots, (\ell_{i_K}, f_{i_K}) \},$$

and the set of edges in P(M) is equal to $M \oplus M_n^*$. The uniqueness of P(M) follows since I(M) is unique by Lemma 4 and there is no other way to connect the poor leader ℓ_{i_0} and the unmatched follower f_{i_K} with a path. This suggests that, given a matching $M \in \mathcal{M}_n$, the unique deficit-decreasing path P(M) must be "solved" in order to reach the stable matching of G_n .

B. The tree T_m^*

Definition 9: Let T_1 be a labeled rooted tree with a singleton node with label 1. Inductively, for $i \le 2$, let T_i be the labeled rooted tree whose root is labeled with i and its i - 1 children are the roots of copies of T_1, \ldots, T_{i-1} . We define T_m^* to be the tree with a root with label m + 1 whose only child is the root of a copy of T_m (see Figure 11 for a visual representation). Let r^* denote the root of T_m^* .

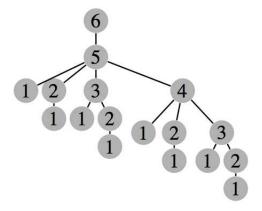


Fig. 11. The three T_m^* for m = 5.

We show that the hitting time of r^* for a random walk on T_m^* starting at any node $u \neq r^*$ is exponential in *m* with high probability. For a node $u \neq r^*$, we call the edge that connects *u* to its parent *u*'s *exit* edge. For any subtree $T_i \subset T_m^*$, let Z_i be the random variable denoting the number of steps that it takes for a walk starting at the root of T_i to exit T_i (that is, to hit the parent of the root of T_i). The following lemma provides an exponential lower bound on Z_i .

Lemma 5: There exist positive constants $\alpha, \gamma > 0$ such that, for all $i \ge 2$,

$$\Pr[Z_i \ge \gamma \cdot 2^{i/(\alpha \log^2 i)}] \ge 1 - \frac{1}{\log i}.$$

Proof: We proceed by induction on *i*. For convenience, define $g(i) = \alpha \log^2 i$ and $f(i) = \gamma \cdot 2^{i/g(i)}$ for some $\alpha, \gamma > 0$. For any $\alpha > 0$ and $i \ge 2$, we can choose $\gamma > 0$ such that $f(i) \le 1$; therefore, as $Z_i \ge 1$ with probability 1, the claim holds trivially for any $i \le i^*$, where i^* is a suitably large constant.

Now consider any $i \ge i^*$ and suppose the claim holds up to i - 1. Every time the walk is on the root of T_i , it exits T_i with probability 1/i (since the root of T_i has i neighbors: one parent and i - 1 children). Therefore, letting E_t be the event that the first t times the walk is on the root of T_i it does *not* exit T_i , we have $\Pr[E_t] \ge 1 - t/i$. Let $t = i/(2\log i)$, and let D_j , $1 \le j \le t$, be the event that, when it is on the root of T_i for the *j*-th time, the walk moves to the root of one of the subtrees $T_{i-g(i)}, \ldots, T_{i-1}$ and takes at least f(i - g(i)) steps to exit that subtree. For $1 \le j \le t$, we have

$$\Pr[D_j \mid E_t] \ge \frac{g(i)}{i} \cdot \Pr[Z_{i-g(i)} \ge f(i-g(i))]$$
$$\ge \frac{g(i)}{i} \cdot \left(1 - \frac{1}{\log(i-g(i))}\right),$$

by the induction hypothesis on $Z_{i-g(i)}$. Letting χ_j be the indicator function of the event D_j for $1 \le j \le t$, the probability that at least two of the events D_j happen, given E_t , is lower bounded by:

$$\Pr\left[\sum_{j=1}^{t} \chi_j \ge 2 \mid E_t\right] \ge \Pr\left[\sum_{j=1}^{t/2} \chi_j \ge 1, \sum_{j=t/2+1}^{t} \chi_j \ge 1 \mid E_t\right]$$
$$= \Pr\left[\sum_{j=1}^{t/2} \chi_j \ge 1 \mid E_t\right]^2.$$

By union bound, we can write

$$\Pr\left[\sum_{j=1}^{t/2} \chi_j \ge 1 \mid E_t\right]$$

$$\ge 1 - \prod_{i=1}^{t/2} \left(1 - \Pr[D_j | E_t]\right)$$

$$\ge 1 - \left(1 - \frac{g(i)}{i} \left(1 - \frac{1}{\log(i - g(i))}\right)\right)^{t/2}$$

$$\ge 1 - \exp\left[-\frac{\alpha \log i}{4} \left(1 - \frac{1}{\log(i - g(i))}\right)\right] \ge 1 - \frac{1}{i^{\alpha/8}},$$

where the last step holds for *i* sufficiently large so that $log(i - g(i)) \ge 2$. This implies that

$$\Pr\left[\sum_{j=1}^{t} \chi_j \ge 2 \mid E_t\right] \ge \left(1 - \frac{1}{i^{\alpha/8}}\right)^2 \ge 1 - \frac{2}{i^{\alpha/8}}.$$

Therefore, we conclude that

$$\Pr[Z_i \ge 2 \cdot f(i - g(i))] \ge \Pr\left[\sum_{j=1}^t \chi_j \ge 2\right]$$
$$\ge \Pr\left[\sum_{j=1}^t \chi_j \ge 2 \mid E_t\right] \Pr[E_t]$$
$$\ge \left(1 - \frac{2}{i^{\alpha/8}}\right) \left(1 - \frac{t}{i}\right) \ge 1 - \frac{1}{\log i},$$

where the last step holds by choosing α sufficiently large. The claim follows since $2 \cdot f(i-g(i)) \ge f(i)$.

Note that a random walk starting at any node $u \neq r^*$ has to exit T_m before hitting r^* . Therefore, an application of Lemma 5 to T_m yields a lower bound to the hitting time of r^* when starting at any node $u \neq r^*$.

Corollary 2: The hitting time of r^* of a random walk starting at any node $u \neq r^*$ is $2^{\Omega(n/\log^2 n)}$ with high probability.

C. The dynamics of the algorithm starting from $M \in \mathcal{M}_n$

For ease of presentation, we set the probability parameters of the algorithms to p = q = 1. Setting p = 1 means that a poor leader always proposes to a follower. Setting q = 1 means that a follower always accepts an incoming request. Our result holds for any choice of p and q.

By Lemma 4, every matching $M \in \mathcal{M}_n \cup \{M_n^*\}$ is uniquely identified by the set $\mathcal{I}(M) = \{k : (\ell_k, f_k) \notin M\}$.

Definition 10 (The height of a matching): Let $M \in \mathcal{M}_n$, $\mathcal{I}(M) = \{i_0, \dots, i_K\}$. The height h(M) of M is defined as follows. If K = 0 then h(M) = 0. If $K \ge 1$ then $h(M) = i_{K-1} \in \{1, \dots, n-1\}$.

For a matching $M \in \mathcal{M}_n$ such that h(M) > 0 we can write $\mathcal{I}(M) = \{i_0, \dots, h(M), i_K\}$. For each $t \ge 0$, let M(t) be the matching at the beginning of round *t* of the algorithm, and for ease of notation let $\mathcal{I}(t) = \mathcal{I}(M(t))$. For a matching $M \in \mathcal{M}_n$ let

$$\tau^*(M) = \min\{t : M(t) = M_n^* | M(0) = M\}$$

be the number of steps that the algorithm needs to reach the stable matching starting from M.

Note that, with p = q = 1, $t^*(M) = 1$ for every $M \in \mathcal{M}_n$ such that h(M) = 0 (that is, $|\mathcal{I}(M)| = 1$), since according to the algorithm leaders prefer unmatched followers. We are interested in relating $\tau^*(m)$ and h(M) for every matching $M \in \mathcal{M}_n$ such that h(M) > 0 (that is, $|\mathcal{I}(M)| > 1$).

We study how the matching evolves over time through the Markov process $\{I(t) : 0 \le t \le \tau^*(M)\}$. Since $I(M_n^*) = \emptyset$, $\tau^*(M) = \min\{t : I(t) = \emptyset\}$. The state space of the Markov process is given by the set *S* defined in Lemma 4. The transition probabilities are characterized by the following lemma.

Lemma 6: Conditional on $I(t) = I \in S$, |I| > 1, the transition probabilities at time t are given by

$$\Pr\left(\mathcal{I}(t+1) = I' \middle| \mathcal{I}(t) = I\right) = \frac{1}{\min I} \quad \text{if} \quad I' \in \left\{I \cup \{k\} : k < \min I\right\} \cup \left\{I \setminus \{\min I\}\right\},$$

and 0 otherwise. Moreover $Pr(\mathcal{I}(t+1) = \emptyset | \mathcal{I}(t) = \emptyset) = 1$, and $Pr(\mathcal{I}(t+1) = \emptyset | \mathcal{I}(t) = I) = 1$ for every *I* such that |I| = 1.

Proof: The case of $I(t) = \emptyset$ corresponds to the stable matching M_n^* , which is an absorbing state for the Markov process. In the case of |I(t)| = 1, we have that h(M) = 0, and p = q = 1 implies that that $I(t+1) = \emptyset$.

Consider now |I| > 1. Conditional on I(t) = I, the poor leader is $\ell_{\min I}$ and has degree min I and neighborhood $N_{\min I} = \{f_1, \ldots, f_{\min I}\}$, and chooses one of the followers in $N_{\min I}$ uniformly at random. If $\ell_{\min I}$ chooses follower f_k for some $k < \min I$ then the leader ℓ_k becomes poor, since by property (3) of Lemma 3 ℓ_k was matched to f_k in M(t), and we have that $I(t+1) = I \cup \{k\}$. If instead $\ell_{\min I}$ chooses follower $f_{\min I}$ (matched to $\ell_{\min(I \setminus \min I)}$ in M(t) by property (4) of Lemma 3), then $I(t+1) = I \setminus \{\min I\}$.

For every matching $M \in \mathcal{M}_n$ such that h(M) > 0 and $\mathcal{I}(M) = \{i_0, \dots, i_K\}$, define the matching $\mathcal{L}(M) = \{(\ell_j, f_j) : j \neq i_K\}$ and $\tau(M) = \min\{t : M(t) = \mathcal{L}(M)\}$, and observe that $h(\mathcal{L}(M)) = 0$ and $\tau^*(M) > \tau(M)$ (in particular, $\tau^*(M) = 1 + \tau(M)$ for p = q = 1).

For every matching M such that $|\mathcal{I}(M)| > 1$, let $\mathcal{R}(M)$ be the set of the matchings in \mathcal{M}_n that can be reached from M (after one or multiple steps). According to the transition probabilities defined by Lemma 6, it is easy to see that

$$\mathcal{R}(M) = \left\{ \mathcal{L}(M) \right\} \cup \left\{ M' \in \mathcal{M}_n : I(M') = A \cup \{h(M), i_K\}, A \subseteq \{1, \ldots, h(M) - 1\} \right\}.$$

Observe that every $M' \in \mathcal{R}(M) \setminus \{\mathcal{L}(M)\}$ has height h(M') = h(M). The following lemma characterizes the one-to-one correspondence between matchings in $\mathcal{R}(M)$ and nodes of the tree $T^*_{h(M)}$.

Lemma 7: Consider the mapping $\omega(\cdot)$ from $\mathcal{R}(M)$ to $T^*_{h(M)}$ defined as follows. Let $\omega(\mathcal{L}(M)) = r$, where *r* is the root of $T^*_{h(M)}$. For $M' \in \mathcal{R}(M) \setminus \{\mathcal{L}(M)\}$ and $\mathcal{I}(M') = I$, let $\omega(M')$ be the node of $T^*_{h(M)}$ with label min *I* and connected to the root with a path of nodes labeled by the sorted indexes in $I \setminus \{\min I\}$. Then $\omega(\cdot)$ is a bijection.

The proof is omitted since it directly follows from the construction of the tree $T^*_{h(M)}$ and the mapping $\mathcal{I}(\cdot)$.

Lemma 8: The stochastic process $\{I(t): 0 \le t \le \tau(M) | M(0) = M\}$ is equivalent to a random walk on $T^*_{h(M)}$ starting at $\omega(M)$.

Proof: It suffices to show that the transition probabilities between two matchings $M_1, M_2 \in \mathcal{R}(M)$ are nonzero if and only if the nodes $\omega(M_1)$ and $\omega(M_2)$ are adjacent in $T^*_{h(M)}$. To prove the "only if" direction, assume that $M_1, M_2 \in \mathcal{R}(M)$ are such that there is a nonzero transition probability from M_1 to M_2 (and therefore from M_2 to M_1). Let $\mathcal{I}(M_1) = I_1$ and $\mathcal{I}(M_2) = I_2$. According to the transition probabilities given above, there are two possible cases. In the first case, $I_2 = I_1 \cup \{k\}$ for some $k < \min I_1$, and $\omega(M_1)$ is a child of $\omega(M_1)$. In the second case $I_2 = I_1 \setminus \{\min I_1\}$ and $\omega(M_2)$ is the parent of $\omega(M_1)$. The proof of the other direction is similar.

To summarize, the number of steps that the algorithm needs to reach the stable matching of G_n starting from $M \in \mathcal{M}_n$ with h(M) > 0 is upper bounded by the time $\tau(M)$ to reach the matching $\mathcal{L}(M)$, and reaching $\mathcal{L}(M)$ is equivalent to reaching the root of $T^*_{h(M)}$ starting from the node $\omega(M)$. By Corollary 2, $\tau(M)$ is exponentially large in h(M) with high probability. To complete the proof of the theorem, we show that, for any constant $0 < \gamma < 1$, a $1 - O(n2^{-(1-\gamma)n})$ fraction of the matchings $M \in \mathcal{M}_n$ have $h(M) \ge \gamma n$. This is done through a counting argument.

D. The fraction of the matchings $M \in \mathcal{M}_n$ such that $h(M) \ge \gamma n$

Let *N* be the number of matchings in \mathcal{M}_n . Fixed a constant $0 < \gamma < 1$, let $\mathcal{M}_{\gamma} = \{M \in \mathcal{M}_n : h(M) < \gamma n\}$ and let $N_{\gamma} = |\mathcal{M}_{\gamma}|$. For j = 0, ..., n-1, let N(j) be the number of matchings $M \in \mathcal{M}_n$ such that h(M) = j. It follows that

$$N = \sum_{j=0}^{n-1} N(j), \qquad N_{\gamma} \leq \sum_{j=0}^{\lceil \gamma n \rceil - 1} N(j).$$

Lemma 9: N(0) = n and $N(j) = (n - j)2^{j-1}$ for all j = 1, ..., n - 1.

Proof: N(0) = n since there are *n* matchings *M* with h(M) = 0, that is, the matchings $\{(\ell_j, f_j) : j \neq k\}$ for $1 \le k \le n$.

Fix $j \in \{1, ..., n-1\}$. By Lemma 4, a matching $M \in \mathcal{M}_n$ with h(M) = j is uniquely identified by a set $\mathcal{I}(M) = \{i_0, ..., i_{K-1}, i_K\}$ for some $1 \le K \le n-1$ and $i_{K-1} = j$. Since $\mathcal{I}(\cdot)$ is a bijection, to determine N(j) we need to count all subsets of $\{1, ..., n\}$ of the form $\{i_0, ..., j, i_K\}$. There are 2^{j-1} subsets of $\{1, ..., j-1\}$ and n-j ways to choose $i_K \in \{j+1, ..., n\}$, thus $N(j) = (n-j)2^{j-1}$.

We now show that for any constant $0 < \gamma < 1$, the fraction of matchings $M \in \mathcal{M}_n$ such that $h(M) < \gamma n$ goes to zero exponentially fast in n

Lemma 10: Fix $0 < \gamma < 1$. Then, $N_{\gamma}/N = O(n2^{-(1-\gamma)n})$.

Proof: We first compute *N*.

$$N = \sum_{i=0}^{n-1} N(i) = n + \sum_{i=1}^{n-1} (n-i)2^{i-1} = n + n \sum_{i=0}^{n-2} 2^i - \sum_{i=1}^{n-1} i2^{i-1}$$

The second sum can be shown (e.g. by induction) to be equal to $(n - 1) + (n - 2)(2^{n-1} - 1)$. Therefore,

$$N = n + n(2^{n-1} - 1) - (n - 1) - (n - 2)(2^{n-1} - 1) = 2^n - 1 = \Omega(2^n).$$

Similarly, letting $k = \lceil \gamma n \rceil$ we have that,

$$N_{\gamma} \leq \sum_{i=0}^{k-1} N(i) = n + n \sum_{i=0}^{k-2} 2^{i} - \sum_{i=1}^{k-1} i 2^{i-1}$$
$$= n + n(2^{k-1} - 1) - (k - 1) - (k - 2)(2^{k-1} - 1)$$
$$= 2^{k-1}(n - k - 2) - 1 = O(n2^{\lceil \gamma n \rceil}).$$

Therefore, the fraction of matchings in \mathcal{M}_n with height $h(M) < \gamma n$ is $N_{\gamma}/N = O(n2^{-(1-\gamma)n})$.

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