

# Reaction-Diffusion on Dynamic Inhibition Areas: A Bio-Inspired Link Scheduling Algorithm

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**Abstract**—We present the *Dynamic Inhibition Areas Reaction-Diffusion (DIA-RD)* algorithm, a distributed medium access control protocol that globally maximizes the spatial reusability (number of simultaneous transmissions per unit area) of wireless sensor networks. This algorithm is able, in consequence, to minimize the number of time slots needed to schedule the set of demanded links, making it very efficient to solve the *Shortest Link Schedule* problem. DIA-RD combines accurate interference management, provided by the use of dynamic inhibition areas based on the *physical interference model*; and global intelligent behavior, provided by the bio-inspired technique known as *Reaction-Diffusion*. This technique ensures global convergence to dense feasible transmission patterns (no active link inside the inhibition area of other active link) in a decentralized way. Experimental results show that our DIA-RD algorithm provides superior performance, in terms of spatial reusability, than the best state-of-the-art approaches, namely the DIA-LS, RD-MAC, GOW\* and ML<sup>2</sup>S algorithms.

## I. INTRODUCTION

Time Division Multiple Access (TDMA) protocols [4] have been shown to be the most suitable access control (MAC) techniques [6] for wireless ad-hoc networks. While Carrier Sense Multiple Access (CSMA) protocols [3] tend to behave in a very conservative way, specially when Collision Avoidance (CSMA/CA) stage is used, TDMA protocols are able to deal with the high traffic loads demanded by wireless ad-hoc network applications.

The main objective of this work is the design of an efficient TDMA medium access control technique for wireless ad-hoc networks. An easy way to evaluate and compare different TDMA approaches is to make them tackle the *Shortest Link Schedule* (SLS) problem [2]. Given a set of demanded transmissions or *demanded links* (pairs of transmitter-receiver nodes) to be scheduled, the target is to build as short as possible schedules, in terms of time slots, where every demanded link is *active* (carrying out a transmission) during one of these time slots. Defining a *feasible transmission pattern* as a subset of demanded links that can be simultaneously active while ensuring a Signal to Interference Noise Ratio (SINR) greater than a given threshold  $\beta$  at each receiver node, denser feasible transmission patterns provide shorter schedules. Thus, our

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purpose is to build as dense as possible feasible transmission patterns.

In this paper, we present the so called *Dynamic Inhibition Areas Reaction-Diffusion (DIA-RD)* link scheduling algorithm. It is based on three design principles: *a)* it is based on the physical interference model, which provides accurate interference management; *b)* *dynamic inhibition areas* [2], making the DIA-RD algorithm adaptable to the changeable wireless environment. Every demanded link has an associated inhibition area, which is defined as a circular region around the corresponding receiver node, where no node can transmit without causing a collision at this receiver node; *c)* reaction-diffusion mechanism [5], providing a global clever behavior of the system, based on local and simple decisions (*emergent behavior* [9]). We show that the DIA-RD link scheduling algorithm obtains denser feasible transmission patterns than both the *Reaction-Diffusion MAC (RD-MAC)* [5] and the *Dynamic Inhibition Areas Link Scheduling MAC (DIA-LS)* [2] algorithms do. The DIA-RD algorithm, like DIA-LS, also outperforms GOW\* [1] and ML<sup>2</sup>S [8] algorithms, the main related works in the literature, when solving the SLS problem.

The remainder of this paper is organized as follow: In section II we motivate this work while discussing about the main state-of-the-art approaches. Section III introduces the formulation of our problem. The DIA-RD algorithm is described in detail in Section IV. In section V we prove that the DIA-RD algorithm always converges to feasible transmission patterns. Finally, section VI includes the numerical results and conclusions of this work.

## II. MOTIVATION AND RELATED WORK

Wireless ad-hoc networks does not rely on predefined infrastructures and are, by definition, decentralized and self-organized. Thus, every algorithm designed for them, must be distributed. A very interesting way of designing decentralized algorithms is to imitate some mechanisms present in the nature, where simple decisions based on local information, lead to global intelligent behavior (*emergent behavior* [9]). Typical examples of these processes are zebra stripes formation.

*Reaction-Diffusion MAC (RD-MAC)* [5] is a bio-inspired TDMA medium access protocol that obtains feasible transmission patterns in a distributed way. RD-MAC assigns an *inhibition area* and an *activation area* to every demanded

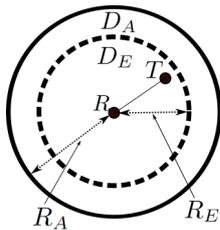


Fig. 1. Example of inhibition and activation areas defined by Reaction-Diffusion mechanisms around a receiver node.  $D_E$  and  $D_A$  are the sets of other links (not in the figure for the sake of simplicity) whose transmitter nodes are placed in its inhibition and activation areas respectively.

link (see Fig.1). The activation area of a demanded link is the region where the presence of another active link is encouraged in order to enhance the spatial reusability. Every demanded link also has an associated *transmission probability* that is iteratively updated as a function of the transmission probabilities associated to the links within its inhibition and activation areas. Authors in [5] show that, after a finite number of iterations, every transmission probability converges to either 1 or 0. The set of links with transmission probability equal to 1 form a feasible transmission pattern because they are never placed inside each others inhibition area.

RD-MAC presents two important drawbacks: *a)* The interference model assumed is not well defined nor realistic and *b)* inhibition areas are predefined, time invariant and uniform for every link. This makes RD-MAC not suitable for wireless ad-hoc networks, where nodes are usually randomly placed, not either suitable for wireless environments, where the channel conditions are time variant.

The key issue when designing medium access control (MAC) algorithms for wireless ad-hoc networks is to accurately manage the interference. Using realistic interference models, able to adapt to the changeable wireless environment, leads to a high performance in terms of throughput, simultaneous transmissions and spatial reusability  $\rho$  (number of active links per area unit) of the network

Authors in [2] present the so called *Dynamic Inhibition Areas Link Scheduling* (DIA-LS) algorithm. A distributed TDMA medium access control algorithm that efficiently solves the Shortest Link Schedule (SLS) problem. DIA-LS builds feasible transmission patterns, where the number of simultaneous successful transmissions is maximized, thanks to the use of the *physical interference* model and to the use of dynamic inhibition areas. Authors show that the DIA-LS outperforms the GOW\* [1] and ML<sup>2</sup>S [8] algorithms, which represent the main related works in the literature.

The weak point of the DIA-LS algorithm is the fact that, at each iteration of the algorithm, the links forming a feasible transmission pattern are randomly chosen among the available candidates. A more clever way of choosing that links, can enhance the performance of the algorithm. This happens because the inhibition areas, around the links forming a feasible transmission pattern, are smaller, more simultaneous links fit

in the same network area and denser feasible transmission patterns are obtained. Therefore, the spatial reusability of the network is increased and the throughput is enhanced.

The Dynamic Inhibition Areas Reaction-Diffusion (DIA-RD) algorithm that we present in this paper, combines the strengths and avoids the weaknesses of both RD-MAC and DIA-LS algorithms. It accurately manages the interference, by using individual and adaptive inhibition areas, and chooses every active link in a clever way, by imitating biological emergent behaviors [9] where local decisions lead to a global performance enhancement.

### III. PROBLEM FORMULATION

The inputs of our problem are the following: first, the random network itself, which is a set  $\mathbf{V}$  of  $N$  nodes, randomly placed in a square area; the second input is the set of *demanded links*  $\mathcal{L}$ , containing pairs of *transmitter-receiver* nodes from the set  $\mathbf{V}$ . The result provided by the *Dynamic Inhibition Areas Reaction-Diffusion* (DIA-RD) algorithm is a set  $\mathcal{S}$  of disjoint subsets  $S_t \subset \mathcal{L}$ , such that  $\cup_{t=1}^M S_t = \mathcal{L}$ . Each  $S_t$  represents a *feasible transmission pattern*, containing the links that will be simultaneously active, at time slot  $t$ . Every receiver node in those sets has an  $\text{SINR} \geq \beta$ . The objective of the DIA-RD algorithm is to obtain as dense as possible feasible transmission patterns, thus, minimizing the number of subsets  $S_t$  (schedule length, denoted as  $M$ ) needed to schedule every demanded link.

In the next subsections, we briefly describe how the two different approaches, in which our DIA-RD algorithm is based, solve the proposed problem.

#### A. Description of the Reaction-Diffusion mechanism

In the work by Durvy *et al* [5], authors propose a model, called RD-MAC. Circular *inhibition* and *activation* areas are associated to every demanded link (see Fig. 1). The radii corresponding to the inhibition and activation areas are defined by  $R_E$  and  $R_A$ , respectively. This radii are predefined, time invariant and homogeneous for every link. In addition, each link has an associate *transmission probability*  $p_i[m]$  such that  $p_i[m] = 1$  indicates that link  $i$  carries out a transmission at iteration  $m$ . Initial transmission probabilities  $p_i[m = 1]$  are shown to be irrelevant. Each link iteratively updates its transmission probability according to the expression:

$$p_i[m + 1] = f \left( l p_i[m] - s \sum_{y \in \mathcal{D}_E^i} p_y[m] + r \sum_{z \in \mathcal{D}_A^i} p_z[m] \right) \quad (1)$$

where  $l$ ,  $s$  and  $r$  are the self-activation, inhibition and activation parameters respectively,  $\mathcal{D}_E^i$  is the set of links in the inhibition area of link  $i$  and  $\mathcal{D}_A^i$  is the set of links in the activation area of link  $i$ . Parameters  $l$ ,  $s$  and  $r$  are time and spatial invariant. Function  $f(\cdot)$  is a piecewise linear such that:

$$f(x) = \begin{cases} 1 & \text{if } x \geq 1. \\ 0 & \text{if } x \leq 0. \\ x & \text{otherwise} \end{cases} \quad (2)$$

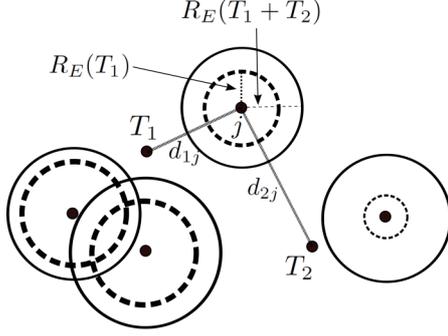


Fig. 2. Example of inhibition radii updates. Scenario with two transmitters and four receivers. Dashed circumferences represent the inhibition areas when only T1 was present. Solid circumferences represent the inhibition areas when T1 and T2 are present. Inhibition areas grow depending on the distance to the transmitters.

Authors in [5] show that if  $\mathcal{D}_E^i$  and  $\mathcal{D}_A^i$  are time invariant:

- Transmission probabilities, for every link, converge to equilibrium points.
- If parameter  $l > 1$ , every transmission probability is either 0 or 1 at equilibrium points.
- If  $l > 1$ ,  $s > l - 1$  and  $0 < r < \frac{1}{A_{max}}(1 - l + s)$ , being  $A_{max}$  the average number of nodes in the activation areas and  $d$  the communication range; two active links are at least at distance  $R_E$  from each other and within a distance  $2(R_E + d)$ . This property defines the density and spatial reusability provided by the feasible transmission patterns obtained by the RD-MAC algorithm.

### B. Description of the Dynamic Inhibition Areas link scheduling algorithm

In this case, authors in [2], propose an iterative process that obtains dense feasible transmission patterns. At each iteration  $m$ , a new demanded link is included in the transmission pattern until no more links can be added without corrupting any link already included.

In each iteration, every demanded link is classified into one of the next three categories:<sup>1</sup>:

- **Active**( $\mathcal{A}(m)$ ): Links carrying out a transmission at a given time slot. These are the links that have been included in the feasible transmission pattern.
- **Candidate**( $\mathcal{C}(m)$ ): Non active links that have the chance of being active at the current time slot.
- **Discarded**( $\mathcal{D}(m)$ ): Links that do not have the chance of being active at the current time slot.

The demanded links, which are included in the feasible transmission pattern, are randomly chosen among the set of candidate links and become active links. Every demanded link has an associated inhibition area, centered at its corresponding

<sup>1</sup>Transmitter and receiver nodes belonging to a link included in one category, also receive the same treatment (e.g. active transmitter, candidate receiver, etc)

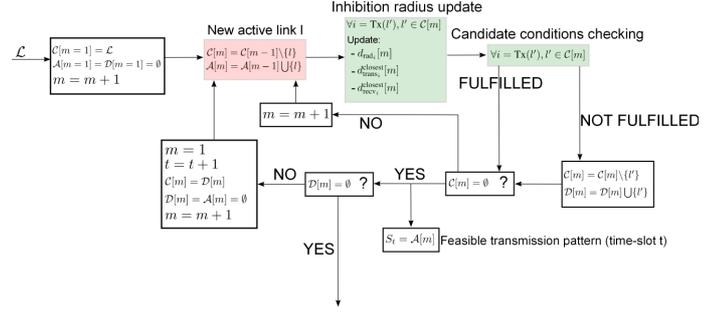


Fig. 3. Block diagram representing the DIA-LS algorithm. The block “New active link  $l$ ” represents the random choice of a new active link among the remaining candidate links.

receiver node. When a new active link is chosen, the transmitter nodes corresponding to the remaining candidate links update their inhibition radius, depending on the distance to the transmitter node belonging to the chosen active link. Fig. 2 shows how inhibition areas around each candidate receiver node are updated as more active links appear. According to their new inhibition radius some candidate links become discarded links (if a transmitter node belonging to an active link is placed inside their inhibition area). Finally, a new iteration  $m + 1$  starts with the random election of a new active link among the remaining candidate links. Fig. 3. shows a diagram block that represents the DIA-LS algorithm.

## IV. DYNAMIC INHIBITION AREAS REACTION-DIFFUSION ALGORITHM DESCRIPTION

The DIA-RD algorithm is run by all nodes that want to transmit some information at a given time. It is a distributed algorithm that obtains dense feasible transmission patterns by enhancing the number of simultaneous transmissions. Each feasible transmission pattern is built by iteratively adding new transmissions to them, until no more simultaneous transmissions can be added without corrupting any other.

### A. Previous considerations

The DIA-RD algorithm needs some assumptions to be made:

- Each node knows its own location.
- Both nodes (transmitter-receiver) belonging to a given link know each other positions.

The proposed DIA-RD maintains the classification of the demanded links into *Active*( $\mathcal{A}(m)$ ), *Candidate*( $\mathcal{C}(m)$ ) and *Discarded*( $\mathcal{D}(m)$ ) links, proposed in [2]. The concepts of *inhibition* and *activation* areas [5], defined by the inhibition  $R_E^i$  and activation  $R_A^i$  radii respectively, are also present in the DIA-RD algorithm. In this case, an inhibition and activation areas are associated to each demanded link  $i$ . A *transmission probability*  $p_i[m]$  is also associated to each demanded link  $i$ , indicating whether a link is classified as active ( $p_i[m] = 1$ ) or it is classified as candidate/discarded link ( $p_i[m] < 1$ ) at iteration  $m$ . Initial values of those probabilities are shown, in [5], to be irrelevant.

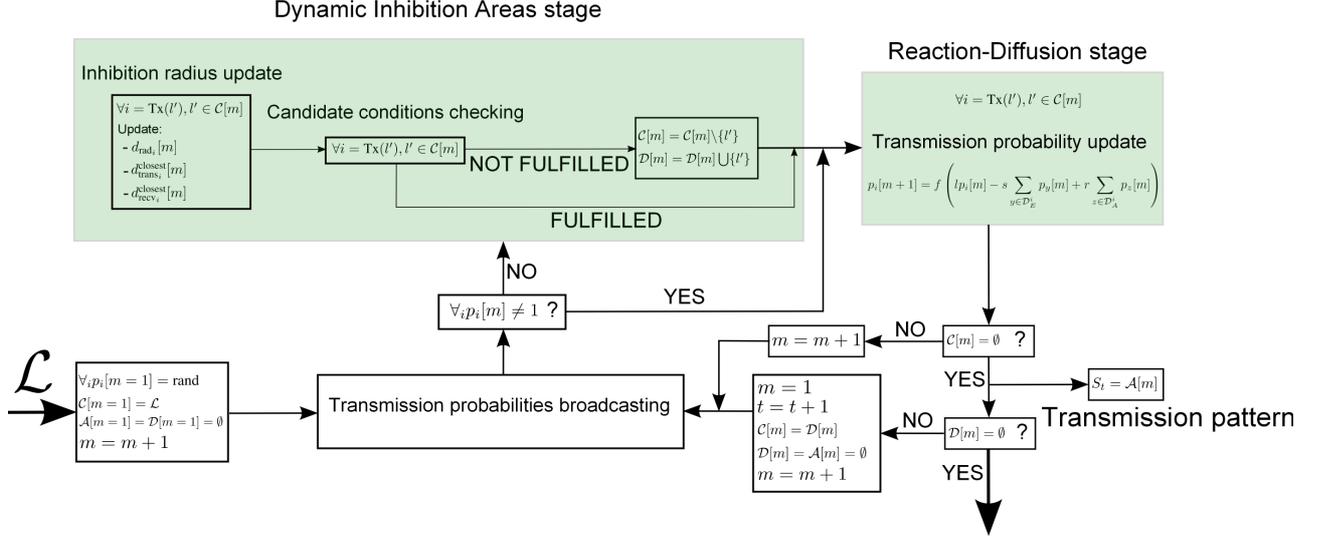


Fig. 4. Block diagram representing the DIA-RD algorithm. The block “Dynamic Inhibition Areas stage” and “Reaction-Diffusion stage” represent the two main building blocks of the algorithm.

Every node running the algorithm keeps and updates the following information:

- Its current Inhibition Radius  $R_E^i$ .
- The distance to the closest transmitter node belonging to an active link.
- Its transmission probability at the current iteration  $m$ ,  $p_i[m]$ .

According to the physical interference model, the *Signal to Interference plus Noise Ratio* (SINR) at the receiver node is the parameter that determines whether a transmission is correctly received or not. The SINR, at a node  $i$ , is given by the expression:

$$\text{SINR}_i = \frac{\frac{P}{d_{ii}^\alpha}}{\sum_{j \neq i} \frac{P}{d_{ji}^\alpha} + \sigma^2} \geq \beta \quad (3)$$

where  $d_{ji}$  is the distance between the transmitter node belonging to link  $j$  and the receiver node belonging to link  $i$ . A successful reception occurs if  $\text{SINR}_i \geq \beta$ . The *Log-distance path loss* is the chosen signal propagation model. Under this model, the power received at a given point is given by the expression  $\frac{P_t}{d^\alpha}$ , where  $P$  is the transmission power,  $d$  is the distance to the transmitter and  $\alpha \geq 2$  is the path-loss exponent. For the sake of simplicity, we assume that the channel is static during the time needed by a node to sense the channel and transmit a packet.

## B. DIA-RD process description

*Dynamic Inhibition Areas Reaction-Diffusion* (DIA-RD) algorithm is run by every transmitter node belonging to a *demanded link* that is classified as *candidate link*. It is an iterative process that obtains a dense *feasible transmission pattern* for the current time slot  $t$ . Fig. 4 shows a block diagram that represents the DIA-RD process.

Initially (iteration  $m = 1$ ), every demanded link is classified as candidate link. Since no active links are present yet, each transmitter node belonging to a candidate link calculates its own *inhibition radius*  $R_E^i$  as a function of its corresponding transmitter-receiver distance, according to the expression:

$$R_E^i[m = 1] = \left( \frac{P}{\frac{P}{d_{ii}^\alpha \beta} - \sigma^2} \right)^{1/\alpha} \quad (4)$$

which directly follows from the Signal to Noise Interference Ratio (SINR) expression (3) and where  $d_{ii}$  is the transmitter-receiver distance of link  $i$ . The corresponding activation radius  $R_A^i$  is calculated as  $R_A^i = R_E^i C$ , being  $C > 1$  time and spatial invariant. It can not be equal to 1 because it implies that  $R_A^i = R_E^i$ , eliminates the *activation area* and makes  $\mathcal{D}_A^i$  to be an empty set.  $C$  can not be very large either because active links should be close to each other, in order to maximize the spatial reusability.

Subsequent iterations  $m > 1$  start with the transmitter nodes belonging to candidate links, waiting for a random timer to expire and, then, broadcasting their own transmitter and receiver node locations, as well as their current *transmission probabilities*  $p_i[m]$ . Thus, transmitter nodes belonging to candidate links, placed within their transmission range, receive the transmission probabilities from other candidate links.

If the transmitter node belonging to a candidate link  $i$  receives a transmission probabilities equal to 1, from the transmitter node belonging to link  $j$ , this means that link  $j$  became active in the previous iteration. In this case, the transmitter node belonging to link  $i$  runs the *Dynamic Inhibition Areas* (DIA) stage. The inhibition radius belonging to the candidate link  $i$  is updated according to the expression:

$$R_E^i[m + 1] = \frac{d_{ji}}{\left( \left( \frac{d_{ji}}{R_E^i[m]} \right)^\alpha - 1 \right)^{1/\alpha}} \quad (5)$$

where  $d_{ji}$  is the distance between their own receiver node and the transmitter belonging to the new active link  $j$ . This distance can be computed by each candidate link because every link has been broadcasting its transmitter and receiver locations. Fig. (2) shows how inhibition areas around each candidate receiver node are updated as more active links are included in a feasible transmission pattern. Candidate links also update, if necessary, the location of the closest transmitter node belonging to an active link. The DIA stage finishes when the transmitter node belonging to the candidate link  $i$ , checks if the closest transmitter node belonging to an active link is **not inside** its inhibition area. If this condition is fulfilled, link  $i$  remains as a candidate link and keeps running the algorithm. Otherwise, link  $i$  becomes a discarded link and stops running the (DIA-RD) algorithm. Active links just keep broadcasting their location and transmission probability ( $p_i[m] = 1$ ) in each iteration.

If none of the transmission probabilities  $p_j[m]$ , received by the transmitter node belonging to link  $i$ , is equal to 1, this means that no candidate link became an active link in the previous iteration. Thus, inhibition and activation areas are not updated, that is,  $R_E^i[m+1] = R_E^i[m]$  and  $R_A^i[m+1] = R_A^i[m]$ . The DIA stage is **no executed**.

Regardless of whether the DIA stage is executed or not, the *Reaction-Diffusion* (RD) stage is executed by every candidate link  $i$ , at every iteration  $m$ . In this stage, the transmitter node belonging to candidate link  $i$ , updates its own transmission probability  $p_i[m]$ , according to the Reaction-Diffusion update expression (1). It is a function of its own transmission probability at iteration  $m-1$ , but also function of the transmission probabilities received from transmitter nodes belonging to other candidate and active links, placed inside its own inhibition  $\mathcal{D}_E^i$  or activation area  $\mathcal{D}_A^i$ .

When no candidate links are left (every link is classified as active or discarded), active links at this iteration form the feasible transmission pattern corresponding to the current time slot  $t$  (subset  $S_t$ ). Then, discarded links become candidate links again and the whole process is repeated for these remaining candidate links, in order to obtain a new feasible transmission pattern for the next time slot  $t+1$ . The DIA-RD algorithm finishes when, after assigning a set of active links to the corresponding time slot, no discarded links are left.

## V. DYNAMIC INHIBITION AREAS REACTION-DIFFUSION CONVERGENCE

In [5], the convergence of the Reaction-Diffusion process is shown for time invariant *inhibition* and *activation areas*. Concretely, the process always reaches equilibrium points where every *transmission probability*  $p_i[m]$  becomes either 1 or 0, forming a *feasible transmission pattern*. Since our DIA-RD algorithm is based on dynamic inhibition and activation areas, in the next paragraphs we show that:

**Proposition 1.** *The Reaction-Diffusion process converges to equilibrium points that yield dense feasible transmission patterns when inhibition and activation radii ( $\mathcal{R}_E^i$  and  $\mathcal{R}_A^i$ ),*

*around each receiver node belonging to a candidate link, are updated according to our DIA-RD algorithm.*

*Proof:* This proof is based on the one that authors use in [5] to show convergence to equilibrium points when inhibition areas are time invariant. First, the function  $V[\mathbf{p}]$  is defined by:

$$V[\mathbf{p}] = -\frac{1}{2} \sum_{i=1}^N \sum_{j=1}^N a_{ij} p_i p_j + \frac{1}{2} \sum_{i=1}^N p_i^2 \quad (6)$$

where

$$a_{ij} = \begin{cases} l & \text{if } j = i. \\ -s & \text{if } j \in \mathcal{D}_E^i. \\ r & \text{if } j \in \mathcal{D}_A^i. \\ 0 & \text{otherwise} \end{cases} \quad (7)$$

By LaSalle's Theorem [7], every trajectory of a system converges to equilibrium points if:

$$\mathbf{p}[m+1] \neq \mathbf{p}[m] \Rightarrow V[\mathbf{p}[m+1]] - V[\mathbf{p}[m]] < 0 \quad (8)$$

which defines  $V[\mathbf{p}]$  as a Lyapunov function.

Without loss of generality, authors assume that, at iteration  $k + \frac{1}{N}$ , link 1 is the only one that has updated its transmission probability  $p_1[m+1]$  (see details in [5]). Then, (8) can be rewritten, in terms of (6) as

$$V[\mathbf{p}[m + \frac{1}{N}]] - V[\mathbf{p}[m]] = -\frac{1}{2}(p_1[m+1] - p_1[m]) \cdot \left( (a_{11} - 1)p_1[m+1] + 2 \sum_{j=1}^N a_{1j} p_j[m] - (a_{11} + 1)p_1[m] \right) \quad (9)$$

and

$$p_1[m+1] = f \left( \sum_{j=1}^N a_{1j} p_j[m] \right). \quad (10)$$

Considering the three segments of the piecewise linear function  $f(\cdot)$ , given by (2):

- If  $\sum_{j=1}^N a_{1j} p_j[m] \geq 1$  then  $p_1[m+1] = 1$  and

$$V[\mathbf{p}[m + \frac{1}{N}]] - V[\mathbf{p}[m]] = -\frac{1}{2}(1 - p_1[m]) \left( (a_{11} + (2 \sum_{j=1}^N a_{1j} p_j[m] - 1)) - (a_{11} + 1)p_1[m] \right) < 0. \quad (11)$$

- If  $\sum_{j=1}^N a_{1j} p_j[m] \leq 0$  then  $p_1[m+1] = 0$  and

$$V[\mathbf{p}[m + \frac{1}{N}]] - V[\mathbf{p}[m]] = \frac{1}{2} p_1[m] \left( 2 \sum_{j=1}^N a_{1j} p_j[m] - (a_{11} + 1)p_1[m] \right) < 0. \quad (12)$$

- If  $0 < \sum_{j=1}^N a_{1j} p_j[m] < 1$  then  $p_1[m+1] = \sum_{j=1}^N a_{1j} p_j[m]$  and

$$V[\mathbf{p}[m + \frac{1}{N}]] - V[\mathbf{p}[m]] = -\frac{1}{2}(a_{11} + 1)(p_1[m+1] - p_1[m])^2 < 0. \quad (13)$$

Therefore,  $V[\mathbf{p}[m + \frac{1}{N}]] - V[\mathbf{p}[m]] < 0$  for every region of function  $f(\cdot)$ , given by (2). This proves the convergence of the

system to equilibrium points when inhibition and activation areas are time invariant.

In some iterations  $m$  of our DIA-RD algorithm, the inhibition  $R_E^i[m]$  and activation  $R_A^i[m] = R_E^i[m]C$  radii, corresponding to every *candidate link*, are updated according to (5). Thus,  $\mathcal{D}_E^i[m]$  and  $\mathcal{D}_A^i[m]$  become time variant. Regarding the convergence proof, the elements  $a_{1j}$  in (9) and (10) also become time variant, resulting in

$$V[\mathbf{p}[m + \frac{1}{N}]] - V[\mathbf{p}[m]] = -\frac{1}{2}(p_1[m + 1] - p_1[m]).$$

$$\left( (a_{11} - 1)p_1[m + 1] + 2 \sum_{j=1}^N a_{1j}[m]p_j[m] - (a_{11} + 1)p_1[m] \right) \quad (14)$$

and

$$p_1[m + 1] = f \left( \sum_{j=1}^N a_{1j}[m]p_j[m] \right). \quad (15)$$

Observe that the same derivation as in (11), (12) and (13) can be used to proof that  $V[\mathbf{p}[m + \frac{1}{N}]] - V[\mathbf{p}[m]]$  in (14) is less than 0 for each of the three regions of the piecewise linear function  $f$ . The fact that the elements  $a_{1j}[m]$  are time variant does not affect the convergence because, independently of their evolution,  $\sum_{j=1}^N a_{1j}[m]p_j[m]$  always corresponds to one of the regions of function  $f$ . Thus, (11), (12) or (13) can be applied and the convergence is always guaranteed. ■

## VI. NUMERICAL RESULTS AND CONCLUSIONS

Simulations have been performed on 100 random networks consisting of 1000 nodes, randomly placed in a 5000 long side square area, using the following set of parameters.  $P = 100\text{mW}$ , path loss exponent  $\alpha = 3$ , minimum SINR threshold  $\beta = 10\text{dB}$  and background noise  $\sigma^2 = 10^{-9}\text{mW}$ . Reaction-Diffusion parameters were fixed to values  $l = 1.01$ ,  $s = 1.01$  and  $r = 0.25$ , which are the same parameters used in [5], in order to ensure fair comparisons.

Fig. 5 shows the evolution of the number of *discarded links* as more active links are assigned to the same time slot. According to the parameters shown above, the DIA-LS algorithm presented in [2], the RD-MAC algorithm [5] and our DIA-RD were run in order to solve the *Shortest Link Schedule* problem. For each algorithm, the average number of active and discarded links was calculated. Additionally, the average value of the spatial reusability indicator  $\rho$  (number of active links per area unit) is also obtained for the RD-MAC and the DIA-RD algorithms. Fig. 5 shows that the number of discarded links, as a function of the number of active links, grows much slower for our DIA-RD algorithm than for the DIA-LS and RD-MAC algorithms.

Regarding the spatial reusability, our DIA-RD algorithm obtains an average value of  $\rho = 0.21$ , while the RD-MAC algorithm obtains an average value of  $\rho = 0.14$  (33% larger spatial reusability).

The fact that our DIA-RD algorithm outperforms both the DIA-LS and RD-MAC algorithms confirms that the DIA-RD algorithm combines the advantages of both DIA-LS and RD-MAC algorithms and avoids their main drawbacks,

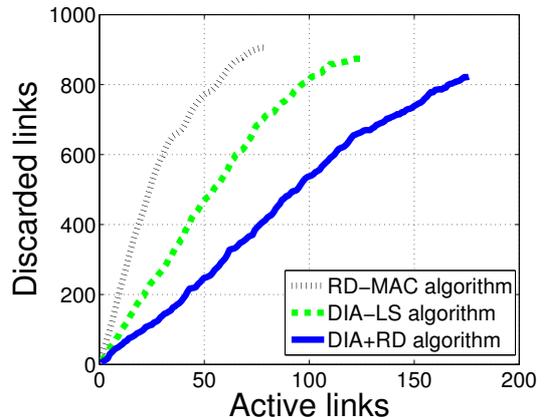


Fig. 5. Average number of discarded links as a function of the number of simultaneous active links included in a feasible transmission pattern. RD-MAC, DIA-LS and our DIA-RD algorithms are compared.

commented in section II. On the one hand, adaptive and individual inhibition areas (DIA-RD), whose radius are based on the physical interference model, lead to a more accurate interference management than the use of uniform and static inhibition areas (RD-MAC), whose radius are predefined. On the other hand, the reaction-diffusion mechanism (DIA-RD), which allows for an intelligent global behavior from simple local decisions, leads to denser feasible transmission patterns than choosing each active link that is included into a feasible transmission pattern randomly (DIA-LS).

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