Reaction-Diffusion Inspired Sensor Networking: From Theory to Application

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Abstract: Alan Turing introduced a novel Reaction-Diffusion (RD) model in 1952 to explain biological pattern formation found in animals. Since then, studies based on the RD model have long proved the feasibility of adapting it to spatial patern formation in distributed systems, especially in networking systems. In the past two decades, RD mechanism started being applied to Wireless Sensor Networks, and the possiblity of expanding to new applications is promising. In this paper, we first review the original RD model and further show its variants, known as activator-inhibitor models. Several research efforts on applying them to model tasks in wireless sensor networks will be presented and summarized.

1 INTRODUCTION

Studies in morphogenesis and mathematical chemical processes suggest ways how biological objects develop complex organisms with decentralized coordination and control. Observables are, among others, animal coats and skin pigmentation, such as spots and stripes on the skin of zebra and leopard. Indeed for networking systems demanding autonomous agents benefit from these works. Alan Turing proposed a mathematical model (Turing, 1952), known as the Reaction-Diffusion (RD) model, to explain the main phenomena of morphogenesis. The RD equations describe the chemical interaction of two morphogens, and the movement of chemical substances (i.e., morphogens) following the concentration gradients. The RD equations are partial differential equations that have the possibility of achieving analytical solutions.

Wireless Sensor Networks (WSNs) are widely applied in many fields such as military, transportation, environment monitoring, surveillance, etc. Typically, a WSN is deployed in an application environment with a set of base stations and small, low-cost, autonomous computation devices, called sensor nodes. Data transmission and routing are standard operations between sensor nodes and base stations and among sensor nodes themselves in the networks. These operations consume electrical energy that is usually supplied by the battery. Consequently, the lifetime of a WSN highly depends on the aggregated effect of battery constraints from all network components.

One of the research objectives in the wireless sensor network applications is to optimize the network lifetime which is manifested by emerging developments of energy-efficient protocols for routing in the networks. Specifically, these protocols aim to reduce energy consumption in order to maximize the network lifetime. This can be accomplished by either selecting optimal routing paths for communications between sensor nodes and the base stations, or by decreasing the volume of required data transmission or both.

In addition, due to the limited energy and network resources, applications in wireless sensor networks shall consider to be distributed and self-organizing. A robust WSN should also be scalable to the number of sensor nodes, adaptive to changing communication and resilient to failure. Under these considerations, biological mechanisms have attracted the research community of wireless sensor networks to pay more attentions to. Comprehensive surveys can be found in (Ren and Meng, 2006; Dressler and Akan, 2010b; Dressler and Akan, 2010a; Nakano, 2010; Zheng and Sicker, 2013; Nakas et al., 2020; Singh et al., 2021).

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Since the Turing Reaction-Diffusion model had been proposed in 1952 (Turing, 1952), many subsequent studies for modeling biological pattern formation have been proposed. Reaction-diffusion mechanisms started to gain interests in the research community of wireless sensor networks researchers about two decades ago. However it has not yet been widely applied. Apart from the application of the reaction-diffusion mechanism in WSNs proposed in 2020 (Wu et al., 2020), the most recent research related to reaction-diffusion was presented in 2014 (Henderson et al., 2014).

In this paper, we will give an overview to Turing's RD model and introduce some notable activator-inhibitor based models inspired by the Turning RD model. The feasibility of applying reaction-diffusion models to WSNs will also be discussed, particularly the Turing reaction-diffusion model. Selected papers will be discussed to present the applications of reaction-diffusion mechanisms in the wireless sensor networks, including sensor data relaying, data gathering and so on. We hope more researchers and practitioners in wireless sensor networks gain an interest in this beautiful theory and take advantage of it.

2 REACTION DIFFUSION MODELS

2.1 Turing Reaction-Diffusion Model

The Turing reaction-diffusion model (Turing, 1952), or RD model, proposed by Alan Turing is a well-known mathematical model that explains the development of biological structures or patterns autonomously in a system of hypothetical chemical substances, called morphogens. In a system of cells, morphogens in each cell interact and diffuse to neighbor cells. If two types of morphogens are considered, called activator and inhibitor, both are assumed to regulate their own and mutual production, and diffuse spatially at their specific diffusion rates in the system. Consider that each cell in the system contains two diffusible ligand U and V, and also equips with receptors that accept U and V. When a cell is producing a morphogen and also resulting in the production of the same morphogen in adjacent cells, it is *activating*. When a cell causes other cells not to produce a morphogen, it is *inhibiting*. On this basis, U could be locally activated whereas V is capable of long-range inhibition. An individual cell can interact with a region of adjacent cells whose size is controlled by the diffusion rate of the chemical in consideration.

Given an initial state of the system, activating and inhibiting interactions exhibit chemical concentration (i.e., u, v) gradients in space and time. Under certain conditions, the system can reach a dynamic equilibrium state. Eq. (1) and (2) describe the dynamics of morphogen concentrations u and v in a RD system in the form of partial differential equations over the time step t.

$$\frac{\partial u}{\partial t} = F(u,v) - \mu_u u + D_u \nabla^2 u \tag{1}$$

$$\frac{\partial v}{\partial t} = G(u,v) - \mu_v v + D_v \nabla^2 v \tag{2}$$

In Eq. (1) and (2), $F(u,v)$ and $G(u,v)$ are the reaction terms that describe the activation and inhibition among morphogens. μ_u and μ_v represent the decay rate of U and V respectively. D_u and D_v represent the rates of diffusion or the diffusion coefficients. ∇^2 is the Laplacian operator.

The emergence of periodic patterns is formed by the following processes. First, the activator enhances both its own and the inhibitor's production. A slight perturbation of the activator's concentration will activate both the activator and the inhibitor. On the other hand, the inhibitor restrains the production of activator and decays with time. Because the diffusion coefficient of the inhibitor is assumed to be larger than the activator's, the inhibitor concentration peaks will be less steep than the activator concentration peaks. Consequently, the concentration peaks of activator and inhibitor emerge as a homogeneous pattern.

2.2 Activator-inhibitor Models

The activator-inhibitor model is a RD model that considers the activator and inhibitor described above. A few variants are seen in the literature. Each of them differs in either the hypothetical chemical ingredients, mechanisms of local interactions, or the types of patterns achieved. In the remainder of this section, we introduce three of the notable activator-inhibitor-based models.

2.2.1 The Gierer-Meinhardt Activator-inhibitor Model

The Gierer and Meinhardt activator-inhibitor model (Meinhardt, 1982) is described by equation (3) and (4), as follows:

$$\frac{\partial a}{\partial t} = \frac{\sigma a^2}{h} - \mu_a a + \rho_a + D_a \nabla^2 a \tag{3}$$

$$\frac{\partial h}{\partial t} = \sigma a^2 - \mu_h h + \rho_h + D_h \nabla^2 h \tag{4}$$

where (A,a) and (H,h) pairs correspond to the short-range autocatalytic and long-range antagonist substances/concentrations as the activator and the inhibitor respectively. In Eq. (3), $\frac{\sigma a^2}{h}$ is the growth term of the activator, where σ is the growth rate. $\frac{1}{h}$ represents the inhibition effect to the growth of the activator. $-\mu_a a$ represents the decay of the activator. ρ_a is the external source or inflow of the activator, A. Similarly in Eq. (4), the growth of the inhibitor is catalyzed by the local activator with no inhibition. ρ_h is the natural inflow of the inhibitor, H. D_a, D_h are the constant diffusion coefficients. The basic mechanism of activator-inhibitor model is depicted in Figure 1.

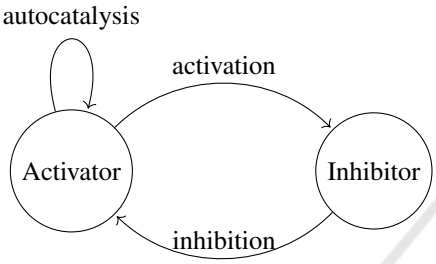

Figure 1: Relationship between Activator-inhibitor interactions.

Gierer and Meinhardt activator-inhibitor model (Meinhardt, 1982) requires some conditions to achieve the emergence of patterns. First, the diffusion rates differ significantly: $D_h \gg D_a$. Second, the inhibitor decays faster than the activator does, or $\mu_h > \mu_a$. As mentioned above, in Eq. (3), the activator concentration, a, grows proportionally to σa^2, but slows down by a factor $\frac{1}{h}$ contributed by the inhibitor, H. Particularly, the term $\frac{1}{h}$ likely comes from a third hypothetical substance, a catalyst C (Bar-Yam, 2003). Based on the existence of C, Yamamoto et al. attempted to infer a set of chemical reactions that correspond to Eq. (3) and (4). Detailed chemical formulas and reactions can be found in (Yamamoto et al., 2011).

2.2.2 The Activator-Substrate Model

Meinhardt also created the Activator-Depleted Substrate model (Meinhardt, 1982), or Activator-Substrate model based on the activator-inhibitor model. The main idea is that a substrate, S, is depleted during the autocatalytic production of the activator A. This model is described as the following Eq. (5) and (6).

$$\frac{\partial a}{\partial t} = \sigma_a s a^2 - \mu_a a + \rho_a + D_a \nabla^2 a \tag{5}$$

$$\frac{\partial s}{\partial t} = -\sigma_s s a^2 - \mu_s s + \rho_s + D_s \nabla^2 s \tag{6}$$

where (S,s) represents the substrate and its concentration. ρ_a, ρ_s are the natural inflows of A and S respectively. σ_a, σ_s are the coefficients of the growth of A and S respectively. D_a, D_s are constant diffusion coefficients of A and S. $D_s \gg D_a$ also needs to hold. In this model, the growth of the activator actually consumes the substrate S, but not affected by the inhibitor.

2.2.3 The Gray-Scott Model

The Gray-Scott Model (Gray and Scott, 1990; Pearson, 1993) is an activator-substrate-based model that considers a special set of chemical reactions. It is represented by the following equations, which describe three sources of increase and decrease for each of the two chemicals U and V:

$$\frac{\partial u}{\partial t} = -uv^2 + F(1-u) + D_u \nabla^2 u \tag{7}$$

$$\frac{\partial v}{\partial t} = uv^2 - (F+K)v + D_v \nabla^2 v \tag{8}$$

where F and K are parameters of the system. $(U,u), (V,v)$ and D_u, D_v are analogous to the parameters of A and S described in section 2.2.2. Under a well-perturbed initial state, the Gray-Scott model exhibits bistability and oscillations for a range of parameters (Gray and Scott, 1990). Moreover, the Gray-Scott model is able to form various types of spatial patterns, such as spots, strips, hexagons, and self-replicating spots (Pearson, 1993).

3 FEASIBILITY AND PRACTICABILITY OF REACTION-DIFFUSION MECHANISM IN WSNs

Characterized by autonomous pattern formation, the reaction-diffusion mechanisms are practically suited for applications that demand autonomous control mechanisms. Moreover, RD systems can help generate observable and appealing topology useful for networking purposes. For instance, Turing's reaction diffusion mechanism can generate strip patterns, which provide *path markers* for data transmission in sensor networks. Nevertheless there are several issues may influence pattern formation, such as the number of cells, uniformity of cell placement, and initial condition variations. Further whether these factors influence the feasibility of adapting the reaction-diffusion mechanism to wireless sensor networks is required to take into account.

Henderson et al. (Henderson et al., 2004; Henderson et al., 2014) showed that patterns in sensor networks can be indeed formed using Turing's reaction-diffusion mechanisms. In general, Turing's reaction-diffusion model is situated in a uniform cell environment with the equal inter-cell distance. Consider the field deployment of a wireless sensor network, sensor devices are typically dropped into the environment randomly, and inter-node distances are unlikely equal. In particular, *non-uniform placement of cells* is considered a significant issue in the pattern formation. Henderson et al. (Henderson et al., 2004; Henderson et al., 2014) investigated the effect of non-uniform spacing on the pattern computing. Their results (Henderson et al., 2004) showed that patterns can be formed by the reaction diffusion mechanisms. Specifically, computing the partial differential equations (PDEs) of the Turing's reaction diffusion model does converge under various initial conditions and random errors. The generated patterns vary based on inter-node distances of the network at different converging time or iterations.

Hyodo et al. (Hyodo et al., 2007) investigated the practicability of adopting the reaction-diffusion mechanisms in wireless sensor networks. The reaction diffusion system employed in the study is based on Eq. (1) and Eq. (2) without the decay effect. The reaction parts, $F(u,v)$ and $G(u,v)$, use the model for an emperor angel fish pomacanthus imperator (Kondo and Asai, 1995), as follows:

$$F(u,v) = max\{0, min\{au - bv + c, M\}\} - du \quad (9)$$

$$G(u,v) = max\{0, min\{eu + f, N\}\} - gv \quad (10)$$

The coefficients a and b correspond to the rates of activation and inhibition respectively. For per unit time, c and f represent the increase of morphogens, while d and g represent the decrease of morphogens. M and N are constants of limit. To assess that patterns can actually be generated in time, the wavelength l of the patterns is used as one of the measures, as follows :

$$l = 2\pi\sqrt[4]{\frac{D_u D_v}{eb-(a-d)g}} \quad (11)$$

l is derived by averaging the widths of black and white strips, where the white color represents a point or spot whose concentration of activator exceeds a certain threshold, and otherwise black.

For the simulation experiments, sensor nodes in the study are arranged in a grid. Each node can communicate with its direct neighbors. For instance, an edge node has three neighbors, which a corner node has two. The equation Eq. (1) and Eq. (2) are discretized to reflect the discrete nature of the node arrangement and information exchange. The discretization from Eq. (1) and Eq. (2) results in the following (Hyodo et al., 2007):

$$u_{t+1} = u_t + \Delta t\{F(u_t, v_t) + D_u \frac{u_t^n + u_t^e + u_t^s + u_t^w - 4u_t}{\Delta h^2}\} \quad (12)$$

$$v_{t+1} = v_t + \Delta t\{G(u_t, v_t) + D_v \frac{v_t^n + v_t^e + v_t^s + v_t^w - 4v_t}{\Delta h^2}\} \quad (13)$$

In Eq. (12, 13) , Δh and Δt represent the distance between nodes and the discrete time step respectively. u and v represent the concentrations of neighbors, n, e, s and w. The discretization is characterized by both the temporal and the spatial dimensions. Specifically, the discrete step interval of time Δt should satisfy the following condition in order to reach the convergence.

$$0 < \Delta t < min\{\frac{2}{d + 4D_u(\Delta x^{-2} + \Delta y^{-2})}, \frac{2}{g + 4D_v(\Delta x^{-2} + \Delta y^{-2})}\} \quad (14)$$

The discretization approach is verified by both analytic analysis and simulation experiments. Both results show consistent and matching wavelength measured from the generated patterns in the converged stages. In addition, two methods are proposed to accelerate the generation of patterns. Simulation results show that the number of communication and calculation required for activator's concentration to converge is decreased by increasing Δt. Nevertheless, it is also observed that larger Δt lowers the calculation accuracy. As a result, Δt needs to satisfy the condition specified in Eq. (14). The second method deals with the number of calculation of the reaction-diffusion equations, K, at each control timing. As the simulation results show, a larger K would decrease the number of communication required for the activator concentration to converge. Specifically, the effective range of K is between 0 and 40.

Besides the simulation experiments, practical prototype experiments using nodes of OKI Electric Industry verified that the prototype can generate the same pattern as in the simulation.

4 APPLICATION OF REACTION-DIFFUSION MODELS IN WSNs

Reaction-diffusion mechanisms started to gain interest in the research community of wireless sensor net-

works researchers about two decades ago, however it has not yet been widely applied. Except the application of the reaction-diffusion mechanism combining with the Gür game in WSNs to form clusters and improve the lifetime of clusters proposed by Wu et al (Wu et al., 2020) in 2020, the most recent application in WSNs was presented in 2014 by Henderson et al. (Henderson et al., 2014). In this section, we present selected examples of how the reaction-diffusion models were applied in the wireless sensor networking. We will present in these applications, if a reaction-diffusion model is selected appropriately, the desired spatial patterns can be generated autonomously to achieve the goals, such as topology control, routing and cluster head election.

4.1 Topology Control for Periodic Data Gathering

Wakamiya et al. (Wakamiya et al., 2008) proposed a reaction-diffusion based topology control mechanism to achieve energy-efficient and low-delay for periodic data gathering in wireless sensor networks. The first task is to find the best topology for the target system, which is a WSN with one sink node. The topologies considered are categorized into direct and tree topologies. In the direct topology case, sensor nodes send data to a sink directly. The direct topology consumes the most energy because of the distances between each sensor node and the sink. Among six topologies considered: direct, tree, single-multi, multi-single, and multi-multi, cluster-based topology with multi-hop transmission makes the best energy efficient and low-delay data gathering in wireless sensor networks, as shown in the Figure 2.

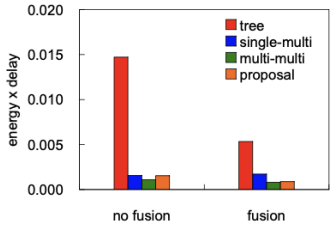

Figure 2: Comparison of topologies in terms of energy efficient and low-delay data gathering (Wakamiya et al., 2008).

4.2 Data Highway for Efficient Routing

Lowe et al. (Lowe and Miorandi, 2009) described a distributed reaction-diffusion based approach to form data highways in dense ad hoc wireless sensor networks. This approach employed data highways originated from (Franceschetti et al., 2007), which applied the Percolation Theory to construct fast-lane paths for data transmission. Specifically, data highways are cross-section data transmission paths in a network that are characterized by the high source-destination throughput. Such data highways are spatially optimized so every non-highway node is within one hop away from at least one data highway in the network.

The data highways of a network originally described in (Franceschetti et al., 2007) relied on a prior analysis of the network topology to determine the highway paths within. To enhance the flexibility and robustness of the model, Lowe et al. (Lowe and Miorandi, 2009) used a self-organizing activation-inhibition diffusion mechanism and the diffusion filter to determine the optimal data highways through a WSN.

Consider a WSN where all nodes are underlined with variables that denote temporally and spatially varying concentrations of a pair of competing substances: short-range activator and long-range inhibitor. For nodes that will serve as data highways to emerge, additionally, diffusion filters with the controlled activation axis or orientation are applied so that stripped patterns or ridges can be generated during the diffusion process in the WSN. The orientation of the diffusion filters also need to be carefully selected so the activation bands are oriented towards the data sink in the network, such as in Figure 3.

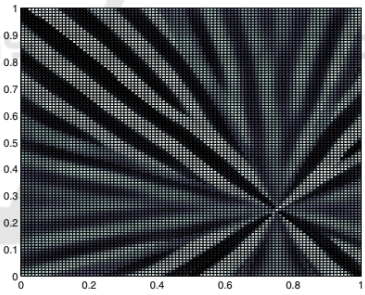

Figure 3: Sensor activation and inhibition with diffusion filters oriented towards a single data sink (Lowe and Miorandi, 2009).

For the WSN with more data sinks, the direction of the diffusion filter at node N_i can be given by the vector D_i, as follows:

$$D_i = \frac{\Sigma_{j\in S}(N_i - S_j)|N_i - S_j|^{-2}}{\Sigma_{j\in S}|N_i - S_j|^{-2}} \qquad (15)$$

where S is the set of data sinks S_i.

Once the data highways are generated, each non-highway node needs to find the closest data highway by broadcasting until it receives an acknowledge from a node that belongs to a data highway. The responding node is then used as an entry point for the broadcasting node to forward its data to the data highway and

in turn being relayed to the data sink. Additional optimization is required to ensure that data entering the data highway needs to be routed to the closest and one data sink only. This is achieved by broadcasting and exchanging the distance information along nodes on a given data highway. Numerical experiments provided in (Lowe and Miorandi, 2009) showed results that are analogous to the example in Figure 3.

In (Miorandi et al., 2009), Miorandi et al. described a refined approach based on (Lowe and Miorandi, 2009) to accommodate the fact that all nodes may not have the perfect information on the relative locations of data sinks in the WSN. The same reaction-diffusion-based data highway approach was used to construct high-throughput data highways. First, for all nodes to estimate the distance and direction to data sinks, each data sink broadcasts a beacon with its ID so all nodes can receive, update and rebroadcast the distance information.

Second, each node derives its neighborhood by broadcasting a message to its immediate or one-hop neighbors in order to learn their one-hop neighbors until all neighbors located at most R-hop are discovered, along with neighbors' level of activation.

Third, each node constructs its local *activator* and *inhibitor* regions as its *diffusion filter*, which will guide the ridge peak in the activation level to emerge and orient toward the data sinks. Specifically, for a given node n_i, if a neighbor node, n_j is on the shortest path to or from a data sink, n_j therefore is considered a activator node for the given node. That is: $n_i \in R_a$ where R_a is the activation region. In contrast, if n_j is not on the shortest path, n_j is an inhibitor node, or $n_j \in R_i$ where R_i is the inhibition region. The activation level is updated based on the discrete reaction-diffusion equation with one activation level variable u, as follows (Lowe and Miorandi, 2009; Miorandi et al., 2009):

$$u(k,t+1) = g[\phi_s u(k,t) + \Sigma_{j\in R_i}\phi_i(j)u(k+j,t) + \Sigma_{j\in R_a}\phi_a(j)u(k+j,t)] \quad (16)$$

where k is the location; R_a and R_i are the regions of activation and inhibition respectively; ϕ_a, ϕ_i, and ϕ_s are coefficients of self-activation, activation, and inhibition respectively; and g is a normalizing function. Processes of the second and the third steps are repeated until a stable pattern is formed.

The approach and the protocols have been implemented and simulated in the event-driven network simulator, Omnet++ (Varga, 2010). The simulation showed that using the described approach is able to construct valid routes (i.e. data highways) to data sinks. Two performance evaluation metrics are applied in the simulation. The first is for a given node the time of acquiring and reaching a valid data highway path to the data sink, which is shown in Figure 4. While the resulting minimum and average time are slightly sensitive to the number of nodes of the network, the maximum time attained positively depends on the number of nodes in the network.

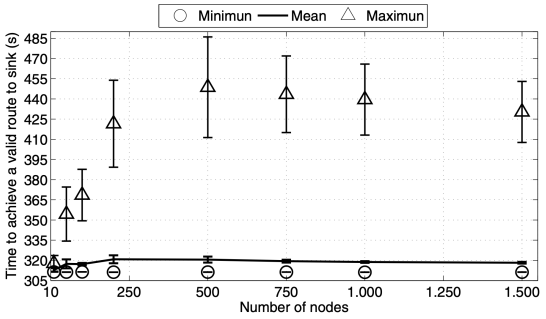

Figure 4: Bootstrapping time as a function of the network size (Miorandi et al., 2009).

The second metric was related to the overhead of the number of message-exchange needed until reaching a valid *data highway* to the data sink, as shown in Figure 5. The result shows that the number of control messages required increases linearly in the number of nodes.

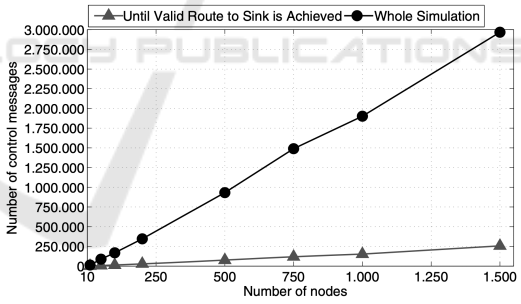

Figure 5: Number of Control messages as a function of the network size (Miorandi et al., 2009).

4.3 Cluster Formation and Cluster Head Election

In (Yamamoto and Miorandi, 2010) Yamamoto et al. evaluated two well-known activator-inhibitor models, Gierer-Meinhardt model and Activator-Substrate model, on their performance of recovery from perturbation or attacks in the case of the distributed cluster head computation. The two activator-inhibitor models are engineered to form spot patterns that correspond to activator concentration peaks. The location of such a peak is considered an autonomous processor elected

to execute important commands designated for a cluster head. As a result, the formation of the spot patterns is much analogous to the cluster head election problem.

With the goal of preserving the compatible with future artificial chemistry implementation or natural chemical computing, such as reaction-diffusion processors, the approach presented in (Yamamoto and Miorandi, 2010) first derived the chemical reactions from the reaction terms of the reaction-diffusion equations for the two models by employing the Law of Mass Action and considered an additional substance, the catalyst. The set of chemical reactions can be described by a system of ordinary differential equations (ODE), in contrast to the original reaction-diffusion equations being partial differential equations (PDE). The chemical reaction system is then simulated deterministically by integrating the system of derived ODE from the chemical reactions.

Gierer–Meinhardt activator-inhibitor model (Gierer and Meinhardt, 1972) is one of the most widely used activator–inhibitor models. Yamamoto et al. (Yamamoto and Miorandi, 2010) reverse-engineered the equations (3) and (4) to derive corresponding chemical reactions. Similarly a set of corresponding chemical reactions were derived for the activator-depleted substrate model (Meinhardt, 1982) and Gray-Scott model (Gray and Scott, 1990). These three activator-inhibitor based models were simulated according to the derived chemical reactions. Their experiment results showed a tournament between the stability of network patterns and the ability to recover upon disruption. Specifically, for a method that is more stable with rare failure, it recovers slower from disruption and vice versa as shown in Figure 6. For instance, The Gierer-Meinhardt model is more stable, but slower to recover from disruptions. The activator–substrate model is neutral that sits between the above two extremities.

Wu et al. (Wu et al., 2020) presented a Gierer-Meinhardt activator-inhibitor model (Gierer and Meinhardt, 1972) and Gür game (Tsetlin, 1973; Tung and Kleinrock, 1993; Tung, 1994; Tung and Kleinrock, 1996) based routing algorithm that tries to reduce the energy consumption of a WSN to maximize the network lifetime. The Gierer-Meinhardt activator-inhibitor model (Gierer and Meinhardt, 1972) is applied for cluster head selection and autonomous clusters formation. Within each cluster, the Gür game is to determine the active sensor nodes so that only the active nodes transmit sensing data to its cluster head to relay the aggregated data to the base station.

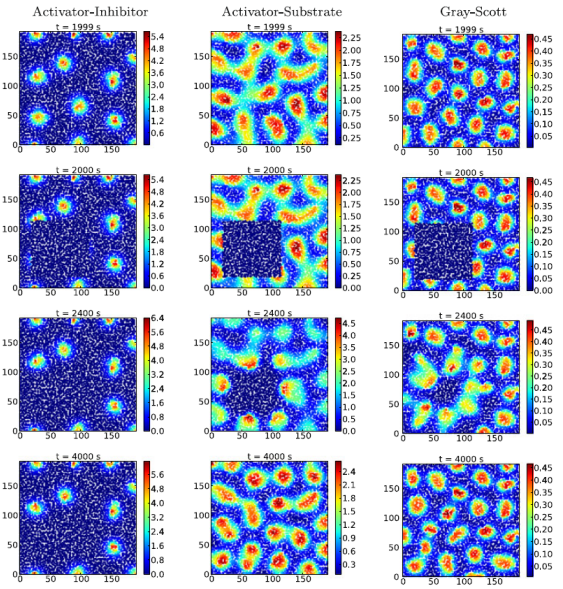

Figure 6: Recovery behavior of the three reaction–diffusion models at different time steps: t = 1999 s (before perturbation), t = 2000 s (start to introduce a perturbation), t = 2400 s (recovering), and t = 4000 s (end of simulation). (Yamamoto et al., 2011).

5 CONCLUSION

Since the first reaction-diffusion model had been proposed by Alan Turing in 1952, many subsequent studies for modeling biological pattern formation have been proposed. Reaction-diffusion mechanisms started to gain interest in the research community of wireless sensor networks researchers about two decades ago, however it has not yet been widely applied. In this paper, we gave an overview to the RD model and introduced three notable activator-inhibitor based models inspired by the RD model. Selected papers have been discussed to present the applications of reaction-diffusion mechanisms in the wireless sensor networks, including sensor data relaying, data gathering, and cluster formation and cluster head election.

In the RD-based models presented in this paper, we observe that several valuable variant models that well-suit the algorithmic purposes of assisting high level computing tasks in WSNs, such as routing and cluster head election. It is worth of further exploring whether there is a trade-off among various parameters and models when a synergy is envisioned. Although the mathematical theories of reaction-diffusion mechanics require sometimes to narrow parameter choices, the results can be useful for autonomous systems like sensor fields with distributed control.

REFERENCES

Bar-Yam, Y. (2003). *Dynamics of Complex Systems*. Westview Press.

Dressler, F. and Akan, O. B. (2010a). Bio-inspired networking: from theory to practice. *IEEE Communications Magazine*, 48(11):176–183.

Dressler, F. and Akan, O. B. (2010b). A survey on bio-inspired networking. *Computer networks*, 54(6):881–900.

Franceschetti, M., Dousse, O., Tse, D. N., and Thiran, P. (2007). Closing the gap in the capacity of random wireless networks via percolation theory. *IEEE Transactions on Information Theory*, 53(ARTICLE):1009–1018.

Gierer, A. and Meinhardt, H. (1972). A theory of biological pattern formation. *Kybernetik*, 12(1):30–39.

Gray, P. and Scott, S. K. (1990). *Chemical oscillations and instabilities: non-linear chemical kinetics*. Oxford: Oxford Science.

Henderson, T. C., Luthy, K., and Grant, E. (2014). Reaction-diffusion computation in wireless sensor networks. *Jounral of Unconventional Computing*.

Henderson, T. C., Venkataraman, R., and Choikim, G. (2004). Reaction-diffusion patterns in smart sensor networks. In *IEEE International Conference on Robotics and Automation, 2004. Proceedings. ICRA'04. 2004*, volume 1, pages 654–658. IEEE.

Hyodo, K., Wakamiya, N., Nakaguchi, E., Murata, M., Kubo, Y., and Yanagihara, K. (2007). Experiments and considerations on reaction-diffusion based pattern generation in a wireless sensor network. In *2007 IEEE International Symposium on a World of Wireless, Mobile and Multimedia Networks*, pages 1–6. IEEE.

Kondo, S. and Asai, R. (1995). A reaction–diffusion wave on the skin of the marine angelfish pomacanthus. *Nature*, 376(6543):765–768.

Lowe, D. and Miorandi, D. (2009). All roads lead to rome: Data highways for dense wireless sensor networks. In *International Conference on Sensor Systems and Software*, pages 189–205. Springer.

Meinhardt, H. (1982). *Models of biological pattern formation*. Academic Press, London.

Miorandi, D., Lowe, D., and Gomez, K. M. (2009). Activation–inhibition–based data highways for wireless sensor networks. In *International Conference on Bio-Inspired Models of Network, Information, and Computing Systems*, pages 95–102. Springer.

Nakano, T. (2010). Biologically inspired network systems: A review and future prospects. *IEEE Transactions on Systems, Man, and Cybernetics, Part C (Applications and Reviews)*, 41(5):630–643.

Nakas, C., Kandris, D., and Visvardis, G. (2020). Energy efficient routing in wireless sensor networks: a comprehensive survey. *Algorithms*, 13(3):72.

Pearson, J. E. (1993). Complex patterns in a simple system. *Science*, 261(5118):189–192.

Ren, H. and Meng, M. Q.-H. (2006). Biologically inspired approaches for wireless sensor networks. In *2006 International Conference on Mechatronics and Automation*, pages 762–768. IEEE.

Singh, A., Sharma, S., and Singh, J. (2021). Nature-inspired algorithms for wireless sensor networks: A comprehensive survey. *Computer Science Review*, 39:100342.

Tsetlin, M. (1973). *Automaton theory and modeling of biological systems: by ML Tsetlin. Translated by Scitran (Scientific Translation Service).*, volume 102. Academic Press.

Tung, B. and Kleinrock, L. (1993). Distributed control methods. In *High Performance Distributed Computing, 1993., Proceedings the 2nd International Symposium on*, pages 206–215. IEEE.

Tung, B. and Kleinrock, L. (1996). Using finite state automata to produce self-optimization and self-control. *Parallel and Distributed Systems, IEEE Transactions on*, 7(4):439–448.

Tung, Y.-C. (1994). Distributed control using finite state automata.

Turing, A. M. (1952). The chemical basis of morphogenesis. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences*, 237(64):37–72.

Varga, A. (2010). Omnet++. In *Modeling and tools for network simulation*, pages 35–59. Springer.

Wakamiya, N., Hyodo, K., and Murata, M. (2008). Reaction-diffusion based topology self-organization for periodic data gathering in wireless sensor networks. In *2008 Second IEEE International Conference on Self-Adaptive and Self-Organizing Systems*, pages 351–360. IEEE.

Wu, S.-Y., Brown, T., and Wang, H.-T. (2020). A reaction-diffusion and gür game based routing algorithm for wireless sensor networks. In *International Conference on Mobile, Secure, and Programmable Networking*, pages 223–234. Springer.

Yamamoto, L. and Miorandi, D. (2010). Evaluating the robustness of activator-inhibitor models for cluster head computation. In *International Conference on Swarm Intelligence*, pages 143–154. Springer.

Yamamoto, L., Miorandi, D., Collet, P., and Banzhaf, W. (2011). Recovery properties of distributed cluster head election using reaction–diffusion. *Swarm Intelligence*, 5(3):225–255.

Zheng, C. and Sicker, D. C. (2013). A survey on biologically inspired algorithms for computer networking. *IEEE Communications Surveys & Tutorials*, 15(3):1160–1191.