Dynamic Sensor Collaboration in Chemical Sensor Networks

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***Abstract*—Dynamic Sensor Collaboration (DSC) is an attractive approach to address the challenge of optimal control and management of chemical sensor networks. This paper proposes two analytical models to study the effects of DSC in a network of chemical sensors. Our first analytical model employs the known analogy between the information spread in a sensor network and the propagation of epidemics across a population. The second model describes the same process (DSC) by using a framework of network theory. We derive analytical expressions which relate the parameters of the network (e.g., network topology, number of sensors, sensing time), with its performance characteristics (probability of detection, response time of a network, fraction of active senors, etc.) and the parameters of the external challenge (the chemical pollutant and environment). The paper also presents numerical simulation results in support of the analytical models.**

I. Introduction

Chemical sensor networks have a wide range of applications spanning from technological and environmental monitoring to defence and security systems (see [1],[2],[3],[4] and references therein).

The optimal control and management of such networks is a challenging task, which often requires employment of many optimisation criteria to achieve the best performance for a given set of operational scenarios and, if possible, to prolong the lifespan of the network. One attractive approach to this optimisation problem is to employ so-called Dynamic Sensor Collaboration (DSC) [1],[5],[6]. DSC implies that a sensor in the network is invoked (activated) only when there is an information gain for its activation [6]. For each individual sensor, this information gain can be evaluated against other performance criteria of the networking system (e.g., power and other resources constraints, detection time) to find an optimal solution in given circumstances. Consequently, the DSC-based approach provides a rigorous framework to develop algorithms for optimal scheduling of sensing resources.

For a network of chemical sensors, the optimisation problem becomes even more important because modern chemical sensors usually have a sampling unit (fan, mixer, etc.) that is resource demanding (energy, maintenance). This necessitates an application of the DSC approach to reduce the average sampling time of the chemical sensors and thus extend the network lifespan.

A rigorous framework for DSC algorithms involves continuous estimation of the state of each sensor in the network which usually requires extensive computer simulations [1],[5],[6]. These simulations may become unpractical as the number of sensors in the network increases. This motivates the development of another, perhaps less rigorous, but certainly simpler, approach to the problem of sensor network management and optimisation (see [2],[7],[8],[9],[10],[11],[12]) which is based on physics-based consideration. The main idea of the alternative approach is to phenomenologically employ the so-called bio-inspired (quorum sensing, epidemiology, population dynamics) or physics-inspired (graph, self-organisation and percolation theories) models to describe DSC. Because the theoretical framework for the bio-inspired or physics-inspired models is well established, it enables development of feasible theoretical models for DSC in order to evaluate (and possibly optimise) the effectiveness of DSC analytically. Evidently, the analytic (or equation-based) approach is much simpler and less computationally intensive than the simulation-based approach. Another benefit of the analytic approach is that it often leads to valuable insights into the performance of the proposed sensor system by providing simple analytical expressions to calculate vital network parameters, such as scalability, robustness, responsiveness and stability.

In the current paper, we develop and validate two simple models in which DSC is driven by the concentration of a pollutant (the external challenge) on each individual sensor.

Our first analytical model employs the known analogy between the information spread in a network of communicating agents and the propagation of epidemics across a population [9]. We extend the model initially proposed in [10].

Our second model describes the same process (DSC) by using the framework of graph theory. In this approach, the information epidemic corresponds to the percolation threshold of the network and can be described by the well-known methods of percolation theory.

We derive analytical expressions for the two models mentioned above which relate the parameters of the network (e.g., network topology, number of sensors, sensing time), with the network performance characteristics (probability of detection, response time of a network, fraction of active senors, etc.) and the parameters of the external challenge (the chemical pollutant and environment). We also present numerical simulation results in support of our analytic expressions.

Although the models presented in this paper is specific to a network of chemical sensors, the underlying analytical approach can be easily adapted to other applications (e.g., SECOAS project [2]) and other types of networks by a simple change of the model of the external challenge.

The rest of the paper is organised as follows. Section II describes the related work. A model of the environment and a model of a chemical sensor are presented in Section III. Section IV presents our first analytical model for DSC which is based on epidemic theory. Section V presents our second analytical model for DSC which combines network theory and percolation theory. Our observations related to the two analytical models are summarised in Section VI. Section VII describes the simulations and presents the numerical results. Conclusions are drawn and future work is described in Section VIII.

II. Related Work

Bio-inspired and physics-inspired algorithms have been known in computer communication for a long time (e.g., genetic and gossip algorithms, quorum sensing, epidemiological models, graph and percolation theories, chaos, and self-organisation), and they have recently become a topic of intensive research in wireless sensor networks (there is a vast list of publications on this topic; for initial review see [1],[9],[3] and refs. therein.). For instance, bio-inspired and physics-inspired models are commonly used to describe worm propagation in computer network [13], to study connectivity properties of randomly activated nodes [11], to simulate network resilience, to estimate coverage area or even to model "peer-to-peer" communication over the Internet [12]. Some publications contain rigorous derivation of these models [14], but very often, they are successfully applied based on a semi-empirical or pure heuristic approach by using a visual similarity between "breakthrough" plots of the observed variables (e.g., number of infected nodes, fraction of coverage area, transmission distance) and the logistic curves associated with the models [2],[8],[13],[11]. An extensive discussion of this subject can be found in [9].

The novelty of our approach is:

1. Application of the bio-inspired and physics-inspired algorithms to a new domain - network of chemical sensors, when the probability of hazard detection of an individual sensor is driven by the turbulent dispersion (mixing) in the environment and the underlying probability density function (PDF) has a strongly non-Gaussian shape (power-law tail with arbitrary intermittency, see (1)).

2. Development of an integrated analytical framework (sensor + network + environment) for modelling of the effect of DSC and providing analytical relationships between key parameters of the chemical sensor network (topology, response time, detection threshold, etc.) and concentration of external challenges to be detected.

3. Inter-comparison (consistency check) of bio-inspired (epidemiology) and physics-inspired (percolation) algorithms resulting in an "analytical" calibration of the proposed models (i.e., in establishing values of some configuration parameters) and refinement of the overall analytical framework for DSC.

III. Models of the Environment and the Sensors

We model DSC using a modelling framework, initially proposed in [10], which includes separate models for the environment, an individual sensor, and the whole network. It provides a modular framework that can be used to extend and improve the model incrementally.

A. The Model of the Environment

The external challenges are modelled by random time series which mimic the turbulent fluctuations of concentration at each sensor of the network. In this approach, the fluctuations in concentration C are described by the power-law probability density function of concentration $\rho(C)$. The probability density is parameterised by the mean concentration of the pollutant in the area, C_0 [15],[16]:

$$\begin{aligned}\rho(C) &= (1-\omega)\delta(C) \\ &\quad + \frac{\omega^2}{C_0}\frac{(\gamma-1)}{(\gamma-2)}\left(1+\frac{\omega}{(\gamma-2)}\frac{C}{C_0}\right)^{-\gamma}. \quad (1)\end{aligned}$$

Here the value $\gamma = 26/3$ has been chosen to make $\rho(C)$ compliant with the theory of tracer dispersion in Kolmogorov turbulence (see [15]), but it may vary with meteorological conditions. The parameter ω, which models the tracer intermittency in the turbulent flow, is in the range $[0, 1]$, with $\omega = 1$ corresponding to the non-intermittent case.

The measured concentration time series can be simulated by drawing random samples from the probability density function $\rho(C)$ at each time step. The random number generator is implemented using the *inverse transform* method based on the following steps [4] :

1) Draw a sample u from the standard uniform distribution: $u \sim U[0, 1]$.
2) Compute the value of C that satisfies $F(C) = u$, where $F(\cdot)$ is the cumulative distribution function (CDF) of the distribution of (1).

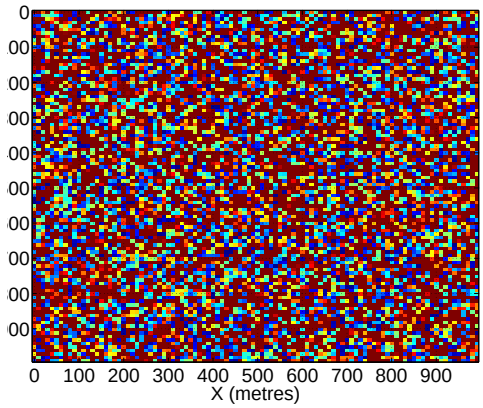


Fig. 1. An example of random concentration realisation where different concentrations are represented by different colours

We ensure that the generated concentration values are nonnegative by applying the following condition:

$$C = \begin{cases} C_0 \left(\frac{\gamma-2}{\omega}\right) \left[\left(\frac{1-u}{\omega}\right)^{-\frac{1}{\gamma-1}} - 1 \right], & u \geq 1-\omega \\ 0, & u < 1-\omega. \end{cases} \quad (2)$$

A reasonably accurate model of the contaminated environment can be implemented with the above approach which allows us to generate the concentration realisation at each sensor over time. The parameters γ and ω are typically extracted from meteorological data and will be assumed known. Fig. 1 shows an example concentration realisation generated using this algorithm; different colours are used to represent different concentrations of contaminant. In this work we do not consider any spatial correlation in the containment concentration levels.

B. The Model of a Chemical Sensor

We adopt a simple binary (or "threshold") model of a sensor, with the sensor reading V given by:

$$V = \begin{cases} 1, & C \geq C_* \\ 0, & C < C_*, \end{cases} \quad (3)$$

where threshold C_* is an internal characteristic of the sensor, unrelated to C_0 in (1). This threshold is another important parameter of our model. A conventional chemical sensor with bar readings, which includes many subsequent levels for concentration thresholds mapped into a discrete sensor output, is an evident generalisation of (3).

Using the sensor model described by Eq. 3 and the concentration PDF defined by Eq. 1, the probability of detection p for an individual sensor embedded in the environment [10] can be expressed as:

$$p = 1 - F(C_*|C_0). \quad (4)$$

This aggregated parameter links the characteristics of a specific sensor (C_*), the parameter of the external challenge (C_0), and the parameters of the environment (γ, ω).

IV. The Epidemiological Model of a Chemical Sensor Network

To describe DSC in a network of chemical sensors we employ the "epidemiologic" model (EM) initially proposed in [10] and extended in this work. We adopt the following network protocol for DSC [10]. Each sensor can be in only one of two states: *active* or *passive*. The sensor can be activated only by a message it receives from another sensor. Once activated, the sensor remains in the active state during an interval of time τ_*; then it "dies out" (i.e., becomes passive). While being in the active state, the sensor senses the environment and, if the chemical tracer is detected, it broadcasts a (single) message to its neighbors[1].

It is easy to see from a mathematical point of view that this model is similar to the epidemic SIS (Susceptible-Infected-Susceptible) model [17] and can be described by the following system of equations [10]:

$$\frac{dN_+}{dt} = \alpha N_+ N_- - \frac{N_+}{\tau_*}, \quad (5)$$

$$\frac{dN_-}{dt} = -\alpha N_+ N_- + \frac{N_+}{\tau_*}, \quad (6)$$

where N_+ and N_- denote the number of active and passive sensors, respectively. The nonlinear terms on the right hand side of (5) and (6) are responsible for the interaction between individuals (i.e., sensors), with the parameter α being a measure of this interaction. The population size (N) is conserved; that is, $N_+ + N_- = N = const$.

The main feature of the proposed model is that it supports an "information epidemic" which is associated with the "collective" detection of a pollutant. Our aim is to configure the network system in a such way that it would provide an "epidemic" (explosive) response to the threats to be detected.

An expression for parameter α in (5) and (6) can be derived by invoking the epidemiological analogy [10] and results from graph theory for networks with random breakdowns [18]:

$$\alpha = G\frac{pk}{N\tau_*}, \quad (7)$$

where k is the degree of associated graph and G is a constant calibration factor of order unity (it can be estimated during the network calibration; see below). Generalisation of k for a random network can be achieved by the standard substitution [18]

$$k \mapsto 1/(\langle k^2\rangle/\langle k\rangle - 1). \quad (8)$$

We assume this substitution in all expressions below when we need to generalise our results for the case of a sensor network with random connectivity.

By using the "conservation law" $N_+ + N_- = N$, and by a simple change of variables, Eq. 5 can be reduced to the standard logistic equation with the well-known solution

$$\eta = \frac{N_+}{N} = \frac{c}{(a-1)\exp(-bt)+1}, \quad (9)$$

[1]The described protocol assumes that a certain small fraction of, not necessarily the same, sensors is permanently active (otherwise the scheme would not work)

where $b = \alpha N - 1/\tau_*$, $c = b/(\alpha N)$, $a = b/(\alpha N_0)$ and N_0 is the value of N_+ at $t = 0$.

We can see that if $b < 0$ then $N_+ \to 0$ as $t \to \infty$ for any a, so any individual sensor activation in the network will "die out", that is, the network will not be able to detect the external challenge. The same is valid for $b = 0$ when $N_+ = const$ (no response to external challenges). We can see that an "information epidemic" occurs only if the condition $b > 0$ is satisfied. Then N_+ increases and, after some activation time τ (see below), it reaches a new steady state saturation level (a steady state):

$$\eta_s = 1 - \frac{1}{\alpha \tau_* N}. \tag{10}$$

From here, it follows that the typical time scale for the network to reach the new state (the activation or response time) is given by:

$$\tau \approx \frac{1}{b} = \frac{\tau_*}{\alpha \tau_* N - 1} = \frac{\tau_*}{Gpk - 1}, \tag{11}$$

i.e., an "epidemic threshold" for the sensor network is defined by a simple condition,

$$R_0 = \alpha \tau_* N = Gpk > 1, \tag{12}$$

or

$$p > p_c = 1/(Gk). \tag{13}$$

For a random network, the generalisation of this condition is evident.

The parameter R_0 is well known in epidemiology where it has the meaning of a *basic reproductive number* [17]. Observe that sensor sampling time τ_* will disappear from the expression for R_0 for any topology (7). This means that it is possible to create an "information epidemic" (i.e., detect a chemical pollutant) for any value of τ_* provided this time is long enough for a sensor to detect the chemical tracer.

From (10) and (11), we can deduce a few important expressions for the activation time (network response) and for the fraction of active sensors (they will be later validated by our computer simulation):

$$\frac{\tau_*}{\tau} = \alpha \tau_* N - 1 = Gpk - 1 = q(k)(p - p_c), \tag{14}$$

$$\eta_s = 1 - \frac{1}{Gpk} = \frac{p - p_c}{p}, \tag{15}$$

$$\eta_s \approx q(k)(p - p_c), \quad p \approx p_c, \tag{16}$$

where $q(k) = Gk$ and p_c is determined by (13).

V. The Percolation Model of a Chemical Sensor Network

Another analytical model that can provide important insights into the properties of a network of chemical sensors can be derived by applying ideas from percolation theory to the underlying graph. Hereinafter, we call this the Percolation Model (PM).

Let us suppose that the i-th sensor node has a set of *neighbours*, $\mathcal{K}_i$. The number of elements in $\mathcal{K}_i$, k_i, is referred to as the degree of node i and, in general, may vary from node to node. Because a sensor cannot send an activation message to itself, the network is an undirected graph without self loops.

We analyse the behavior of this networking system in discrete time steps assuming a completely synchronised mode of operation of the sensors in which all sensors start and complete the sensing activity during a single time step. The time step is chosen to be greater than or equal to τ_*, which ensures that all active sensors complete their detection activity during a single time step. Each active sensor that detects the chemical trace during the discrete time step corresponding to time $t - \tau_*$ sends an activation message to its neighbours, and the system moves to the next time step. The equation for network dynamics can be written in the form

$$p_i^a(t) = 1 - \prod_{j \in \mathcal{K}_i} (1 - p_j^b(t - \tau_*)), \tag{17}$$

where

$$p_i^b = p_i^a \times p_i^d, \tag{18}$$

$p_i^b(t)$ is the probability of broadcasting of the i-th sensor, $p_i^a(t)$ is the probability for the i-th sensor to be active and $p_i^d(t)$ is the probability for the i-th sensor to detect tracer. The fraction $\eta(t)$ of active nodes in the network can therefore be given as the average of p_i^a computed over all nodes:

$$\eta(t) = \tfrac{1}{N} \sum_{i=1}^{N} p_i^a(t). \tag{19}$$

Because we consider the case where the concentration level of the chemical tracer is homogeneous with respect to space, all nodes have identical detection probabilities p. That is,

$$p_i^d = p, \tag{20}$$

where p is given by Eq.(4).

Eqs. (17), (18), and (19) provide a framework for our numerical simulations (see below).

Let us now consider a network that is homogeneous with respect to node connectivity with each node having a degree k (deterministic network). It is evident that at steady state the probability of activation of nodes will be equal. Therefore, the probability of activation at steady state will be equal for each node and Eq.(17) reads

$$\eta_s = 1 - (1 - p\eta_s)^k. \tag{21}$$

This equation can be simply derived from the "mean-field" arguments widely used in percolation theory [18], [19]. The value of η_s can be considered as the probability that a randomly selected sensor is in the active state. Then $p\eta$ is the probability that this sensor detects a pollutant and sends a message to its k neighbors in the network; so, $1 - p\eta$ is the probability for a sensor not to send an activation message. On the other hand, the probability that a randomly selected sensor is in passive state is $1 - \eta$. Thus, we arrive at the condition $1 - \eta_s = (1 - p\eta_s)^k$ from which follows Eq.(21). This is the equation for a "giant" cluster in percolation theory [18],[19].

By setting $\eta_s = 0$ in (21), we can find a percolation point for this system:

$$p_c = 1/k, \tag{22}$$

which corresponds to the "information epidemics" in EM. This immediately fixes the only calibration constant in the EM (13), i.e., we can set $G = 1$.

From this equation, we can find an asymptotic for η when it is far from the percolation point p_c:

$$\eta_s = 1 - \exp(-pk), \quad p \gg p_c. \tag{23}$$

It is worth noting that, in contrast to the EM, the PM approaches the saturation level much faster (exponential against power law, see (15) and Fig. 2). It will be later confirmed by our numerical simulations.

Since $\eta = 0$ at $p = p_c$, we need to modify this expression in the following way

$$\eta_s = 1 - \exp[-q(k)(p - p_c)]. \tag{24}$$

where $q(k) = k$. A more accurate representation for η near the percolation point p_c can be obtained by using series expansion of (22) for small values of η_s and keeping only the first two terms in the expansion. Thus, we can arrive at

$$\eta_s = \frac{2(p - 1/k)}{p^2(k-1)} \approx q(k)(p - p_c), \quad p - p_c \ll p_c, \tag{25}$$

where $q(k) = 2k^2/(k-1) \approx 2k$ for $k \gg 1$.

The simple equation describing the evolution of $\eta(t)$ in the PM (a continuous analogue of (17) can be derived from (17), (21)

$$\frac{d\eta}{dt} = 1 - \eta - (1 - p\eta)^k, \tag{26}$$

and reduced to a simplified form based on the phenomenological arguments

$$\frac{d\eta}{dt} = -\frac{B}{\tau_*}\eta^\nu(\eta - \eta_s). \tag{27}$$

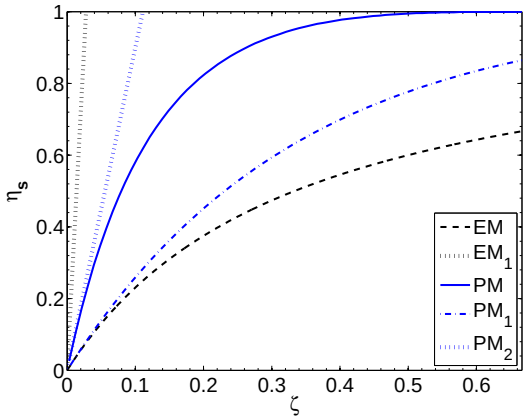
Here η_s is the solution of (21), $B = const$, and parameter $\nu(k)$ is undetermined within the phenomenological approach, but can be derived from numerical simulations (see below). This generalised logistic equation (27) simply captures the fact that $\frac{d\eta}{dt} = 0$ at the equilibrium ($\eta = \eta_s$) and (possibly) at the percolation point ($\eta = 0$), see Fig 3,4. Near the equilibrium point, this equation has an obvious solution

$$\eta - \eta_s \sim \eta_s \exp(-t/\tau), \ \tau = \tau_*/(B\eta_c^\nu), \tag{28}$$

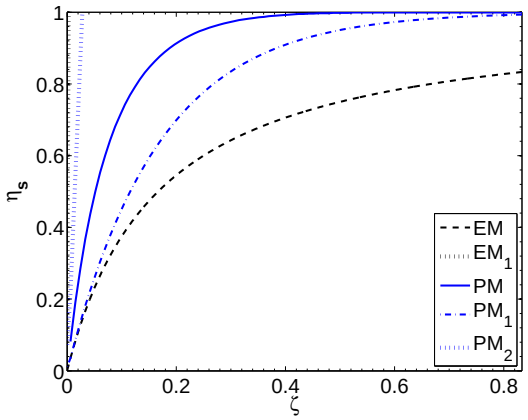
where τ is the network response time. The comparison with (25) provides a scaling law for the network response (activation) time

$$\frac{\tau_*}{\tau} \sim [k(p - p_c)]^\nu. \tag{29}$$

The parameters ν and B can be derived either from numerical simulations (see below) or by comparison with other models. A comparison with the EM (15) provides a simple estimate $\nu \approx 1$ (see Fig. 7).



(a) $k = 3$



(b) $k = 6$

Fig. 2. Summary of analytical model predictions: EM - Epidemiological Model (15), EM_1 - EM approximation (16), PM - numerical solution of Percolation Model (21), PM_1 - PM approximation (24), PM_2 - PM approximation (25)

VI. Analytical Observations

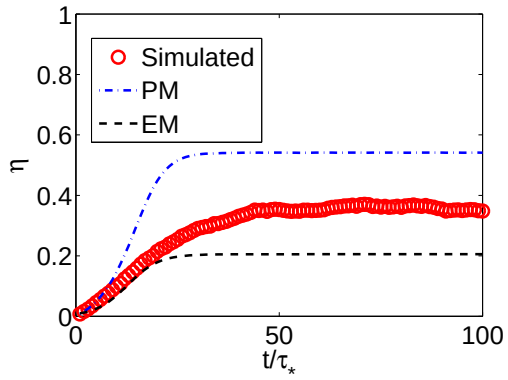
The inspection of the analytical expressions (15), (21), (24), (25) and (29) provides an important observation that the saturation limit η_s and the activation time τ of the network are determined not by values of p and k separately, but only by the combination pk. This property of "particular self-similarity" allows us to introduce a new "scaling" variable

$$\zeta = k(p - p_c) = kp - 1, \tag{30}$$

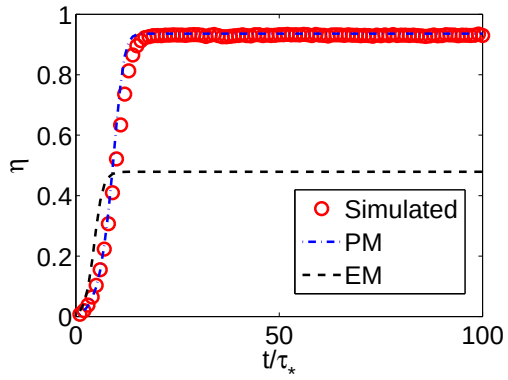
and to present our simulation results in a general form for all p and all k. For instance, the percolation point always corresponds to the origin on the graphs (i.e., $\zeta = 0$) regardless of the underlying network topology (k), detection threshold (C_*) and characteristics of the environment (i.e., p).

The results of our analytical findings are summarized in Fig. 2, where we plot the fraction of active sensors at steady state (η_s) as a function of ζ. We use Eq. (7) with $G = 1$ for parameter α in EM, and Eq. (24) with the "shape function" $q(k) = k$ (Eq. (16)), and $q(k) = 2k^2/(k-1)$ (Eq. (24)) in PM. Presented in the figure is also a numerical solution for

PM (Eq. (21)) with its analytical asymptotics (Eq. (24) and Eq. (25)) and analytical solution of EM (Eq. (15)) with the linear asymptotic (Eq. (16)). We can see that in the interim range of p ($p_c < p < 1$), corresponding to $\zeta > 0$ in Fig. 2, EM always provides much lower estimation of η_s. The linear asymptotics (dotted lines) are valid only in the very narrow region around $p - p_c$ (i.e., $\zeta \approx 0$), where EM-based expression (16) seems to provide better approximation.



(a) $p = 0.42$



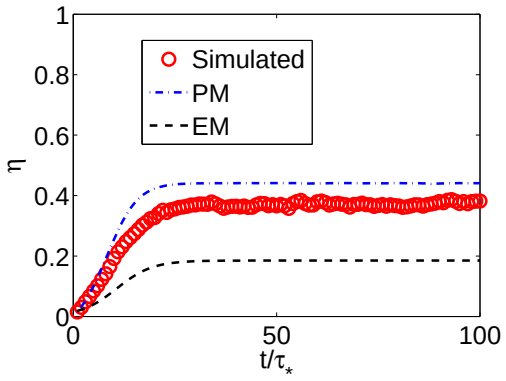
(b) $p = 0.64$

Fig. 3. Fraction of active nodes vs. time step for k = 3

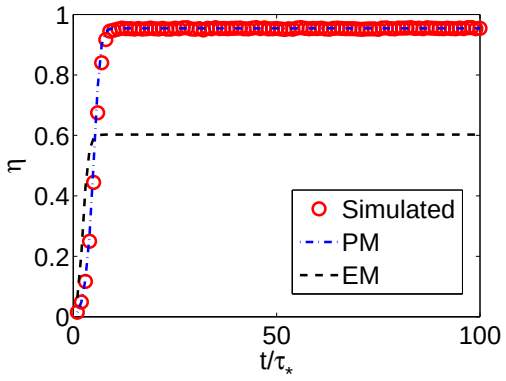
VII. Numerical Simulations

To validate the analytical models, we developed a MATLAB simulation of a network of chemical sensors operating in the turbulent environment (1) collaborating according to the adopted protocol. Numerical simulations were carried out for various values of the parameters of the network (p, k, τ_*, C_*, N) and the environment (C_0), each distinct combination of parameter values defining a different scenario. Hundred Monte Carlo runs were performed on each scenario to suppress fluctuations and produce meaningful "ensemble-averages". Then these averages were compared with the predictions of the Epidemic Model (EM) and Percolation Model (PM) presented in Sections IV and V respectively.

The aims of our study were:



(a) $p = 0.20$

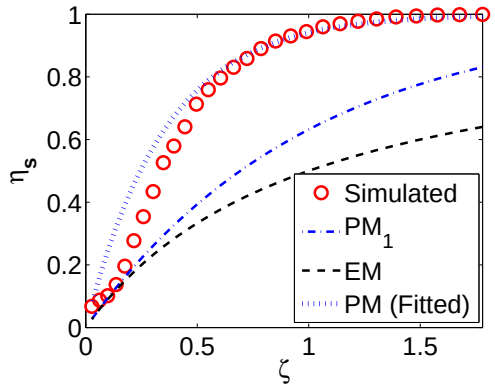


(b) $p = 0.42$

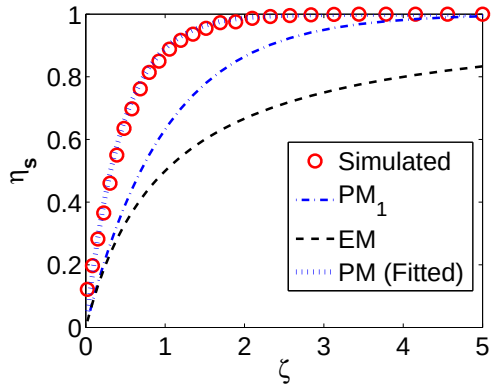
Fig. 4. Fraction of active nodes vs. time step for k = 6

1) To simulate conditions for IE (i.e., $pk > 1$) and observe this effect in the network of chemical sensors. Identify the influence of topology (parameter k) and the main parameters of the environment and individual sensor (p, τ_*, C_*, C_0, and N) on the "information epidemic";
2) To compare saturation limits and activation times with the values predicted by the analytical models (EM and PM);
3) To validate some universal relationships (scaling laws) predicted by the model (i.e., (29));
4) To derive the best fit for the the "shape function" $q(k)$ in (24) from computer simulations (i.e., from the solution (15)) and compare it with the analytical expressions provided by models (7);

Figs. 3 (a) and (b) compare η vs. time step from EM (Eq. (9)) and PM (Eq. (19)) with the results of the simulation for two different values of p: one near the percolation point, and the other far from the percolation point for a network with $k = 3$ and $N = 400$. Fig. 4 shows similar plots for a network with $k = 6$ and $N = 400$. We observed that for values of p further from the percolation point, PM provided better agreement with simulation. For values of p close to the percolation point, EM sometimes performed better. In general, the simulation results lie between the predictions provided by PM and EM, rapidly



(a) $k = 3$



(b) $k = 6$

Fig. 5. Fraction of active sensors as a function of probability of detection (30)

approaching PM for higher values of p. Figs. 5 (a) and (b) compare η_s from the numerical simulation with η_s predicted from EM (15) and PM approximation (24) ($q(k) = k$), for $k = 3$ and $k = 6$ and network size $N = 400$.

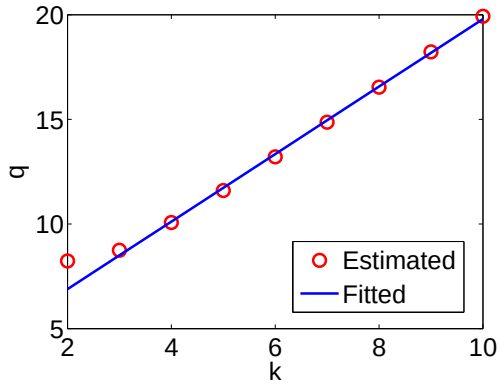
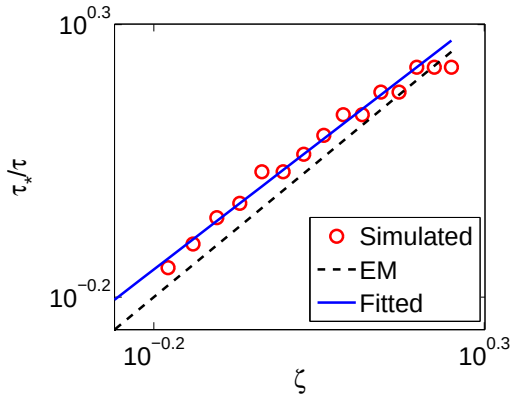
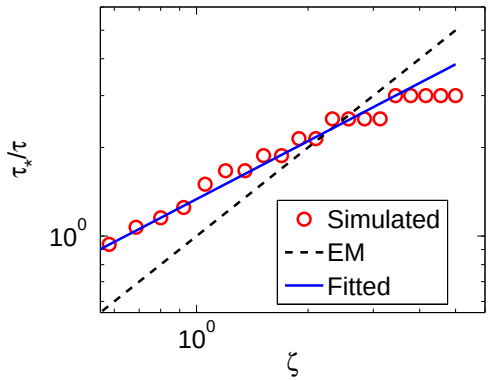


Fig. 6. Fitting values for "shape function" $q(k)$ for different k

Our next step was to find a universal approximation for the "shape function" $q(k)$ (24) by treating it as a fitting function. Motivated by the analytical solutions (16), (25), we proposed a linear fit $q(k) = ak + b$ and found an excellent agreement of this "shape function". The dotted lines in Fig. 5 (a) and (b) show η_s obtained by fitting $q(k)$. Fig. 6 shows the values of q obtained by curve fitting plotted as a function of k, and the corresponding linear fit with $a = 1.7$ and $b = 3.7$. It is worth noticing that the estimated value of a resides within the range $1 \leq a \leq 2$ imposed by EM and PM (see (16) and (25)).



(a) $k = 3$



(b) $k = 6$

Fig. 7. Scaling law for network activation time (29) as a function of probability of detection (30)

Our last step was to verify a scaling law for network activation time predicted by (29). We plotted (τ_*/τ) against ζ in log-log scale and derived slopes of the graphs (the values of the slopes are equal to ν in (29)). Because prefactor B in (29) was not defined, we were able to shift plots vertically for a better visual comparison. The derived value of ν, which was ≈ 1 for $k = 3$, gradually reduced to $\approx 1/2$ for $k = 6$ (see Fig 7). This behaviour leads to a simple approximation formula $\nu(k) = a/k$ with $a \approx 2.9$. The latter relationship provides the last undetermined parameter in the phenomenological equation for PM (27), explicitly linking it with the connectivity of network (constant B can be absorbed in the definition of τ_*).

VIII. Conclusions and Future Work

We proposed and validated two analytical models of a network of chemical sensors with DCS for the purposes of

energy/resourse conservation and information gain. The proposed models leverage on the existing theoretical discoveries from epidemiology and percolation theory for the analysis of network dynamics. The Epidemiological and Percolation models enabled us to formulate analytically the conditions for the network to respond in the coherent regime to the external challenges (“information epidemic”). Thus, we found an optimal configuration which, within the underlying assumptions, yields a balance between the network topology, number of sensors, detected concentration, the sampling time and the threshold of an individual sensor. The findings are partly supported by numerical simulations.

The numerical results presented above are mostly for illustration purposes only. More extensive simulations will be required to validate these models and underlying assumptions under more general conditions (random topology, random thresholds of individual sensors, high intermittency, etc.). The modular architecture of the proposed simulation framework (sensor + network + environment) provides flexibility to make incremental improvements by enhancing individual components while keeping the whole framework unchanged. For instance, we plan to use a more complex model for intermittency parameter ω in (1) to parameterise turbulent dispersion in canopies (see [20],[16]), “bar-reading” chemical sensors [21], and more advanced algorithms for activation message processing (when probability of detection by an individual sensor is conditioned on the number of messages received). These enhancements will be addressed in a separate publications.

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