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Energy-Aware Tracking of Mobile Targets by Bacterial Nanonetworks

Nabiul Islam, Saswati Pal, Sasitharan Balasubramaniam, *Senior Member, IEEE*, Sudip Misra, *Senior Member, IEEE*

Abstract—The functioning of bacterial nanonetworks as a "drug delivery system" requires the engineered bacteria to track the targets, such as harmful micro-organisms, pathogens, or chemical weapons to release drug molecules effectively. The coordinated and intelligent movement of energy-constrained engineered bacteria is desired for successful tracking of mobile targets. In this work, first, we analyze the energy consumption by engineered bacteria for releasing molecules and propagating for the tracking process. Then we show that the events of the release of molecules by engineered bacteria and their propagation are interlinked in such a way that the strategy of releasing attractants upon detecting the target is coupled to the energy available with the engineered bacteria. Based on the finding, we propose an energy-aware algorithm, named as EnPoS, which probabilistically selects a group of engineered bacteria among the deployed bacterial population to release signaling molecules over a particular time period in order for engineered bacteria to track the mobile targets. The simulation results show better performance of the proposed algorithm as compared with the basic algorithm incorporating continuous releasing of signaling molecules, concerning the energy expenses, mean displacement over time, and distribution of the engineered bacteria around the targets.

Index Terms—Mobile target, target tracking, energy-aware, bacterial nanonetwork, drug delivery system.

1 Introduction

The design and development of target drug delivery systems using emerging communication and networking technologies, such as nanoscale communication networking have gained increased attention recently [1], [2]. This is due to the fact that it is possible to reach unprecedented locations of the environment of interest with higher precisions and accuracies using nanonetworks. Bio-inspired molecular communication which allows information transfer among biological and artificial components, serves as potential carriers of active drug molecules which are released eventually upon reaching the desired target areas. The widely reported biosensors include genetically *Engineered Bacteria* (EBs) or genetically modified cells [3]. EBs are the bacteria that are genetically modified in order to achieve specific features via the tools of synthetic biology [4]. Henceforth in the paper, we use the acronym EBs for biosensor nodes. The area of interest to be targeted can be either static or mobile or both. Targets are the harmful micro-organisms, pathogens, unhealthy cells, or chemical weapons that impose a potential threat to the environment as well as inside human body. Earlier works [5], [6] in target tracking using biological entities, such as bacterium-based biosensors modeled the process through two types of signaling molecules namely, repellents and attractants. They focused on the continuous release of repellent molecules that would diffuse in the environment. However, in fluidic environment diffusion is a slow process which results in delayed tracking process [7]. Moreover, the detection and tracking of the target following the diffusive process occur over a long distance, which incurs sufficient energy of the EBs limiting the performance of the tracking. Most of the works on target tracking focus on static targets as in targeted drug delivery systems [1], [8], [9]. To track the mobile targets, previous works in [5], [10] have considered the continuous release of signaling molecules, such as repellents and attractants by the deployed EBs in a specified environment. Upon detecting a target, the EBs emit attractant molecules, thereby attracting other EBs around the target. The successive propagation and continuous release of repellent molecules incur a good deal of resource utilization limiting the EBs in sufficient concentration of attractants. By the time EBs harvest energy through chemical reactions from the environment, the mobile target moves to some other position. Therefore, a more generic energy-aware model is required to design the tracking of mobile targets.

Most of the approaches focus on the foundations of mobility model and networking without considering the energy requirement. The sensor nodes in conventional networking system are equipped with external power supplies or batteries. However, the energy for bioinspired sensor node is scarce and limited. The EBs need to harvest energy from the nutrient-rich environment. For example, a bacterium needs to consume food via chemical reactions to gain energy from the surrounded environment. The limited energy storage in a typical bacterium-based biosensor motivates us to propose an energy-aware mobility model for tracking of mobile targets.

In this work, a novel energy-aware mobile target tracking protocol is proposed using the novel properties

N. Islam and S. Balasubramaniam are with the TSSG, Waterford Institute of Technology, Ireland. (E-mail: nislam@tssg.org; sasib@tssg.org)
S. Pal is with the School of Nano-Science and Technology, Indian Institute of Technology Kharagpur, India. (Email: saswatipal@iitkgp.ac.in)
S. Misra is with the Department of Computer Science and Engineering, Indian Institute of Technology Kharagpur, India. (E-mail: sudip_misra@yahoo.com)

of the EBs. While the continuous release of signaling molecules provides a platform to track moving targets, it is highly resource demanding. Hence, to judiciously employ the resources in the tracking of multiple moving targets, we consider a probabilistic approach, which aims to minimize the resources consumed in the network, by selecting a group of EBs based on their energy profiles in releasing the signaling molecules. Based on this probabilistic scheme, we propose an energy-aware scheme for the biased random walk model. Finally, we propose an energy-adaptive mobility model to improve the efficiency of multiple target tracking.

Numerous target tracking applications have been explored widely in wireless sensor networking domain. Few applications based on molecular communication are recently proposed.

1.1 Wireless Sensor Networks

In conventional Wireless Sensor Networks (WSNs) a considerable amount of work on energy efficient target tracking is documented concerning the trade-off between energy and quality [11] [12]. Generally, activation of multiple sensors achieve better tracking performance but at the cost of high energy consumption. In this regard, they concluded that selective activation of sensors and selective operation yields better tracking quality along with energy savings. Theoretically, the energy-efficiency in a collaborative WSN-based target tracking scheme was compared for several approaches and it was shown that selective activation for both communication and sensing operations were required for dynamic target tracking [13] [14]. To achieve improved collaborative target tracking and maximize the network lifetime, the protocol either followed a scheduling scheme [15] [16], or other routing schemes [17]. The conservation of energy was also achieved by adaptively varying the rate of the sensitivity of the network [18] [19]. Additionally, energy optimization techniques at the node, link, and network level enhanced sensor network lifetime [20]. It was also shown that predictive dynamic approaches yielded better target tracking in wireless sensor networks [21].

1.2 Molecular Communication

Initial works on target tracking [5] [10] reported the attraction and repulsion mechanism using signaling molecules for movement of networked biosensors. The mobility models proposed flagellated bacteria as biosensors that spread by the diffusion of continuously emitted repellent molecules. Majority of the works on target tracking follows the distribution of the biosensors in the environment either by diffusion-based approach [2] [22] or non-diffusion methods [23] [24] to reach the targets. A biologically realistic model was used to demonstrate that the chemotactic behavior of bacteria is favorable for target detection and tracking [25]. It is noted that these mechanisms showed low performance in case of distant targets. A decentralized coordination strategy was proposed to overcome this disadvantage by incorporating multi-hop communication among biosensors to track the distant targets. This strategy was achieved by assuming that a biosensor can sense a chemical if it is within the effective range of the chemical.

Few works relevant to energy efficient molecular communication [6] [26] concluded that bacterial relaying process are more energy efficient as compared to diffusion process over long distances. However, our work is distinct with respect to consideration of resource-constrained biosensors EBs to release signaling molecules for a specific time period to track the mobile targets. We analyze the channel model with respect to the energy utilization during propagation and tracking in the aqueous medium.

1.3 Contribution and Organization

In this work, we incorporate heterogenous scenario by considering energy-constrained EBs and multiple mobile targets. The objective of this work is to enable the energy-constrained EBs to release molecules judiciously to achieve energy-efficient tracking of the multiple targets. The specific *contributions* in this work are summarized as follows:

- We propose a novel energy-aware algorithm for bacterial nanonetworks for improved tracking performance considering the limited energy of each EB in such application.
- We obtain expressions for the energy utilized during releasing of molecules and successive propagation in the target tracking process.
- We characterize a probabilistic metric depending on the energy utilized in the tracking process. In particular, we focus on selecting the EBs, taking into account their energy utilization for releasing molecules and for the propagation of EBs.
- We analyse theoretically that the distance until a mobile target is detected by EBs using our proposed algorithm.

The rest of the paper is organized as follows. Section 2 describes the system model. The proposed protocol and the mathematical analysis of the described protocol are given in Sections 3 and 4, respectively. The results are provided in Section 5. Finally, the work is concluded along with the future directions in Section 7.

2 System Model

We consider that EBs are capable of secreting signaling molecules such as repellents and attractants in the environment and propagate in search of the mobile targets. The molecules *indole* and *isatin* are considered in this work as repellents and attractants, respectively [27]. The bacteria produce indole naturally while they lack the enzymes essential to convert indole into isatin. However, synthetic proteins are able to recruit metabolic enzymes which can regulate the conversion to isatin from indole [28]. The release of these signaling molecules is controlled by the intensity of cell-cell interaction. The cellular interaction is carried out by the quorum-sensing molecules such as, *autoinducer-2 ($AI-2$)* [27], which allow EBs to synchronize their behavior in response to the environmental stimulus. The process of *Quorum Sensing (QS)* allows EBs to estimate their local population. The EBs release autoinducers that increase in concentration to sense the local population

density. The detection of the threshold concentration leads to the sensing of the local population, and thus the EBs regulate repellent production. The synthetic quorum sensing system [29] in an EB responds to the presence of a denser local population, sets the timer and the switch on to release repellents. After a certain time interval, the switch is automatically turned off in synchronization with the timer and the chemosensory receptor in the EB monitors the local population of the region as it swims across the environment. When a target is detected, the chemosensory receptor sends a signal to the synthetic circuit of the EB, the timer is again set and the switch toggles to release attractants. This switching process regulated by QS and temporal detection controls the release of repellents and attractants as depicted in Fig. 1.

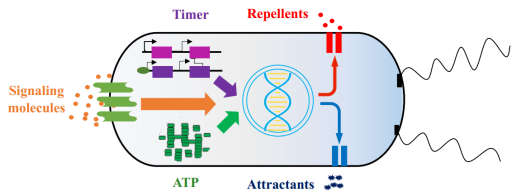


Fig. 1: Model showing switching process regulated by the timer and signaling in EBs

By employing a synthetic interaction, the bacteria that produce indole and $AI-2$ can be engineered to secrete isatin [30]. The synthetic genetic circuits perform logical evaluations of cellular information and control the environmental signals [28]. We envisage that by using synthetic quorum sensing systems and the synthetic genetic circuits, the release of QS as well as signaling molecules can be controlled [29]. The synthetic circuits enable the regulation of the desired cellular activities in EBs. The synthetic toggle switch in cooperation with the synthetic timer achieve simple switching events between two modes of molecular secretion. Firstly, we present some assumptions that are relevant to the model formulation.

Assumption 1. *We consider n number of EBs distributed over an area of $L_x \times L_y$ in a 2D plane including several mobile targets.*

Let $B_s = \{b_1, b_2, b_3, ..., b_n\}$ denotes the set of EBs and $T = \{T_1, T_2, T_3, ..., T_m\}$, a set of mobile targets that are to be tracked by the EBs in B_s.

Assumption 2. *All the EBs are capable of secreting a concentration of chemical substance omni-directionally characterized by radial range, r_{EB}, and the effective communication area is given as, $A_r = \pi r_{EB}^2$. Correspondingly, the targets have a sensing radius, r_T, and move in a straight line [31] with a speed of v_T.*

Assumption 3. *All the EBs are capable of secreting the autoinducers and the signaling molecules, repellents and attractants and assumed to sense the molecules only in its radial range, r_{EB}.*

Each EB has a chemotactic ability to detect the other EBs and change its moving direction based on the concentration gradient of the molecules in the vicinity. This coverage area, with radius, r_{EB}, is also referred to as the communication range of the EB and is considered to be same for all the EBs in B_s.

Assumption 4. *An EB is considered to follow a biased random walk mobility pattern with a step size, μ and changes its moving direction randomly with an angle, θ during each time interval, Δt.*

Considering an aqueous environment filled with uniform random distribution of EBs, the movement of such EBs is characterized by a sequence of *run* and *tumble* motion referred to as bacterial *chemotaxis*. It is determined by the randomized rotation modes of the flagella present in the cell, driven by a reversible rotary motor [32]. In our work, since the run-tumble is influenced by the autoinducers and signaling molecules in the environment, we consider a *biased random walk model* for the movement of the EBs. The detail is provided later in the Subsection 2.1.

Assumption 5. *All the EBs are considered to possess a fixed amount of energy E.*

At any time interval Δt, each EB utilizes energy to propagate and produce molecules for signaling. The energy utilized in propagation (run and tumble) is 2165.4 zJ (zeptoJoule) per second of time interval, whereas in producing one single molecule, either a repellent or an attractant, the energy utilization is 202.88 zJ [6]. However, the energy costs for $AI-2$ production is very low, a maximum of 83 zJ [6], [33]. The further details regarding the processing of energy level are provided in the subsequent Subsection 2.2. However, the nutrients absorbed during propagation is not considered in this work.

2.1 Propagation Model

The propagation mechanism used for representing the motion of an EB is based on the biased random walk. We consider an engineered bacterium, EB releasing repellent molecules in the environment, which are distributed uniformly around the EB. We assume that these repellent molecules diffuse with a constant coefficient. The concentrations of these molecules decrease with the increase in distances from their sources, and is the only phenomenon considered in this work to bias the propagation of any EB sensing the molecules in its range, r_{EB}. The EB tends to walk away from the higher concentration of repellents. On the contrary, they tend to walk towards the higher concentration of attractants. Thus, the propagation is affected by the concentration of both repellent and attractant molecules.

Let $S_i(t)$ be the initial position of an EB, b_i. After each time interval Δt, the EB travels to a new position having x and y components given as:

$$S_i^x(t + \Delta t) = S_i^x(t) + \mu_i cos\theta_i, \tag{1}$$

$$S_i^y(t + \Delta t) = S_i^y(t) + \mu_i sin\theta_i, \tag{2}$$

where μ_i and θ_i correspond to the step size and direction angle of motion in radians, respectively. The parameter θ_i is estimated as [5]:

$$\theta_i = \psi_{b_i} + \psi^r_{b_i} + \psi^a_{b_i}, \tag{3}$$

where ψ_i represents the angle due to the rotational diffusion of the EB b_i, ψ^r_i and ψ^a_i are the drift angles experienced by b_i undergoing repulsion and attraction based on the concentrations of repellents and attractants in the vicinity. The concentration of molecules are characterized in accordance with the Fick's law of diffusion, which exponentially decreases with respect to the square distance from the EB [6]. Note that the biased random walk mobility patterns of the EBs considered in our model bounce off the boundary since we have considered a confined area. This work do not consider the time taken by the repellents and attractants to diffuse away in the environment.

The run and tumble in the random walk pattern represent distance and angle, respectively. The propulsion during the run is approximately constant, and the EB moves along a straight line at a constant speed. On the contrary, during tumbling the EB changes the direction with a certain angle and relocates itself accordingly. The reorientation of the EB during run is characterized by translational diffusion, while rotational diffusion [34] characterizes restoration of equilibrium after the tumble. Thus, each run involves one translation. Since tumbling occurs from the rotation of the flagella twice, each tumble is characterized by two rotations [35]. Therefore, to cover a distance, the EB runs and tumbles alternatively, and we assume that there are $(s-1)$ number of runs while s number of tumbles. So, the time t taken to travel a distance is given as:

$$t = (s-1)\alpha + 2s\beta, \tag{4}$$

$$s = \frac{1}{\alpha + 2\beta}\left(\sqrt{(\Delta S^x)^2 + (\Delta S^y)^2}/\upsilon + \alpha\right), \tag{5}$$

where $\alpha = \frac{<\mu^2>}{6\mathcal{D}_t}$ and $\beta = \frac{<\theta^2>}{2\mathcal{D}_r}$. The terms $\mathcal{D}_t$ and $\mathcal{D}_r$ correspond to translational and rotational diffusion coefficients, respectively.

2.2 Energy Model

The primary source of energy in living micro-organisms is *Adenosine Triphosphate (ATP)* which is generated inside $Mitochondria$ by several chemical procedures, such as oxidation, phosphorylation, and glycolysis [36]. The produced energy is used in the routine activities, such as movement, secretion, and communication. In this work, we consider the energy is utilized by the EB only for releasing molecules and propagating itself. The budget for the consumption of energy E is computed as follows:

$$E = E_Q + E_R + E_P, \tag{6}$$

where E_Q is the energy utilized in releasing QS molecules, E_R and E_P are the energy consumption due to releasing repellent and attractant molecules, and propagation, respectively. The energy utilized by the EB is considered as the energy consumed in releasing the number of molecules over time and the energy consumed during propagation. The energy cost of releasing one QS molecule by a single EB is 1 units of ATP [33], which becomes $83zJ$ [6]. Considering each EB releases n_{mol} QS molecules at each time interval, E_Q in zJ is estimated as:

$$E_Q = n_{mol} \times 83. \tag{7}$$

Once a target is detected, the EB release attractants to attract nearby EB in order to track the same. Considering that the tracking process deals with releasing molecules and propagation until any of the targets are detected, at any time interval Δt the energy consumed in tracking is given as:

$$E_{track} = \sum_{i=1}^{n} E_{Q\,i} + \sum_{i=1}^{\lambda} E^r_{Ri} + \sum_{i=1}^{\Lambda} E^a_{Ri} + \sum_{i=1}^{n} E_{Pi}, \tag{8}$$

where λ denotes the number of EBs releasing repellents, Λ represents the number of EBs releasing attractants, and n denotes the number of deployed EBs. Thus for evaluating E_R, the energy consumed for releasing of repellents and attractants are considered. Following this, for a time duration Δt, E_R is estimated from [37]:

$$E_R = \int_{t_1}^{t_2} r_{EB} C_R \sqrt{2\pi D_R t} dt, \tag{9}$$

where C_R is the concentration of repellents, D_R is the diffusion coefficient of repellents, t_1 is the arbitrary initial time at which the EB starts releasing the repellents whereas, t_2 is the time when it stops releasing them. On the other hand, the energy consumed during propagation, E_P, due to both run and tumble motions, and is given by:

$$E_P = E_{run} + E_{tumble}, \tag{10}$$

$$E_{run} = \frac{KT\mathcal{D}_t t}{\mu^2}, \tag{11}$$

$$E_{tumble} = \frac{2KT\mathcal{D}_r t}{\theta^2}, \tag{12}$$

where E_{run} and E_{tumble} correspond to the energy consumption due to run and tumble, respectively, K is Boltzmann's constant and T is absolute temperature. The terms $\mathcal{D}_t$ and $\mathcal{D}_r$ correspond to translational and rotational diffusion coefficients, respectively.

3 EnPoS : Proposed Protocol

We propose an energy-aware tracking protocol, named *Energy-aware Probabilistic Selection (EnPoS)*, which is outlined in Algorithm 2. Energy utilized in releasing molecules and propagating throughout the environment plays key role to obtain *selection predictability*, which is described in the next Subsection, 4.1. In the proposed energy-aware tracking protocol, the energy utilization levels for E_R and E_P of each EB are divided into high and low energy levels. Then, the repellents are released by a set of selected EBs, which is based on the *selection predictability*. The basic idea behind the metric is not to let all the EBs release repellents continuously till one find the target. Rather, only a set of selected EBs release repellents for a certain duration of

time, Δt based on their energy levels. The diffusion of these repellents biases the movement of the neighboring EBs to detect the targets. After $t + \Delta t$ time, the energy level of all the EBs are calculated, and a new set of releasers with high energy levels are selected to release repellents. If any EB senses the target in its range, then it is considered to release attractants to attract the nearby EBs.

3.1 Selection Predictability

The $EnPoS$ is based on a probabilistic metric, termed as selection predictability, $P(b_i) \in [0, 1]$, which determines whether an EB b_i is able to release repellents, and is given as follows:

$$P^k(b_i) = \begin{cases} 1 - \frac{E_{thres}}{E_k}, & E_k > E_{thres} \\ P_{ini}, & E_k <= E_{thres}, \end{cases} \quad (13)$$

where $P_{ini} \in [0, 1]$ is an initialization constant. Since the EB initially has no prior knowledge about whether it will be selected or not, P_{ini} is set to 0.5. Owing to the fact that the probability of the selection of the EB decreases with the gradual increase in its energy utilization, P_{ini} is a function of the energy utilization. The form of the function depends on the interval since the last selection resulted in an exceed in energy usage level, following that the residual energy falls below the threshold, E_{thres}. The parameters P_{ini} is reset to the initial value 0.5 while $P(b_i)_{prev}$ is reset to 0 when residual energy of the b_i decays below the fixed threshold level, E_{thres}. Finally, if an EB has low energy level for a while, then it is less likely to be selected as a releaser. Thus the initialization constant value is reset thereby reducing the selection predictability in the process:

$$P_{ini} = 0.5 - \Gamma^k, \quad (14)$$

where Γ is the reducing constant, whose value usually is very small (for e.g., 0.01) so as not to significantly restrict the selection predictability value at 0.5 after reset, and k is the number of time intervals that have elapsed since the last time the metric was updated. The modified circadian clock in an EB maintains the metric k [38]. The time interval used is kept constant throughout the target tracking scenario.

The main algorithm, named *Tracking the Mobile Targets (TMT)*, outlined in Algorithm 1, tracks the mobile targets based on the proposed protocol, $EnPoS$ considering the sources of energy for EBs are limited. Towards this approach, we consider the bacteria are engineered so as to update the metric internally for each EB, and this is used to decide which EBs will release repellents. The information from the metric is used to decide which EBs will release repellents. The processing unit, PU in the EB embeds the amount of energy consumption through the synthesis of the energy carrier molecule, ATP [6]. In this design, the bacterial cells are programmed and engineered in gene circuit is coupled to environment-sensing modules that process the information in the surrounding. These gene circuits include sensitive elements that synthesize the information and set a threshold for probability metric and energy, P_{thres} and E_{thres}, respectively. The gene circuits act as a toggle switch when the thresholds for the parameters are reached, and flip from the *ON* state to the *OFF* state. The threshold can be adjusted by altering the RNA sequence [38].

Algorithm 1 TMT: Tracking the Mobile Targets

INPUTS: Set of deployed EBs, B_s and set of targets, T
OUTPUTS: Successful Tracking of mobile targets

while true **do**
  for all $b_i \in B_s$ **do** ▷ The computations are done by $Processing\ Unit$ in EB
    b_i emits QS molecules
    A set of releasers: $\mathcal{R} = \{\mathcal{R}_1, \mathcal{R}_2, ..., \mathcal{R}_\lambda\}$ based on $P(b_i)$ is selected ▷ $\mathcal{R} \subset B_s$
    Each $\mathcal{R}_i \in \mathcal{R}$ emits repellents
    Move b_i based on (1) and (2)
    CALL the procedure EnPoS
    if b_i detects $T_i \in T$ **then** ▷ The set of targets, T traveling either in a certain pattern or randomly
      b_i emit attractants
    end if
  end for
  Measure the mean square displacement of EB and targets
end while

Algorithm 2 EnPoS: Energy-aware Probabilistic Selection

INPUT: Set of releasers, $\mathcal{R} = \{\mathcal{R}_1, \mathcal{R}_2, ..., \mathcal{R}_\lambda\}$
OUTPUTS: Selection Predictability $P(b_i)$ and set of new releasers, $\mathcal{R}$

for $i = 1$ to I **do** ▷ I : Simulation minutes
  Set time $t = 0$
  $k = 0$
  for all $\mathcal{R}_i \in \mathcal{R}$ **do**
    $\mathcal{R}_i$ calculates E_R based on (9)
  end for
  for all $b_i \in B_s$ **do**
    b_i calculates E_Q
    b_i calculates E_P based on (10)
    b_i calculates E_{b_i} based on (6)
    b_i calculates $P(b_i)$ based on (13)
    if $P(b_i)_{prev} = P(b_i)$ **then** ▷ $E_{b_i} < E_{thres}$
      Increase k by 1
      b_i calculates $P(b_i)$ based on (14)
    end if
    if $P(b_i) > P_{thres}$ **then**
      b_i selected to release repellents
      Include b_i in $\mathcal{R}$
    end if
    $P(b_i)_{prev} \leftarrow P(b_i)$
  end for
  Update $t = t + \Delta t$
end for

The design and modification of genetic content in EB using the tools of synthetic biology make it to respond to its environment or a certain stimulus present [38]. The biological parts have the ability to process logical operations due to their circuit-like connectivity [30], [39]. In an EB, periodic synthesis and release of molecules is

autonomously achieved with the synthetic oscillator circuits or programmed time-delay circuits [38]. The selection predictabilities for each EB can be realized in two parts. Initially, the metric is updated after a certain interval of time Δt via a biological timer developed using genetic toggle switches so that EBs that cover relatively small distance have high selection predictabilities. The bacterial cells are programmed and coupled to synthetic oscillator circuits and circadian clocks to keep the track of elapsed time. The time interval considered for the updation of the above metric includes the time period until which the previous releasers release the repellents and the propagation of the EBs during that time. Depending upon the different levels of energy utilized for both releasing and propagation, four conditions may arise:

- Case 1: If the level of energy utilization is high in all the cases of E_Q, E_A, E_R and E_P, then the EB is not considered as a releaser and $P(b_i) = 0$.
- Case 2: If the utilization level is low in all the cases of E_Q, E_A, E_R and E_P, then the EB is considered as a releaser and $P(b_i) = 1$.
- Case 3: If E_Q, E_A, and E_R are high, whereas, E_P is low, then a new set of EBs is taken into consideration as releasers. This is because energy spent for releasing molecules is higher.
- Case 4: If E_Q, E_A, and E_R are low, whereas, E_P is high, the same set of EBs are considered as releasers.

If the EB, b_i has not contributed before as a releaser, then it is more preferable to select it. On the other hand, if it has contributed, it is discarded.

3.2 Description of EnPoS

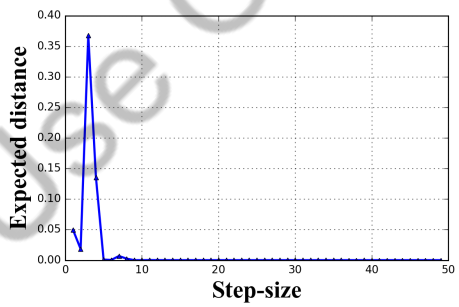
An EB has to optimize its energy utilization essentially to remain active for a longer period of time to track the mobile targets over a longer distance. Since harvesting energy involves several chemical reactions consuming considerable time [36], the performance of resource-constraint EBs degrades. We consider that as the EBs estimate a denser population via QS, they start releasing repellents in order to walk away in search of mobile targets. The major steps of $EnPoS$ are as follows. First, it lets the EBs evaluate their energy consumption in each time interval Δt and update their probability metric, which is described in preceding Subsection 3.1. Second, if the value of the metric exceeds the threshold value, then the EBs release repellents. On the other hand, if it is less then they will only propagate in the environment in search of the mobile targets.

4 Mathematical Analysis

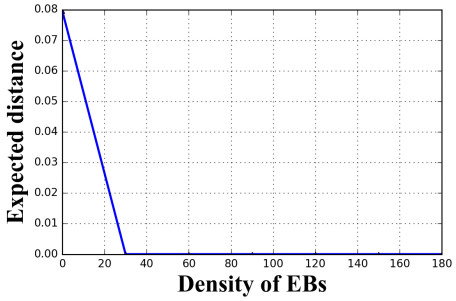
We model the confined area as a rectangle $U \subset \mathbb{R}^2$ with size $L_x \times L_y$. A total of n EBs are deployed with each b_i at locations, $S_i = (x_i, y_i) \in U$. Several mobile targets, $T = \{T_1, T_2, ..., T_j\}$ are considered in the same area with locations $(tx_j, ty_j) \in U$ where $j << n$. For the sake of simplicity, we consider only one mobile target T_j in the environment. To track a mobile target T_j, at least one of the EBs, b_i must detect the location of the target which then emits signal to attract other EBs in the form of attractants. The moving target emits a certain chemical signal which helps the EBs in detecting it. We assume all the EBs are initially concentrated in a circular disk at a location center to the confining area U with the target, T_j located at the periphery of the area. The spreading of the EBs is described with velocity $v(t)$ that depends on the constant speed, v and direction, $\theta \in [0, 2\pi]$. The mean square displacement (MSD) of an EB is given by the $Green - Kubo$ relationship [40]:

$$< \Delta^2 R(t) >= \int_0^t dt_1 \int_0^t < v(t_1).v(t_2) > dt_2, \qquad (15)$$

where $\Delta R(t)$ denotes the displacement. The area confining n number of EBs grows with increasing time as all EBs are considered to take independent random steps. Let the probability for an EB, b_i to be at distance x outside the disk area after N steps is $P_N(x)$. The probability distribution $P_N(x)$ varies with increasing number of steps. Thus the concentration of EB spreads out from the initial area as $< \Delta^2 R(t) > \propto N$ [41].



(a) With μ



(b) With δ

Fig. 2: Variation of the expected distance covered

Theorem 1. *Assuming a target T to be static, after each time interval Δt, the distance, l between the EBs and T decreases by an amount having the following expected value:*

$$< l >= \frac{exp\Big(- \Delta r^2 - \frac{\Delta \mu^2 (1+cos\theta)}{4D\Delta t} \Big)}{4\sqrt{\pi D \Delta t}} + \frac{\delta^{(k-1)} exp(-\delta(1+\pi\Delta r^2))}{2\pi(k!)} \qquad (16)$$

In Theorem 1 [1], we describe the analytical basis for computing the expected distance covered by the EBs in

1. Proof is given in Appendix, which is provided in separate supplementary file.

TABLE 1: Simulation Parameters

Parameter	Value
Simulation area	$10mm \times 10mm$
Speed of EB	50 $\mu m/s$ [6]
Translational diffusion coefficient	0.5 $\mu m^2/s$ [34]
Rotational diffusion coefficient	0.2 rad^2/s [34]
Repellent diffusion coefficient	1 $\mu m^2/s$ [6]
Attractant diffusion coefficient	49 $\mu m^2/s$ [42]
Energy per EB	1000 picoJoule [6]
E_{thres}	100 picoJoule
P_{thres}	0.7

each time interval. It is observed that the expected distance covered, $< l >$, depends on the two factors, namely the step size and density of the set of EBs. Considering one of the factors to be constant, the variations of others are shown in Fig. 2a and Fig. 2b, respectively. Evidently, as both the step-size and density of EBs increase, the expected distance between the set of EBs and the static target, T decreases. Hence, the static targets are tracked by the EBs after some time intervals, the value of which depends on how far the targets are initially away from the EBs. The successful tracking is also confirmed by simulation, as given in next Section. Next, we compute the mean free distance covered by the mobile target, T until the set of mobile EBs detect it.

Theorem 2. *Assuming a target T moving on a straight line, the mean free distance, $\mathbb{E}(\Omega)$, covered by T until it is detected by the set of EBs and tracked thereafter is computed to be,*

$$\mathbb{E}(\Omega) = \frac{e^{-\delta\pi r_T^2}}{2\pi\delta r_T}\left[1 + \frac{1}{2\pi\delta r_T}\right] \tag{17}$$

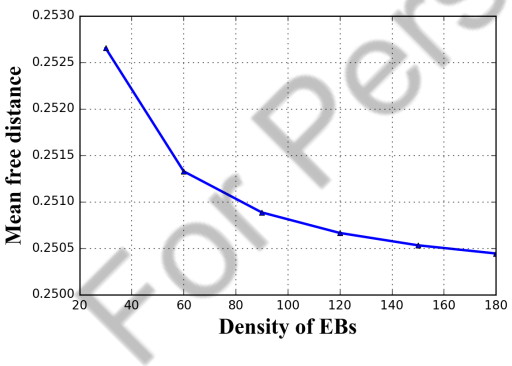


Fig. 3: Variation of the mean free distance

In Theorem 2 [2], we show that the mean free distance between the EBs and the mobile target depends upon the density of the EBs. The variation of the mean free distance with respect to the density of the EBs is shown in Fig. 3. It can be inferred that as the density of EBs increases, the mean free distance covered by the mobile target, T decreases and thus the probability of detection and further tracking increases.

2. Proof is given in Appendix, which is provided in separate supplementary file.

5 Results

We evaluated the performance of the EnPoS algorithm using Python-based simulation. All the values against the parameters used in the simulation are experimental, which are collected from the existing literature. The parameters used in the simulation are listed in Table 1. The values pertaining to energy consumption considered for our work are the average energy. However, the energy consumption in any organism is a stochastic process as the chemical reactions are stochastic in nature. In the simulation results shown below, a varying set of $100 - 500$ EBs and $5 - 20$ static or mobile targets are placed in a confined rectangular space $\mathbb{R}^2$ of $100mm^2$. The EBs are initially located at the center of the simulation area while the targets are located around the EBs at a distance of $1mm$. When the simulation begins, the set of EBs and targets start moving and change their location. Few selected EBs start releasing repellent molecules that bias the random walk motion of the EBs. The performance of $EnPoS$ is evaluated on the basis of a set of parameters that monitor the movement of the set of EBs and the set of targets. Accordingly, we evaluate the efficiency of EnPoS against the following performance metrics. The level of confidence interval in the results is 95%.

5.1 Energy expenses

We observed the amount of energy utilized in the process for a group of 500 mobile EBs during simulations. We computed the results from 50 independent simulations with three different intercation time – low, medium, and high, each for the duration of 15, 30, and 45 simulation minutes. We calculated the selection predictability for each EB and considered a set of those having enough energy to participate in the tracking process actively. Furthermore, we considered each EB has energy, E_{total} to expend to release molecules and propagation. Below a threshold level of E_{thres}, the EB does not release signaling molecules. We showed the variation of residual energy of EBs after tracking the targets for the proposed model and the basic model in Fig. 4. It was observed that the residual energy of the network decreases rapidly for the basic model than for the proposed model. This is attributed to the selective release of molecules by EBs depending on their energy content, which makes the proposed model energy-efficient. In the basic model, the EBs continuously emit repellents assuming that they have unlimited energy. As all the EBs release repellents continuously, the utilization of resource witness a sharp increase. It was observed that the utilization of energy varies closely with or without considering emission of QS molecules as shown by the amount of residual energy of the system in Fig. 5. In the EnPoS, the utilization of energy is relatively very less for releasing QS molecules and propagation as compared to the release of repellent or attractant molecules as shown in Fig. 6. The set of EB is probabilistically chosen to release repellents resulting in less consumption of the resources.

5.2 Tracking targets

We demonstrated that a group of 100 moving EBs was able to track static targets efficiently using $EnPos$ model

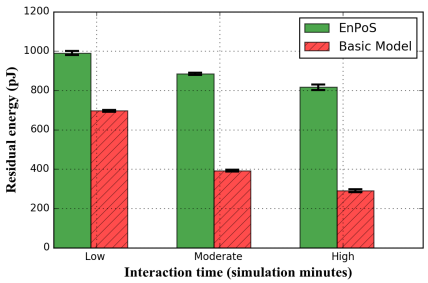


Fig. 4: Residual energy of the EBs in the network

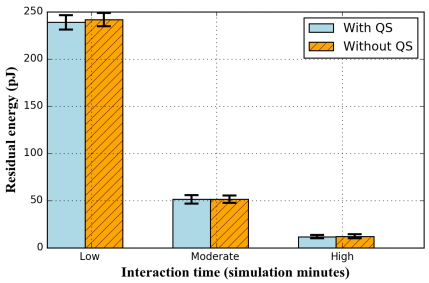


Fig. 5: Residual energy considering QS molecules

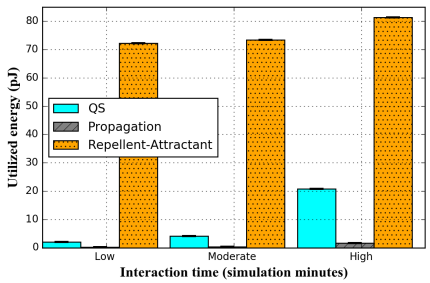
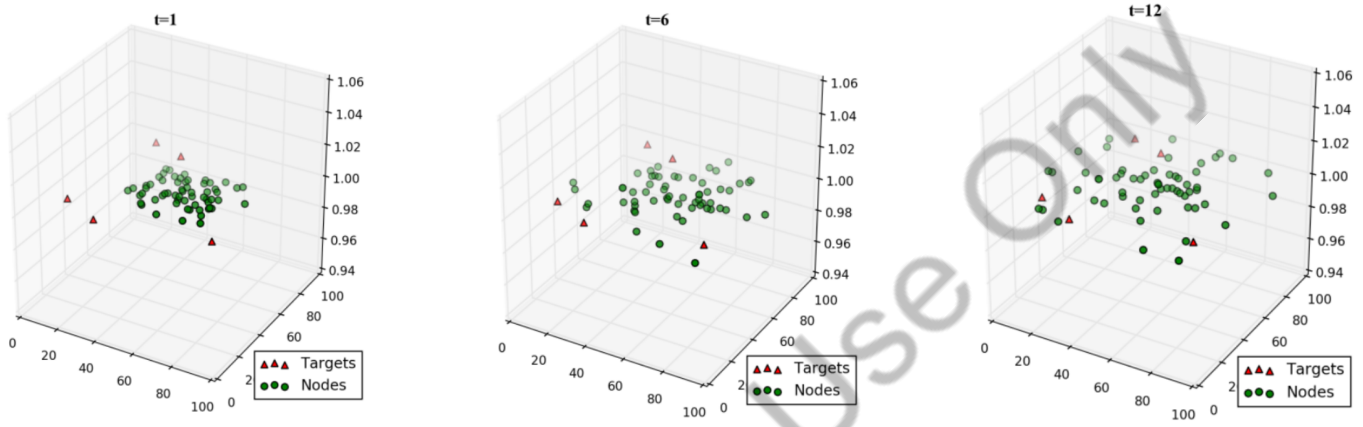
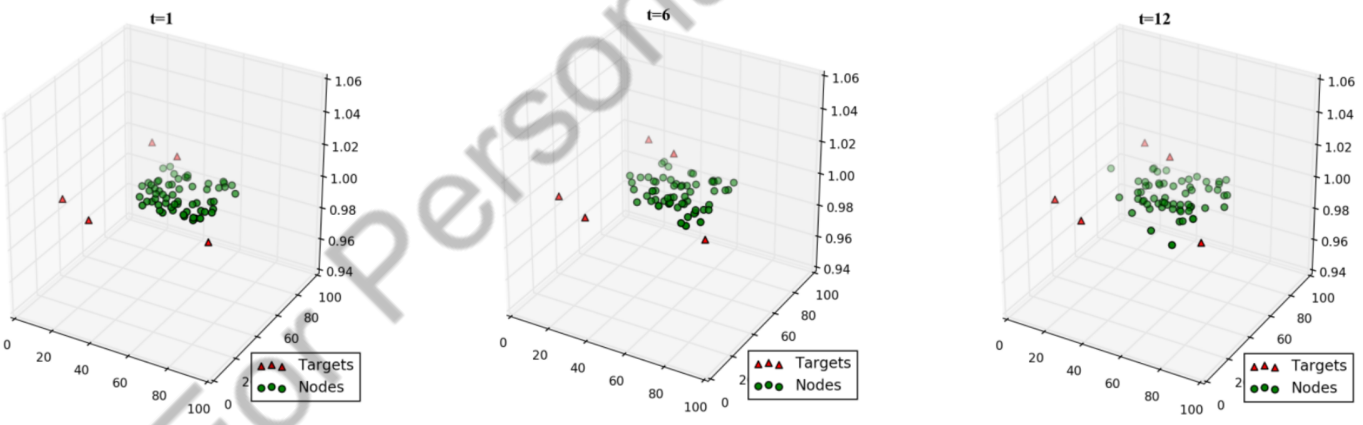


Fig. 6: Energy utilization in different modes



(a) At t = 1 (b) At t = 6 (c) At t = 12

Fig. 7: Tracking of targets in EnPoS

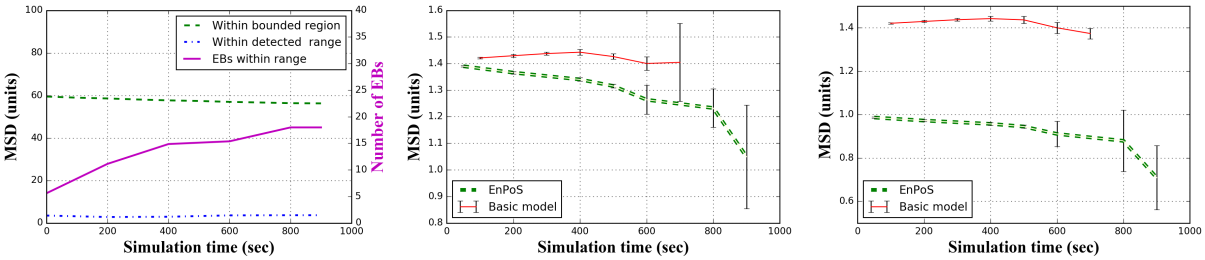


(a) At t = 1 (b) At t = 6 (c) At t = 12

Fig. 8: Tracking of targets in basic model

as shown in Fig. 7 compared to the basic model as shown in Fig. 8. We observed the presence of a significant number of EBs around most of the targets, as evident in Fig. 7. For better visualization purpose, the figures are represented in 3D.

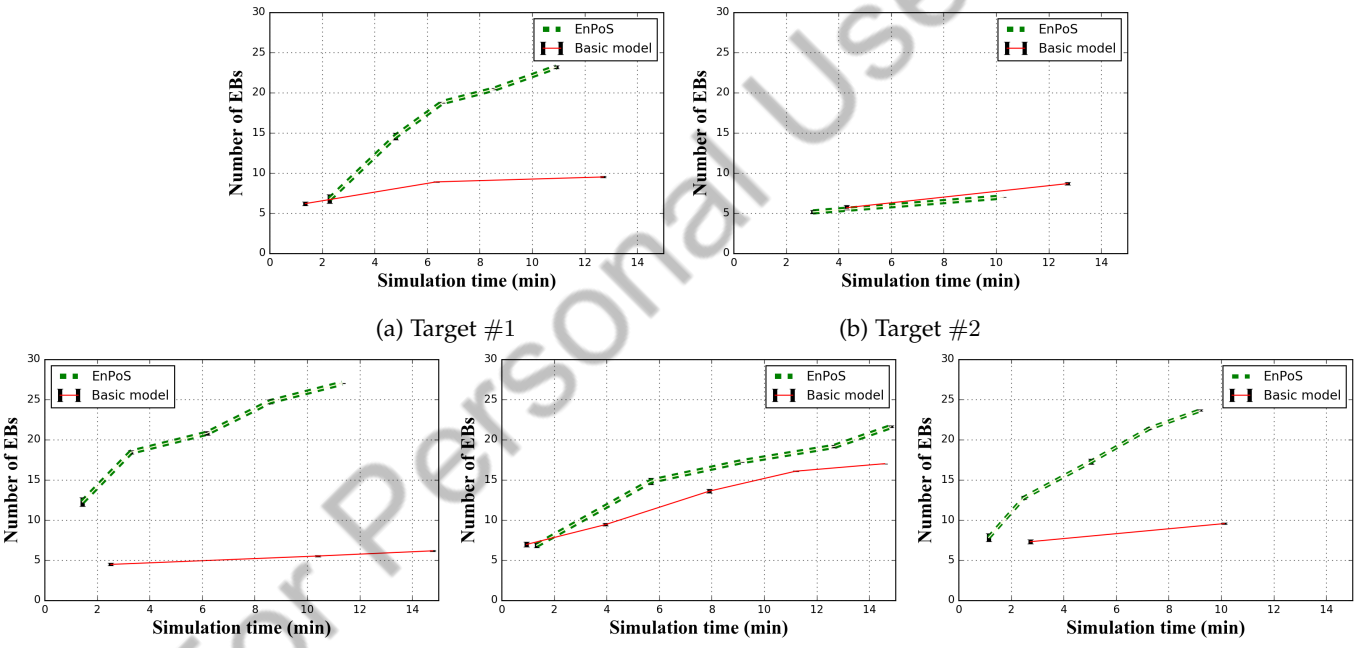
Considering a target moving in a straight line with speed 20 $\mu m/s$, we assumed that an EB detects the target if it is located within target's radius $r_T = 0.5mm$. The successful tracking of targets is shown by quantifying the mean-square distance (MSD) of the set of EBs from the targets. The parameter MSD between the EBs and a certain target indicates how far away the target is from the EBs and is being approached in successive interval. Fig. 9a shows time average of the distance of set of EBs from a particular target within the bounded simulation region as well as within the detectable range of the target. It also shows that the number of EBs increases within the detectable range of the target which is attributed to the secretion of attractants. In Figs. 9b to 9f the variation of MSD for both the basic model as well as $EnPoS$ for 5 different targets are shown.



(a) EBs around a target (b) Target #1 (c) Target #2

(d) Target #3 (e) Target #4 (f) Target #5

Fig. 9: MSD of EBs with respect to targets



(a) Target #1 (b) Target #2

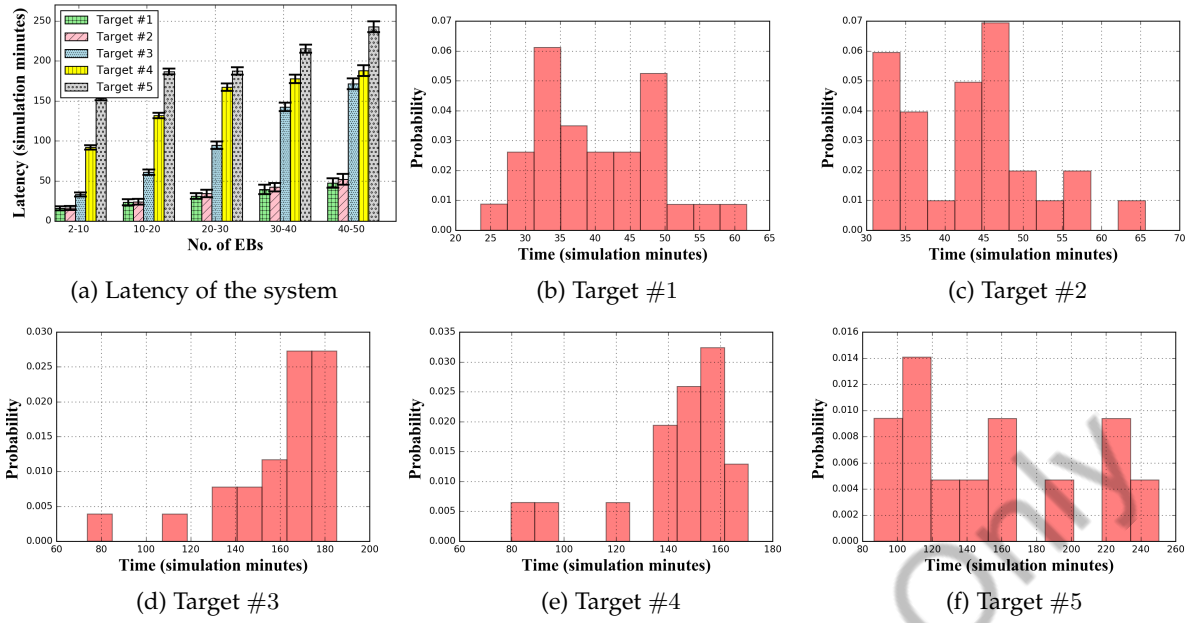
(c) Target #3 (d) Target #4 (e) Target #5

Fig. 10: Distribution of EBs with respect to targets

In basic model the tracking is limited to around 700 seconds as the energy goes below the set threshold level, whereas in $EnPos$ the tracking continues upto the set interaction time of 15 minutes. It was observed that in the proposed model the MSD gradually decreases as the EBs move towards a detected target. The error bars in the figures show the maximum and minimum MSD for each case. This varition is due to the mobility of both the EBs and the targets.

5.3 Distribution of EBs

Figs. 10a to 10e showed the distribution of the average number of EBs around each target over time for 5 different targets. As compared to the basic model, $EnPoS$ has a greater number of EBs around the targets except for Target #2 where both the models witness similar number of EBs. The EBs with more energy content is responsible for this exception seen in the basic model. The increase in the number of EBs around the targets is attributed to the sufficient energy content in the EBs in case of the proposed model. The variation in the number of EBs is shown with the error bars which fluctuates very less depicting a steady presence of EBs in each case. The proposed model



(a) Latency of the system (b) Target #1 (c) Target #2

(d) Target #3 (e) Target #4 (f) Target #5

Fig. 11: Detection and tracking multiple targets

outperforms the basic model with respect to the number of EBs around the targets pertaining to the multiple targets in the scenario. The continuous secretion of repellents consume more energy which affects the number of EBs active and reaching the targets. While considering multiple targets, the energy deprived EBs fail to co-ordinate in the molecular network in continuous search for all the targets.

5.4 Latency and rate of target tracking

We measured the latency of the system attributed to the tracking of multiple moving targets deployed at a distance of $1mm$ from the EBs as shown in Fig. 11a. For simplicity, we considered five different targets in the scenario. It was evident that the targets were well tracked by the EBs over the simulation time. In this context, sequential tracking of multiple targets is considered for a time period of 300 minutes. In particular, after the detection of one target, the EBs search for another and so on. However, the process of secreting attractants to accumulate other EBs is simultaneous. It was observed that due to the sequential detection, the latency encountered in the $EnPoS$ model shows an increasing trend as the proposed model gradually detects all the targets around.

Figs. 11b to 11f showed the probabilities of EBs being around the targets measured from the first detection to the threshold detection over the simulation time. The rate of tracking a target is defined as the time duration which is measured by the moment the EBs first detect the target until the time a threshold parameter of 10% of deployed EBs take to be around the target. It was observed that the targets which are detected initially gather a 10% of EBs faster as well as with higher probability as compared to the targets that are detected later during the simulation process, which is because of the network latency.

6 Discussion

The bacterial movement in fluidic environments is identified by run and tumble model, referred to as chemotaxis. The propulsion and reorientation is achieved by flagellar rotation. During a run, the motion is smooth due to the counterclockwise direction of flagella rotations resulting in nearly constant propulsion. While in a tumble, flagella exert force in different directions and take clockwise rotation forming random propulsion. These rotations are randomized [32] and hence is considered as a random walk model for the random alternating periods of running and tumbling motion of the EBs. This random movement is influenced by the presence of autoinducers as well as the signaling molecules in the environment. These two factors are the necessary conditions that allow us to approximate the run and tumble model as a biased random walk.

7 Conclusion

In this work, we proposed an energy-aware target tracking protocol in order for bacterial nanonetworks to function as drug delivery systems. The protocol enables energy-constrained engineered bacteria to release signaling molecules and track the mobile targets efficiently. We computed the energy utilized in communication process for EBs and then evaluated the performance of the deployed EBs in tracking the moving targets. We also demonstrated the energy-aware tracking process for static targets. Finally, we showed that the EBs are able to track the mobile targets collaboratively. In particular, we compared the performances for both the basic model and proposed selective model, $EnPoS$. Simulation results indicated energy-optimized effective tracking of both static and mobile targets. In future, we intend to explore the aspect of energy utilization in these nanonetworks during chemical operations. We also plan to include a more realistic mobility

model considering the dynamics of molecular motion in the fluidic environment.

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Nabiul Islam Nabiul Islam received the PhD degree from the Indian Institute of Technology (IIT) Kharagpur, India, in 2016, and M.Tech in Computer Science and Engineering from University of Calcutta in 2010. He is currently an EDGE MSCA Research Fellow in TSSG, Waterford Institute of Technology (WIT). From December 2016 to December 2017, he worked as a ERCIM Research Fellow on characterization of the networks of Head Direction neuronal cells at the Department of Electronics and Telecommunications in Norwegian University of Science and Technology (NTNU), Norway from December 2016 to December 2017. His current research interests include molecular communications, terahertz wireless networks and neuroengineering.

Saswati Pal Saswati Pal is an Institute Research Scholar and pursuing her PhD from the School of Nano-Science and Technology, Indian Institute of Technology Kharagpur, India. Prior to that, she was working as a Senior Research Fellow with the Department of Computer Science and Engineering, Indian Institute of Technology Kharagpur, India. She received her M.Tech degree in Electronics and Communication from National Institute of Technology Jalandhar, India in 2016. The current research interests of Ms. Pal include Molecular Communication, Internet of Things, and Wireless Body Area Networks.

Sasitharan Balasubramaniam (SM'14) received the B.E. in electrical and electronic engineering, and PhD degree both from the University of Queensland, in 1998 and 2005, respectively, and the M.E. in computer and communication engineering from the Queensland University of Technology, in 1999. He is currently the Director of Research with the Telecommunication Software and Systems Group, Waterford Institute of Technology, Ireland. His current research interests include bio-inspired communication networks, as well as molecular communications. He has published over 100 articles in various journals and conferences, and actively participates in a number of technical programme committee for various conferences. He is currently on the steering board committee of ACM NANOCOM, which he co-founded, and was the TPC co-chair in 2014, as well as the General Chair in 2015. He is currently an Associate Editor for the IEEE Letters of the Computer Society, Elsevier Nano Communication Networks, and Elsevier Digital Communication and Networks. He was a past Associate Editor for IEEE Internet of Things Journal. In 2018 he was the IEEE Nanotechnology Council Distinguished Lecturer. He is a senior member of the IEEE.

Sudip Misra (M'09 — SM'11) He received the Ph.D. degree in computer science from Carleton University, Ottawa, ON, Canada. He is a Professor with the Department of Computer Science and Engineering, Indian Institute of Technology Kharagpur, India. Prior to this, he was associated with Cornell University (USA), Yale University (USA), Nortel Networks (Canada), and the Government of Ontario (Canada). He possesses several years of experience working in the academia, government, and private sectors in research, teaching, consulting, project management, architecture, software design, and product engineering roles. His current research interests include wireless ad hoc and sensor networks, Internet of Things (IoT), computer networks, learning systems, and algorithm design for emerging communication networks.