Supplementary File for BioBlock: A Blockchain Analogous Mechanism for Integrity in IoBNT-based Drug Delivery Systems

Sudip Misra, *Fellow, IEEE*, Saswati Pal, *Graduate Student Member, IEEE*, and Anandarup Mukherjee, *Member, IEEE*

I. Proof of Lemma 1

Lemma 1. *Considering a single target T_i, the expected number of bionodes $\mathbb{E}(\eta)$ that detect the target is formulated as follows:*

$$\mathbb{E}(\eta) = \left[\frac{e^{-\varrho\pi r_n^2 x} - e^{-\varrho\pi r_n^2}}{1 - e^{-\varrho\pi r_n^2}}\right] \sum_{i=1}^{\varkappa} \eta_i \tag{1}$$

Proof. In this scenario, we consider that there is a single target T_i with traceable radius, r_t^i. The area Λ of the target T_i getting detected by x number of bionodes in its circumference is given by $\Lambda(x) = \pi r_n^2 x$. We consider that the number of bionodes follow a Poisson distribution.

$$P(|\alpha| = \gamma) = \frac{(\varrho\Lambda)^{\gamma} exp(-\varrho\Lambda)}{\gamma!} \tag{2}$$

where ϱ denotes the bionode density given by $\frac{\alpha}{\mathcal{A}}$. The probability that the target, T_i is not detected for the number of bionodes $\eta \geq x$ is computed from the probability that there is no bionode in the circumference of the target, which is computed as follows:

$$P(\eta \geq x) = P(|\alpha| = 0) = exp(-\varrho\Lambda) \tag{3}$$

The expected number of bionodes covering the target is computed as follows:

$$\begin{aligned}\mathbb{E}(\eta) &= \sum_{i=1}^{\varkappa} \eta_i P_i(\eta \geq x) = \sum_{i=1}^{\varkappa} \eta_i [1 - P_i(\eta < x)] \\ &= \left[\frac{e^{-\varrho\pi r_n^2 x} - e^{-\varrho\pi r_n^2}}{1 - e^{-\varrho\pi r_n^2}}\right] \sum_{i=1}^{\varkappa} \eta_i\end{aligned} \tag{4}$$

where $\varkappa$ is the maximum number of bionodes considered in the nanonetwork. When x is very small, $e^{-\varrho\pi r_n^2 x} \approx 1$, so that the term arising from the probability factor reduces to 1. Consequently, the expected value depends on the random variable, η.

$$\mathbb{E}(\eta) \approx \sum_{i=1}^{\varkappa} \eta_i \tag{5}$$

Now, η being a non-negative random variable the series does not converge and is determined by the value of $\varkappa$. When $\varkappa$ is very large, the expected number of bionodes increases to take an infinite value. However, when $\varkappa$ takes a countable value the series converges to a finite value. Thus it can be inferred that a mobile target will be detected by at least η bionodes, all having equal communicating range. □

S. Misra and A. Mukherjee are with the Department of Computer Science and Engineering, Indian Institute of Technology Kharagpur, India. e-mail: (sudip_misra@yahoo.com)

S. Pal is with the School of Nano-Science and Technology, Indian Institute of Technology Kharagpur, India.

II. Proof of Lemma 2

Lemma 2. *Let ϑ be the number of vesicles enclosing information molecules contained in a bionode transmitted to the target T_i and p is the probability of each vesicle reaching the target successfully. Then the probability of successful information delivery $\mathcal{B}$ of the entire system follows a Gaussian distribution formulated as follows:*

$$P(\mathcal{B}_n) = f(\mathcal{B}) = \sqrt{\frac{n}{2\pi p(1-p)\vartheta}} e^{\frac{-n(\beta - p\vartheta)^2}{2p(1-p)\vartheta}} \tag{6}$$

Proof. Once a target is detected by n number of bionodes, each of them transmit the contained vesicles independently. The outcome of these independent transmissions is characterized by either a success or a failure. Based on this scenario, the event is equivalent to the Binomial distribution. The probability that ψ vesicles are successfully delivered to the target out of ϑ vesicles is given as follows:

$$P(\beta = \psi) = \binom{\vartheta}{\psi} \cdot p^{\psi}(1-p)^{\vartheta - \psi} \tag{7}$$

where p is the probability of success with which each vesicle reach the target and β is the random variable which denotes the number of vesicles that reaches the target from one bionode n_i. Thus the probability of successfully receiving Ψ vesicles by the target from n bionodes is given as follows:

$$P(\mathcal{B} = \Psi) = \prod_{l=1}^{n} \left(P(\beta_i = \psi)\right) \tag{8}$$

For n independent bionodes, the expected number of vesicles that reaches the target is computed as follows:

$$\mathbb{E}(\mathcal{B}_n) = \sum_{i=1}^{n} \mathbb{E}(\beta_i) = np\vartheta \tag{9}$$

Since $n \to \infty$, $\mathbb{E}(\mathcal{B}_n)$ diverges to take ∞ value. Thus to limit the overall distribution of $\mathcal{B}_n$, we apply *Central Limit Theorem*. The corresponding mean and variance for $\mathcal{B}_n$ is given as follows:

$$\mathbb{E}(\mathcal{B}_n) = p\vartheta, \; Var(\mathcal{B}_n) = \frac{p(1-p)\vartheta}{n} \tag{10}$$

Thus the probability $P(\mathcal{B}_n)$ converges to a Gaussian function obtained as follows:

$$f(\mathcal{B}) = \sqrt{\frac{n}{2\pi p(1-p)\vartheta}} e^{\frac{-n(\beta - p\vartheta)^2}{2p(1-p)\vartheta}} \tag{11}$$

□

III. Proof of Lemma 3

Lemma 3. *Considering a nanonetwork at any time interval Δt, the total energy utilized $\mathcal{E}_t$ in successful drug delivery is obtained as follows:*

$$\mathcal{E}_t = \frac{KTR^2}{2t_pD} + \kappa\mathcal{E}_r + \mathcal{E}_v + \kappa_a\mathcal{E}_a \tag{12}$$

Proof. We consider an area of $a \times b$ with n uniformly distributed bionodes. Each bionode has a different number of neighboring bionodes in its communication range with radius r_n. In order to relay information in the nanonetwork, the bionode propagates in its neighborhood until the protein sequence matches. The random walk of the bionodes in a confined area can be defined by the transition matrix $T = [T_{ij}]$, where T_{ij} refers to the probability of bionode b_i to go to bionode b_j. We define the time a bionode takes to reach another bionode with matched sequence as the passage time. Thus the passage time refers to the number of steps a bionode takes for its random walk to be stationary. The second largest eigenvalue of the transition matrix T determines the asymptotic rate of convergence of the random walk. Considering that the second largest eigenvalue is close to 1, the passage time t_p is obtained as follows:

$$t_p = \frac{1}{1-e} \tag{13}$$

where $1 - e$ is the rate of convergence of the random walk. Once a bionode b_j with matched sequence is detected, the bionode b_i ensures successful information relaying. Thus a bionode utilizes energy in propagation, releasing plasmids, transferring vesicle containing information molecules, and finally authenticating BioBlock. The energy consumed in propagation $\mathcal{E}_p$ can be computed from the distance covered by a bionode along the random walk until it becomes stationary. Thus we compute the mean distance between any two bionodes is computed as follows:

$$\mathbb{E}(d^2) = \int_{\theta=0}^{2\pi}\int_{r_n=0}^{R} r_n^2\,\rho(r_n,\theta)\,r_n dr_n d\theta = \frac{R^2}{2} \tag{14}$$

where the joint probability density function ρ of the random variables r_n and θ is represented as $\rho(r_n,\theta) = \frac{1}{\pi R^2}$. The energy utilized in releasing plasmids is based on the number of produced plasmids κ, which involves $\kappa \times \mathcal{E}_r\ zJ$ of energy. We consider that after conjugation, the bionode b_i passes one vesicle loaded with drug molecules to the bionode b_j. The energy involved in transferring the vesicle containing information molecules is represented as $\mathcal{E}_v$. To authenticate the BioBlock information, the energy cost involved depends on the number of generated blocks (adhered plasmids) κ_a, which is given by $\kappa_a \times \mathcal{E}_a\ zJ$. Thus at any time interval Δt, the total energy utilized is obtained as follows:

$$\begin{aligned}\mathcal{E}_t &= \mathcal{E}_p + \kappa\mathcal{E}_r + \mathcal{E}_v + \kappa_a\mathcal{E}_a \\ &= \frac{KTR^2}{2t_pD} + \kappa\mathcal{E}_r + \mathcal{E}_v + \kappa_a\mathcal{E}_a\end{aligned} \tag{15}$$

where K is Boltzmann's constant, T is absolute temperature, and D denotes the diffusion coefficient. □