Bounds on Distance Estimation via Diffusive Molecular Communication

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Abstract—This paper studies distance estimation for diffusive molecular communication. The strength of the channel impulse response generally decreases with distance, so it is measured to estimate the distance. The Cramer-Rao lower bound on the variance of the distance estimation error is derived. The lower bound is derived for a physically unbounded environment with molecule degradation and steady uniform flow. The maximum likelihood distance estimator is derived and its accuracy is shown via simulation to perform very close to the Cramer-Rao lower bound. An existing protocol is shown to be equivalent to the maximum likelihood distance estimator if only one observation is made. Simulation results also show the accuracy of existing protocols with respect to the Cramer-Rao lower bound.

I. INTRODUCTION

Applications in areas such as biological engineering and manufacturing could potentially be improved by molecular communication (MC); see [1]. MC is characterized by the encoding of information into molecules that are released by transmitters and are then transported to their intended destinations. Communication via diffusion, where the molecules that are released move randomly due to collisions with other molecules in the environment, is particularly advantageous for ad hoc networks of small devices because there are no fixed connections between devices and no external energy is required for molecule propagation.

Even though diffusive communication is commonly used in biological systems where small molecules need to quickly travel short distances (see [2] Ch. 4), the diffusive transmission of arbitrarily large amounts of information, as would be desired for the aforementioned applications, is severely limited by intersymbol interference (ISI). Signal processing techniques have been proposed to mitigate the impact of ISI, such as those described in [3]–[5]. However, the implementation of such techniques relies critically on the knowledge of the expected channel impulse response, i.e., the number of molecules expected at a receiver over time given that molecules were instantaneously released by a transmitter.

The expected channel impulse response is generally a function of the parameters of the physical environment, including the distance between the devices, the diffusion coefficient, whether there is any flow, and whether the information molecules can participate in chemical reactions. Any of these parameters might also change over time. Depending on the application, specific parameters might need to be individually estimated. For example, knowledge of the distance between devices is essential for applications such as tuning the spatial distribution of a network and device addressing via nodes that release molecules continuously; see [6], [7].

We are interested in studying the problem of distance estimation for diffusive molecular communication. The number of molecules observed from an impulsive release decreases with distance. Thus, we can use the number of molecules observed to estimate the distance. We wish to obtain bounds on estimation so that we can assess the accuracy of any estimator relative to the bound. Existing work has already introduced protocols that we can compare with a bound on distance estimation; see [8]–[11].

Protocols for measuring distance were first described for 1-dimensional environments in [8], where the authors introduced what we call feedback or two-way methods that relied on either an instantaneous (i.e., signal spike or impulse) or a continuous release of molecules. We label these methods two-way because two devices release molecules for one of them to estimate the distance. The same authors expanded their study of impulse-based protocols in [9], where they used the standard deviation of the estimation error as a metric to evaluate and compare protocol performance. In [10], impulse-based distance estimation protocols were introduced for 1-dimensional environments such that no feedback signal must be sent, i.e., one-way protocols. These protocols use additional signal processing at the device where the estimate is made, and use data from multiple observations. Furthermore, the authors proposed a method for measuring the distance by releasing multiple impulses. A 2-dimensional environment was studied in [11], where two-way continuous release and impulse methods were compared, and molecules were either observed or captured until a threshold value was reached.

All existing distance estimation protocols are heuristic, i.e., they were designed based on knowledge of the expected channel impulse response but not with respect to an optimality criterion. The performance of any given protocol has been evaluated in comparison with other protocols and the knowledge of the true distance between devices. However, existing work has not offered insight into the optimality of any protocol.

Suppose that we derive the best possible performance of any estimator under some criterion, given the knowledge required
for its implementation. If we know the best possible estimator performance, then we can perform a complete assessment of protocols because we can evaluate whether a given protocol is making the most accurate estimate for the knowledge that it requires. For example, we would expect that a simple protocol estimating the distance using a single observation would be less accurate than a protocol that makes multiple observations over time. But, the accuracy of the simpler protocol might be much closer to the corresponding optimal accuracy and might provide insight into improving the performance of more complex estimators. Furthermore, if we know that a given estimator is optimal, then we know that we cannot improve the estimator without incorporating additional information such as more observations.

In this paper, we derive a bound on the accuracy of distance estimation protocols as a function of the observations of molecules that are made to calculate the estimate. The primary contributions of this paper are summarized as follows:

1) We derive the Cramer-Rao lower bound (CRLB) on the variance of the estimation error of any unbiased distance estimator as a function of the number of independent observations of a transmitted impulse. We derive the CRLB for an unbounded 3-dimensional fluid environment with steady uniform flow and first-order molecule degradation.

2) We derive the maximum likelihood distance estimator for any number of independent observations of an impulse signal. A closed-form solution exists if there is only one observation, and we show that this special case is equivalent to an existing protocol. In the case of multiple observations, we perform a numerical search to find the maximum likelihood estimate.

3) We extend a selection of existing distance estimation protocols to the physical environment considered in this paper. We transform two-way protocols into one-way form in order to directly compare all protocols.

The rest of this paper is organized as follows. The physical environment is described and existing protocols for distance estimation are reviewed in Section II. In Section III we derive the CRLB on the variance of the estimation error. In Section IV we derive the maximum likelihood distance estimator. Numerical and simulation results are presented in Section V. Conclusions are drawn in Section VI.

II. System Model and Preliminaries

In this section, we describe the diffusive communication environment, including the two devices between which the distance must be estimated. We present the channel impulse response and derive properties that will be useful when designing and analyzing distance estimation protocols. We also review existing protocols for distance estimation and describe how they are executed as one-way methods.

A. Physical Environment

We consider an unbounded, 3-dimensional fluid environment with uniform constant temperature and viscosity. There are two fixed devices, which we label the transmitter (TX) and the receiver (RX) because we are considering one-way distance estimation. The RX is a sphere of radius $r_{RX}$ and volume $V_{RX}$. The coordinate axes are defined by placing the RX at the origin and the TX at Cartesian coordinates $(-d, 0, 0)$, such that $d$ is the distance that is to be measured. There is a steady uniform flow $\vec{v}$ defined by two velocity components, i.e., the component in the direction of a line pointing from the TX to the RX, $v_\parallel$, and the component perpendicular to this line, $v_\perp$.

We note that $v_\perp$ is the component of $\vec{v}$ that lies along the $y_2$-plane but, due to symmetry, the precise direction of this component is not required.

The TX releases type A molecules, which can be detected by the RX. We assume that the RX knows the time when A molecules are released. The constant diffusion coefficient of the A molecules is $D$. The A molecules can also degrade into a form that is not recognizable by the RX via a first-order chemical reaction that can be described as

$$A \xrightarrow{k} \emptyset,$$

where $k$ is the first-order reaction rate constant in $s^{-1}$. We ignore the chemical kinetics of the reception process at the RX by modeling the RX as a passive observer that does not impede the diffusion of the A molecules. By ignoring the reception kinetics, we facilitate our analysis and emphasize the impact of the propagation environment. As an observer, the RX can perfectly count the number of A molecules within its volume $V_{RX}$ at any time instant.

B. Analytical Preliminaries

We require the expected channel impulse response at the RX for the design and analysis of distance estimation protocols. The expected channel impulse response is the number of molecules expected at the RX due to an instantaneous release of molecules by the TX. In this paper, we apply the uniform concentration assumption, i.e., we assume that the A molecule concentration expected at the RX due to molecules released by the TX is uniform throughout the RX and equal to that expected at the center of the RX. We have previously studied the accuracy of this assumption in flowing environments in [14]. If $N_{AEM}$ molecules are instantaneously released by the TX at time $t = 0$, then the number of molecules expected to be observed by the RX, $\overline{N_{A,obs}}(t)$, is given by [4, Eq. (12)]

$$\overline{N_{A,obs}}(t) = \frac{N_{AEM} V_{RX}}{(4\pi D t)^{3/2}} \exp \left(-\frac{|\vec{r}_{eff}|^2}{4Dt}\right),$$

where $|\vec{r}_{eff}|^2 = (d - v_\parallel t)^2 + (v_\perp t)^2$ is the square of the effective distance from the TX to the RX.

All existing impulse-based distance estimation protocols rely on re-arranging [2], where all parameters but $d$ are either given, observed, or removed via substitution, and then solving for the distance $d$. Given a particular observation

1Synchronization strategies include blind synchronization via a maximum likelihood approach in [12] and using inhibitory feedback molecules in [13].
\( N_{A,\text{obs}}(t) = s \) (and not the expected observation \( N_{A,\text{obs}}(t) \)) at a particular time, it can be shown that (2) re-arranges as

\[
d = v_x t \pm \sqrt{4 D t \ln \left( \frac{N_{A,\text{EM}} V_{RX}}{s (4 \pi D t)^{3/2}} \right) - t^2 (v_x^2 + 4 k D)}, \tag{3}
\]

and this equation still applies in the absence of flow and molecule degradation, i.e., if \( v_x = v_\perp = 0 \) and \( k = 0 \).

We note that the “±” in (3) means that there could be two valid solutions for \( d \) if \( v_x > 0 \). At any time \( t \), the largest number of molecules along the \( x \)-axis is expected at the point \( \{v_x t - d, 0, 0\} \), and the distribution of molecules expected along the \( x \)-axis is symmetric about that point. The “±” in (3) represents uncertainty by the RX about whether \( d > v_x t \) or \( d < v_x t \). In this paper, if we evaluate (3) and find two valid solutions, then we choose one via an unbiased coin toss.

There are three cases where (3) could result in no valid distance, as follows:

1) If the observation \( s = 0 \), then the solution is \( d = \infty \). This is more likely if the observation time is long before or long after the peak of the channel impulse response.

2) If \( s \) is sufficiently large relative to the other variables in the logarithm, then the logarithm can evaluate to a negative value and \( d \) would then be a complex number. This is more likely to occur if the observation is made when a large number of molecules is expected.

3) \( d \) could be negative if \( v_x < 0 \).

In this paper, we deal with the first case by setting \( s = 0.1 \) and then solving for \( d \). We deal with the second and third cases by setting \( d = 0 \). Alternative strategies can be considered in future work.

Some existing distance estimation protocols require detecting when the peak number of molecules is observed. By taking the derivative of (2) with respect to \( t \) and setting it equal to 0, it can be shown that the peak number of molecules at the RX, due to an instantaneous release of \( A \) molecules by the TX at time \( t = 0 \), would be expected at time

\[
t_{\text{max}} = \left( -3 + \sqrt{9 + d^2 \eta/D} \right) / \eta, \tag{4}
\]

where

\[
\eta = (v_x^2 + v_\perp^2)/D + 4k. \tag{5}
\]

Interestingly, (4) shows that the direction of flow has no impact on the time when the peak number of molecules is expected; only the magnitude of the flow matters. Thus, (4) is also the time when the peak number of molecules would be expected at the TX due to an instantaneous release of molecules by the RX at time \( t = 0 \).

In the absence of flow and molecule degradation, i.e., if \( v_x = v_\perp = 0 \) and \( k = 0 \), then it can be shown that the peak number of molecules would be expected at the RX at time

\[
t_{\text{max}} = d^2/(6D). \tag{6}
\]

If we substitute (5) into (4), then we can write the number of molecules expected to be observed at \( t_{\text{max}} \) in the absence of flow and molecule degradation as

\[
N_{A,\text{obs}}(t_{\text{max}}) = \frac{N_{A,\text{EM}} V_{RX}}{(2\pi/3)^{3/2} d^3} \exp \left( -\frac{d}{2} \right). \tag{7}
\]

C. Existing Distance Estimation Protocols

The existing distance estimation protocols that we have selected were generally chosen for their accuracy and all rely on impulses sent by the TX at time \( t = 0 \). In order to maintain a consistent comparison between protocols, and also to facilitate tractable analysis, we consider all protocols in one-way form. We transform two-way protocols into one-way protocols with the understanding that we modify the knowledge required to implement those protocols. However, we note that, given the required knowledge, the one-way form of a protocol should be no less accurate than its two-way form. This is because a one-way method estimates the distance from one impulse signal. A two-way method uses a cascade of two impulse signals where the release of the second impulse depends on the detection of the first.

We describe the selected protocols in one-way form as follows:

- The round-trip time from threshold concentration (RTT-T) protocol was proposed in [9] as a two-way method without synchronization. In one-way form, the RX is synchronized with the TX and has a pre-determined threshold observation \( \tau \). When the RX observes a number of \( A \) molecules that is greater than or equal to \( \tau \), it substitutes the current time \( t \) into (3), sets \( s = \tau \), and solves for \( d \).

- The signal attenuation with timer (SA-T) protocol is another two-way protocol that was proposed in [9] but was shown to be a generally inaccurate protocol. We consider it here because we will show in Section 4 that its performance is effectively equivalent to the maximum likelihood distance estimate for one observation. In one-way form, the RX has a pre-determined observation time \( t_{SA} \), when the current observation \( s \) is substituted into (3) and the RX solves for \( d \).

- The envelope detector (ENVD) protocol was proposed in [10] as a one-way protocol without synchronization. The RX tries to estimate the expected peak \( A \) molecule concentration by tracking the upper and lower envelopes of the observations. It is assumed that the time-varying mean of the two envelopes represents the true expected molecule concentration. The peak value of the mean of the two envelopes, \( \bar{s} \), is substituted for \( s \) in (3), and \( t \) is replaced with either (4) or (6) as appropriate, so that the RX can solve for \( d \). In the absence of flow and molecule degradation, substituting (6) into (3) enables us to solve for \( d \) explicitly, such that we can write the estimate as

\[
d_{\text{ENVD}} = (2\pi e/3)^{-\frac{1}{2}} \sqrt{N_{A,\text{EM}} V_{RX}}/\bar{s}. \tag{8}
\]

In the presence of flow or molecule degradation, we must solve (3) for \( d \) numerically because of the \( d^2 \) term inside the square root in (4).
III. BOUND ON DISTANCE ESTIMATION

In this section, we derive the Cramer-Rao lower bound (CRLB) on the variance of any unbiased distance estimation protocol. Due to the noise of diffusion, some of the protocols studied here are biased, i.e., the expected values of their estimates are not equal to the true distance. Nevertheless, the CRLB will provide insight for comparing protocols. We derive the CRLB for an arbitrary number of samples, $M$, taken by the RX.

To derive the CRLB, we need the joint probability distribution function (PDF) of the RX’s $M$ observations. The TX releases $A$ molecules at time $t = 0$ and then the $m$th observation, $s_m$, is taken at time $t_m$. The vector $\vec{s} = [s_1, \ldots, s_M]$ contains all $M$ observations. We assume that the time between consecutive observations is sufficient for each observation $s_m$ to be independent; see [4] for a detailed discussion of observation independence (strictly speaking, protocols that are designed to make observations continuously, such as the RTT-T protocol, should be sampling so fast that consecutive observations cannot be independent). Furthermore, we will assume that the individual observations are Poisson random variables whose means are the expected values of the observations at the corresponding times (this has been shown to be highly accurate in our previous work, including [14]). Thus, the joint PDF of the RX’s observations, $p(\vec{s}; d)$, is

$$p(\vec{s}; d) = \prod_{m=1}^{M} N_{\text{Aobs}}(t_m) s_m^m \exp\left(-N_{\text{Aobs}}(t_m)/s_m\right), \tag{9}$$

where $N_{\text{Aobs}}(t_m)$ is as given by [2]. We write

$$N_{\text{Aobs}}(t_m) = \Lambda_m \exp\left(-d^2 \Phi_m + d \Psi\right), \tag{10}$$

for compactness, where

$$\Lambda_m = \frac{N_{\text{Aexp}} V_{RX}}{(4\pi D t_m)^{3/2}} \exp\left(-kt_m - \frac{t_m}{4D} (v_i^2 + v_f^2)\right), \Phi_m = 1/(4D t_m), \Psi = \nu_i/(2D). \tag{11}$$

For the CRLB to exist, the regularity condition must be satisfied, i.e., for all $d$, [15, Ch. 3]

$$E \left[ \frac{\partial \ln p(\vec{s}; d)}{\partial d} \right] = 0, \tag{12}$$

where $E[\cdot]$ is the expectation taken with respect to $p(\vec{s}; d)$. If (12) is satisfied, then the CRLB on the variance of any unbiased estimator $\hat{d}$ is [15, Eq. 3.7]

$$\text{var}(\hat{d}) \geq -E \left[ \frac{\partial^2 \ln p(\vec{s}; d)}{\partial d^2} \right]^{-1}. \tag{13}$$

We now present the following theorem:

**Theorem 1 (CRLB for distance estimation):** The lower bound on the variance of any unbiased distance estimator, that is evaluated using $M$ independent observations of the channel impulse response, is

$$\text{var}(\hat{d}) \geq \frac{4D^2}{\sum_{m=1}^{M} (v_i - d t_m)^2 N_{\text{Aobs}}(t_m)} \tag{14}.$$
to finding $\hat{d}$ such that $\frac{\partial \ln p(\hat{s}; \hat{d})}{\partial \hat{d}} = 0$. This is the same as satisfying the regularity condition in [12] but without the expectation. In other words, the ML estimate is the distance that satisfies

$$\sum_{m=1}^{M} \left[ -2s \Phi_m \hat{d} + s \Psi \right] - A_m (\Psi - 2 \Phi_m \hat{d}) \exp \left( -\hat{d}^2 \Phi_m + \frac{1}{d} \Psi \right) = 0. \quad (18)$$

If $M = 1$, then it can be shown that (18) is satisfied if the observation $s_1 = A_1 \exp \left( -\hat{d}^2 \phi_1 + \frac{1}{d} \Psi \right)$, i.e., $\hat{d}$ must be the distance whose expected observation $\tilde{N}_{\text{obs}}(t_1)$ is equal to $s_1$. Thus, $\hat{d}$ can be found by substituting $s_1$ and $t_1$ into $\tilde{d}$.

We emphasize that the ML estimate for a given time $t_1$ uses the observation made at that time to estimate $\hat{d}$. Hence, the ML estimate for $M = 1$ is effectively equivalent to the SA-T protocol, even though this protocol was shown to have poor performance in [9]. The reason for its poor performance is that all other existing protocols track the observed signal over time until some criterion is met, i.e., information is combined from multiple observations in order to measure the distance (even though the final calculation might only use the value of a single observation). The SA-T does not track the signal over time but makes the ML estimate for its one observation.

If $M > 1$, then a solution to (18) is non-trivial. We approximate the true ML distance by performing a discretized 1-dimensional search (over non-negative $d$) and choose the distance that maximizes the log likelihood $\ln p(\hat{s}; \hat{d})$ given the vector $\hat{s}$ of $M$ observations. We impose a finite upper bound on $d$, so the estimate is always finite.

For any value of $M$, the RX must know the values of all other environmental parameters, i.e., $v_1, v_{\perp}, D, N_{AEM}, V_{RX}$, and $k$, and be synchronized with the TX, in order to make a ML estimate. This is intuitive; an ML estimate must make use of all knowledge available. Even though the RTT-T and ENVD protocols also require knowledge of all other environmental parameters (in the general case with flow and molecule degradation), they cannot be ML estimates. They make multiple observations but only use a single observation to estimate the distance (actually, in the case of the ENVD protocol, the mean of two filtered observations is used), discarding the information available from all other observations.

V. Numerical Results

In this section, we present simulation results to assess the performance of the distance estimation protocols discussed in this paper, particularly with respect to the CRLB. Our simulations were executed in the particle-based stochastic framework that we described in [16]. Every molecule released by the TX is treated as an independent particle whose location is updated every simulation time step $\Delta t$. The probability of a given molecule degrading via reaction (1) in one time step is $k \Delta t$. We consider two sets of environmental parameters as listed in Table I. The chosen values are consistent with those that we have considered in our previous work, including [14].

The molecule degradation rate for System 2, $k = 62.5 \text{s}^{-1}$, was chosen so that, in the absence of flow, one less molecule is expected at the expected peak concentration time than if $k = 0$, i.e., $\tilde{N}_{\text{obs}}(t_{\text{max}}) = 6.5$ instead of 7.5. We note that we set the velocity of flow perpendicular to the line between the TX and RX (i.e., $v_{\perp}$) to 0. Simulations are averaged over $10^3$ independent realizations.

Prior work on distance estimation has been applied in the absence of flow and molecule degradation, i.e., when $v_1 = v_{\perp} = 0$ and $k = 0$, so most of the results that we present here focus on a similar environment, i.e., System 1, but in 3 dimensions. In Fig. [7] we show how the CRLB varies in System 1 over distance and time for a single observation, i.e., for $M = 1$. An estimate made too soon will have poor accuracy at any distance, because no molecules would have arrived at the RX. An observation made after a long time will also result in poor estimation accuracy because most of the molecules released would have diffused away. Intuitively, the best time for an estimate is during the fastest change in the expected number of molecules. This is confirmed by Fig. [7] where the minimum variance occurs approximately halfway between when the TX releases the A molecules and when the peak number of molecules is expected at the RX. For example, we can calculate from (6) that when $d = 4 \mu m$, $t_{\text{max}} = 2.66 \text{ ms}$, and Fig. [7] shows that the CRLB’s lowest value at that distance is about 1.2 ms after release by the TX. At shorter distances, the CRLB is much more sensitive over time but its minimum is much lower, due to the sudden arrival of a large number of molecules followed by a relatively more rapid dissipation. This can be observed for $d = 2 \mu m$, where the minimum CRLB is much lower than for $d = 4 \mu m$ but becomes higher when time $t > 2.5 \text{ ms}$. When the ENVD protocol was introduced in [10], the authors did not describe their implementation of the upper and lower envelope detectors. We implemented what we refer to as a moving maximum filter and a moving minimum filter, where each filtered observation is found by taking the maximum and minimum of the nearest (in time) RX observations for the upper and lower envelopes, respectively. In Fig. [7] we evaluate the mean square estimation error of the ENVD protocol in System 1 for varying filter window length as a function of the true distance $d$. Shorter filter lengths are better at shorter
Fig. 1. The CRLB on the variance of the error in distance estimation in System 1 as a function of time at varying distances from the TX.

Fig. 2. Mean square error of the ENVD protocol in System 1 for varying filter window length as a function of true distance \(d\).

Fig. 3. Mean square error of the SA-T protocol in System 1 for varying observation time \(t_{SA}\) as a function of true distance \(d\).

Fig. 4. Mean square error in System 1, of all distance estimation protocols being considered, as a function of the true distance \(d\). The CRLB is also shown for \(M = 1\) (to compare with the SA-T protocol) and for \(M = 200\) (to compare with all other protocols).

Distances because the diffusion wave rises and falls more abruptly when the RX is closer to TX. At longer distances, the rise and fall of the diffusion wave is more gradual and so longer filter lengths are more accurate. For example, the shortest window length, 3, is the second best for \(d = 2\) \(\mu m\) and the worst for \(d \geq 3\) \(\mu m\). We choose filter window length 7 for comparison with the other distance estimation protocols.

In Fig. 3 we evaluate the mean square estimation error of the SA-T protocol in System 1 for varying sample time \(t_{SA}\) as a function of the true distance \(d\). We observe that earlier sampling times are generally better, although sampling at time \(t_{SA} = 2.5\) ms has more consistent performance over the range of \(d\) than sampling at \(t_{SA} = 1\) ms. The sampling time \(t_{SA} = 2.5\) ms has fewer occurrences of observations that would, without the corrections proposed in Section II, result in no valid estimate. Due to lack of space, we do not present detailed results of how frequently corrections are required. We choose sampling time \(t_{SA} = 2.5\) ms for comparison with the other protocols in the remaining figures.

In Fig. 4 we compare the mean square error in System 1, of all distance estimation protocols being considered, as a function of the true distance \(d\). For the RTT-T protocol, we chose threshold \(\tau = 2\) for its overall performance over the entire range of \(d\) (a figure similar to Fig. 3 but for the RTT-T protocol and varying \(\tau\) instead of \(t_{SA}\), is not shown). We compare the SA-T protocol with the CRLB for \(M = 1\) and evaluated at the time \(t = 2.5\) ms. The “numerical” ML curve was found by calculating the log likelihood \(\ln p(\vec{s}; d)\) over a range of distances from 0.01 \(\mu m\) to 20 \(\mu m\), given all 200 samples in \(\vec{s}\), and selecting the distance with the largest log likelihood. The CRLB for \(M = 200\) was evaluated by solving (14) for all 200 samples. For clarity of exposition, we do not evaluate the CRLB specifically for the ENVD and RTT-T protocols; the number of samples \(M\) that they observe for a single distance estimate can change with every realization.

Fig. 4 shows that the numerical ML estimate is a lower bound on all distance estimation protocols, and it is also very close to achieving the CRLB given all observations made at the RX (the ML estimate can move closer to the
CRLB by decreasing $M$ so that the observations become more independent and by increasing the resolution of the search over $d$). Thus, the ML estimate is effectively the optimal estimate for $M = 200$. The accuracy of the SA-T protocol is quite poor. However, at shorter distances, i.e., $d \leq 4\mu m$, it rarely requires sample corrections and its accuracy is quite close to the CRLB when $M = 1$. For $d \leq 4\mu m$, it is practically the most accurate unbiased estimate possible for a single observation, and it is equivalent to the single-sample ML estimate when sample corrections are not required. At higher distances, i.e., $d \geq 7\mu m$, the SA-T protocol appears to be more accurate than the CRLB for $M = 1$, and this is because frequent observations of $s_1 = 0$ that are corrected to 0.1 introduce an estimate bias that improves the mean square error over the unbiased case. Finally, we observe that the RTT-T and ENVD protocols are generally more accurate than the SA-T protocol but much less accurate than the CRLB evaluated for $M = 200$.

In Fig. 5 we compare the mean square error in System 2, of all distance estimation protocols being considered, as a function of the flow velocity from the TX towards the RX, $v_1$. We choose the single distance $d = 4\mu m$ because of the accuracy of all protocols at that distance in Fig. 4. All protocols have the same configuration as described for System 1. We see that the numerical ML estimate is still a lower bound on all distance estimation protocols, and it is still very close to the CRLB for $M = 200$. The accuracy of the SA-T protocol is also still close to the CRLB for $M = 1$ for low values of $v_1$, but degrades for $v_1 \geq 1\mathrm{mm/s}$ because of the increasing frequency of corrected estimates that introduce a destructive bias and because we often need to choose between two valid distances via a coin toss (due to the “±” in (3)).

VI. CONCLUSIONS

In this paper, we studied distance estimation for diffusive molecular communication in an idealized 3-dimensional environment. We derived the CRLB on the error variance of any unbiased distance estimator at the RX taking independent samples of an impulsive signal from the TX. The CRLB is a function of the samples expected at the RX. We derived the ML estimator and showed that, in the single-sample case, it is equivalent to the SA-T protocol. A numerical evaluation of the ML estimator that uses all samples at the RX was shown to achieve the CRLB and be more accurate than a selection of the most accurate existing distance estimation protocols.

Our approach for bounding the accuracy of distance estimation protocols can serve as a benchmark for the design of future protocols and as a guide for finding the optimal estimate of other diffusive molecular communication parameters as well as the channel impulse response. Ultimately, we are interested in the design of low-complexity estimators for more realistic environments. Low-complexity protocols might be more practical, and bounds on accuracy give us insight into how much we lose by implementing sub-optimal protocols.

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