Modeling of Viral Aerosol Transmission and Detection

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Abstract

The objective of this work is to investigate the spread mechanism of diseases in the atmosphere as an engineering problem. Among the viral transmission mechanisms that do not include physical contact, aerosol transmission is the most significant mode of transmission where virus-laden droplets are carried over long distances by wind. In this work, we focus on aerosol transmission of virus and introduce the idea of viewing virus transmission through aerosols and their transport as a molecular communication problem, where one has no control over transmission source but a robust receiver can be designed using nano-biosensors. To investigate this idea, a complete system is presented and end-to-end mathematical model for the aerosol transmission channel is derived under certain constraints and boundary conditions. In addition to transmitter and channel, a receiver architecture composed of air sampler and Silicon Nanowire field effect transistor is also discussed. Furthermore, a detection problem is formulated for which maximum likelihood decision rule and the corresponding missed detection probability is discussed. At the end, simulation results are presented to investigate the parameters that affect the performance and justify the feasibility of proposed setup in related applications.

Index Terms

Aerosol transmission, virus detection, Nano-networks, channel modeling, molecular communication, molecular receiver, advection-diffusion channel.

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I. INTRODUCTION

Molecular communication (MC) is an emerging research area that focuses on the communication processes involving biological entities. Unlike conventional wireless communication, where electromagnetic signals are encoded and transmitted to share information, MC uses molecules as signaling sources. The phenomenon is naturally existing in biological systems, however, the recent advancements in nanotechnology and the advent of nanoscale biosensors or nanomachines have boosted the research in this area [2]. The nanomachines have limited capabilities due to their small size, energy resources, memory and processing capacity. Thus, in order to perform complex operations, several nanomachines need to cooperate together and this is where the concept of MC comes into the scene. Thus, MC serves as the link between nanomachines that allows them to work together as a network, where links can not be established through existing electromagnetic or optical technology [3]. This paves the way to develop artificial networks that perform the same job as biological networks inside or outside the human body. Such developments will not only help in understanding the working of complex biological systems such as brain, but also help provide cure for several diseases and disorders that occur due to failure in communication between biological entities. [4]. It is envisioned that the development in MC can lead to biomedical, environmental and manufacturing applications [2]. Some recently explored biomedical applications include neural network modeling, development of ICT-inspired treatments [5] and intelligent drug delivery [6].

MC has been studied from the perspective of not only biomedical applications but also from communications point of view that focuses on the design of efficient receivers, modulation schemes, coding theory and performance analysis, etc. [7]. It must be noted that the existing solutions for conventional communication can not be simply replicated to MC setups due to the complex nature of the process. The challenges in MC appear in the form of non-stationary signal-dependent noise, range limitations that allow nanomachines to communicate over distances not more than few micrometers, large propagation delays, issues concerning chemical reactivity of molecules resulting in high loss rate, limited memory, power constraints and compatibility between bio-nanomachines [2]. These challenges define a significant amount of current and future research dimensions in MC. Other than these, the fact that these nano-sized sensing bodies allow interaction with biological entities such as bacteria have also opened several new avenues for research. For instance, instead of artificially provided molecules and chemicals, chemicals
produced by bacteria serve as messenger for communication between bacterial colonies where receptor bacteria produces light in response to received molecules [8]. Thus, in addition to micro and macro-level applications, research in MC is focused on understanding and successfully replicating chemical and biological processes and systems and interfacing with them through nanomachines.

In this work, we propose a new dimension in MC that focuses on the spread of infections and diseases via aerosols. Aerosol transmission of viruses leads to disease spread with massive impact on larger populations. It has been shown that aerosol transmission serves as an important mode of transmission for several viruses such as influenza A virus [9], severe acute respiratory syndrome (SARS) virus [10], lyssavirus [11], rabies [12] and many other pandemics. Unlike the traditional research in MC, the message-bearing entities can not be modulated and the message can not be embedded as desired. In fact, in the context of this research, we believe that the virus-laden exhaled air from an infected person can serve as a source of useful information and we need to design our receiver in order to retrieve this information. The importance of the proposed research dimension increases in high human population scenarios.

Mass Gatherings are observed when people gather for sports, recreational, social or religious activities. During these gatherings, the large movement of people from different regions pose higher risk of diseases spread to far away places and transport of emerging and reemerging diseases to the gathering place. The higher likelihood of transmission of disease during mass gatherings in reported in [13]–[16]. The detection system proposed in this work can provide solution to this problem. If such a setup is deployed at the entry point of gathering events like railways stations and airports and the likely hosts of diseases and endemics are spotted and treated before they become part of the gathering and transmit diseases to other people, the transport of disease can be checked. Moreover, if accurate models for virus transport and dynamics can be established, a blind localization problem can be formulated that can prove helpful in identification of disease sources. Thus, in order to take preventive measures against disease spread, it is essential to model and analyze the dynamics of virus transport as has been done in this work.

Being the first to study viral aerosol information retrieval, we investigate the detection problem of a single virus released from an infected human in indoor environment. To this end, we develop a mathematical analysis model of aerosol transmission and detection in order to examine the range limitation of virus detection. The main contributions of our work are summarized as
follows\(^1\),

- A new study dimension in MC is proposed, where virus spread through aerosol transmission is studied as a MC problem.
- Mathematical modeling of the wind-aided aerosol transmission channel is presented and insights are drawn into the dynamics of virus spread.
- A virus detection problem is formulated for a biosensor-based receiver architecture and an end-to-end model for proposed setup is presented.
- The performance of the proposed system is studied through numerical simulation scenarios in order to understand the impact of different factors. The performance evaluation is performed by studying the probability of virus miss-detection.

The rest of the paper is organized in the following order: Section II provides a brief description of proposed setup. System modeling is explained in detail and detection problem is formulated in Section III, followed by simulation and results in Section IV. Finally, we conclude the paper in Section V.

**Notations:** As for the mathematical notations, we use the following symbols. The partial derivative of the function \( f \) with respect to \( x \), i.e., \( \frac{\partial f}{\partial x} \), is represented by \( f_x \). Higher order derivatives are represented by repetition of independent variable in subscript, for example \( \frac{\partial^2 f}{\partial x \partial y} \) is represented by \( f_{x,y} \). The \( x \), \( y \) and \( z \) components of \( \vec{F} \) are defined as \( F^x \), \( F^y \) and \( F^z \), respectively. The Laplace transform of a function \( f(x,y) \) with respect to \( x \) is represented by \( \tilde{f}^{(x)}(q,y) \). The two dimensional Laplace transform is represented by \( \tilde{f}^{(x,y)}(q,r) \). \( \vec{F} \) denotes that \( F \) is a vector and \( \nabla \) is the vector differential operator. Thus, the divergence of \( \vec{F} \) is expressed as \( \nabla \cdot \vec{F} \).

**II. System Description**

In this section, we assume a basic architecture of a single source viral aerosol spread system. The proposed system is composed of three major components. The first one is the infected human who acts as a source of pathogen and in the rest of the paper, he or she is referred to as the transmitter. The second component is the aerosol transmission channel through which the virus spreads. The transmission can be subjected to air-flow, i.e., artificial wind. The third component is the receiver side that aims to retrieve information about the virus and/or pathogen.

\(^1\) A part of this work was accepted for presentation at IEEE International Conference on Communications [1].
The respiratory tract of the infected person is assumed to be loaded with virus-containing droplets. The virus can be emitted from the transmitter through different mechanisms of aerosol emission, which are known as breathing, coughing and sneezing. Coughing and sneezing release higher droplets than breathing. However, they are not very frequent compared to the normal breathing that occurs in a continuous manner [17]. Thus, coughing and sneezing account for smaller proportion of bioaerosols generated over the course of the day compared to normal breathing [17].

Once the aerosol is transmitted into the air, the released droplets diffuse in the room. To increase the transmission range and decrease the propagation delay, we apply air flow that is directed towards the receiver side. The released droplets can have different sizes that determine the travel distance of the pathogen. Aerosol transmission can be categorized into two types, airborne transmission and droplet transmission. Airborne transmission is defined as transmission of aerosols with size less than $5\mu$m, which can travel for a large distance in order of meters [18], [19]. On the other hand, droplet transmission refers to transmission of pathogen-laden droplet whose size is usually greater than $5\mu$m with shorter distance spreading [19]. Our focus in this paper is airborne transmission.
Throughout this paper, we are interested in retrieving viral information from the breath of the infected human represented in virus detection, as shown in Fig. 1. The experiment is performed in an indoor environment where we can apply artificial airflow with a specific velocity to drive the aerosols towards the detector. It must be noted that the experimental setup under consideration is very close to real-life situation where viral spread can be directed by the wind. Thus, the models derived in this work can be deployed not only in the development of detection and bio-monitoring applications but also in the qualitative and quantitative analysis of infection transmission.

III. SYSTEM MODELING

In this section, we analyze each block of our system that is shown in Fig. 2. The system is composed of a transmitter, channel, noise and detector. In the following subsections, we provide a detailed mathematical modeling of different system components.

A. Transmitter

As explained earlier, we assume that the infected human releases pathogens into the air through his breath. The normal breathing of an adult occurs at rate of 12-16 breaths per minute [20], which means that each breath takes place in no more than 4.98 seconds. Since the breath time is too small relative to the coarse of experiment which is of the order of several minutes, the variations in emission process due to breathing can be averaged out. Thus, we can model the input signal as a continuous process with constant emission rate which is equal to the average rate i.e $Q$ pathogen amount/sec. It is worth to note that although breathing can be assumed to be continuous in the steady state study, coughing and sneezing as impulsive jet sources can not follow the same assumption.
The droplets’ size from the released aerosol affects the communication performance quality. According to the study in [21], it has been observed that the normal human breathing results in larger fraction of droplets compared to coughing and sneezing, and the droplet sizes are below 1 µm. Hence, the transmitter is assumed to release aerosol with droplets that can travel distances long enough to reach the receiver and remain suspended in air over the course of the experiment. In this work, we focus on the breathing only as it is a permanent source of aerosol transmission compared to coughing and sneezing. Moreover, it is not practical to wait for the infected person to cough or sneeze to begin the experiment of detecting and tracking the infection. However, it is still worthwhile to analyze the performance of coughing and sneezing mechanisms in future studies and other specific scenarios such as transient response studies.

B. Aerosol Transmission Channel Modeling

Once the bioaerosols are released into the air by the infected human, the droplets are carried away by the artificial wind, which is generated to increase the transmission range and decrease the propagation delay. The basic difference between diffusion-based MC (DMC) and aerosol transmission is the propagation mechanism that drives the droplets in the fluid. In DMC, the Brownian motion is responsible for movement of particles and can be modeled as a Wiener process [2], where the molecular diffusion is characterized by molecular diffusivity coefficient. This communication occurs due to thermal movements of molecules and therefore it is a micro-scale communication. On the other hand, aerosol communication is a macro-scale transport of micro-sized particles over larger distances and can be characterized by dispersion models. Moreover, molecular diffusion has negligible contribution in the propagation of bioaerosols in atmosphere and is mainly governed by advection and turbulent diffusion. The wind is responsible for advection and eddies cause turbulent diffusion. It must be noted that eddy diffusivity coefficient is much greater than the molecular diffusivity coefficient, which can be ignored in dispersion models.

Now, we derive the system model for the pathogens concentration emitted from a continuous source at steady state. Assume a source located at \( \vec{r} = [x, y, z] \) emitting pathogens at a rate \( S(\vec{r}, t) \), where \( t \) is the time. From law of conservation of mass we can write [22], [23],

\[
C_t + \nabla \cdot \vec{F} = S, \tag{1}
\]
where $C_t$ is change in concentration of pathogen with time and $\vec{F}$ is the mass flux. Both, the concentration and flux are functions of $\vec{r}$ and $t$. The mass flux is composed of two components resulting from the two phenomenons called diffusion and advection and can be represented as follows,

$$\vec{F} = \vec{F}_{\text{diff}} + \vec{F}_{\text{adv}},$$

where $\vec{F}_{\text{diff}}$ is the diffusion component and $\vec{F}_{\text{adv}}$ is the advection component. The Fick’s law of diffusion states that flux due to diffusion is proportional to concentration gradient,

$$\vec{F}_{\text{diff}} = -\mathbf{K} \nabla C,$$

where $\mathbf{K}$ is the diffusivity matrix defined as

$$\mathbf{K} = \begin{bmatrix} K^x & 0 & 0 \\ 0 & K^y & 0 \\ 0 & 0 & K^z \end{bmatrix},$$

in terms of the eddy diffusivity coefficients $K^x, K^y, K^z$ in the $x, y$ and $z$ direction, respectively, after neglecting the molecular diffusivity. The eddy diffusion coefficients are function of position vector.

$$\nabla \cdot \vec{F}_{\text{diff}} = K^x C_{x,x} + K^y C_{y,y} + K^z C_{z,z}$$  \hspace{1cm} (2)

The second transport phenomenon is the advection which is the bulk transport of particles by a moving fluid. In our case, the driving force responsible for particles’ transportation is wind which is artificially applied. If the flow velocity is represented by $\vec{v} = [u^x, u^y, u^z]$, we can express the advective flux as,

$$\vec{F}_{\text{adv}} = \vec{v} C$$

Then, the divergence of $\vec{F}_{\text{adv}}$ is found to be,

$$\nabla \cdot \vec{F}_{\text{adv}} = \nabla \cdot (\vec{v} C) = C (\nabla \cdot \vec{v}) + \vec{v} \cdot \nabla (\nabla C)$$

For incompressible fluids whose density stays constant [24],

$$\nabla \cdot \vec{v} = 0$$

Thus, the change in advection flux boils down to the following expression,

$$\nabla \cdot \vec{F}_{\text{adv}} = u^x C_x + u^y C_y + u^z C_z$$  \hspace{1cm} (3)
Plugging the flux terms (2) and (3) in (1) and rearranging few terms results in the following expression,

\[ C_t = S + \left( K_x C_{x,x} + K_y C_{y,y} + K_z C_{z,z} \right) - \left( u_x C_x + u_y C_y + u_z C_z \right), \]  

(4)

To find \( C_t \), we solve (4) after stating the following conditions,

1) The infected human is continuously emitting pathogens at a constant rate \( Q \) (discussed in section III.A). The person is standing at origin and his mouth is at height \( H \). Thus, we can represent the source concentration as,

\[ S(\vec{r}, t) = Q \delta(x)\delta(y)\delta(z - H). \]

2) The wind is moving with a constant velocity \( u \) along the \( x \)-axis only and is zero in other directions.

3) The turbulent diffusion is isotropic, while the diffusivity coefficients depends on the downwind distance only, i.e., \( K_x = K_y = K_z = K(x) \).

4) The solution is derived for steady state conditions.

5) Along the downwind direction, the flux due to advection is much stronger than that due to diffusion, therefore, we ignore the diffusion flux, along the \( x \)-direction,

\[ K_x C_{x,x} - u C_x \approx -uC_x. \]

6) The ground doesn’t have any topographical variations and is flat. Thus, \( z = 0 \) is taken as the ground.

7) The pathogen-laden droplets do not penetrate the ground, \( K(x)C_z(x, y, 0) = 0 \)

8) Mass is conserved, i.e., \( C(x, y, \infty) = 0 \), \( C(x, \pm \infty, z) = 0 \), \( C(\infty, y, z) = 0 \)

After considering the conditions in 1-5, (4) reduces to

\[ Q\delta(x)\delta(y)\delta(z - H) = u C_x - K(x)[C_{y,y} + C_{z,z}]. \]  

(5)

To find the concentration at any point in the room away from the source, we use (5) obtaining

\[ \frac{u}{K(x)} C_x = C_{y,y} + C_{z,z}, \]  

(6)

which is a variable coefficient partial deferential equation (PDF). To simplify (6), we adopt a change of variables by defining a new variable \( \eta \) that is related to \( x \) as follows [25],

\[ x_\eta = \frac{u}{K(x)} \]  

(7)
Then, by applying the chain rule, \( \frac{u C_x}{K(x)} \) can be replaced by \( C_\eta \) where

\[
C_\eta = C_x x_\eta.
\]

As a result, \( \eta \) can be expressed as

\[
\eta = \frac{1}{u} \int_0^x K(t) dt.
\]

After the proposed change of variables, the PDE in (6) is written as,

\[
C_\eta = C_{y,y} + C_{z,z}.
\]

One way to solve the simplified PDF (8) is done by break it into two sets of simpler PDEs [25]. So, we break down \( C(\eta, y, z) \) into two functions as,

\[
C(\eta, y, z) = N(\eta, y) M(\eta, z).
\]

Then, we rewrite (8) as,

\[
NM_\eta + MN_\eta = MN_{y,y} + NM_{z,z}.
\]

Now, we divide both sides of the previous equation by \( MN \) to obtain two separate set of equations. The first one in terms of \( M \) and is written along with the corresponding boundary conditions as

\[
M_\eta = M_{z,z} \quad (10a)
\]

\[
M(0, z) = Q \delta(z - H) \quad (10b)
\]

\[
M(\infty, z) = 0 \quad (10c)
\]

\[
M(\eta, \infty) = 0 \quad (10d)
\]

\[
M_z(\eta, 0) = 0, \quad (10e)
\]

while the second equation is in terms of \( N \) and is expressed along with the corresponding boundary conditions as

\[
N_\eta = N_{y,y} \quad (11a)
\]

\[
N(0, y) = \delta(y) \quad (11b)
\]

\[
N(\infty, y) = 0 \quad (11c)
\]

\[
N(\eta, \pm \infty) = 0. \quad (11d)
\]
Now we use Laplace transform to solve the above differential equations to find $M$ and $N$. The Laplace transform variables for $\eta$, $y$ and $z$ are $q$, $r$ and $s$ respectively. Firstly, we solve the equation set (10a)-(10e) to find $M$. We start by finding the Laplace transform of (10a) w.r.t. $z$,

$$
\tilde{M}^{(z)}(\eta, s) = s^2 \tilde{M}^{(z)}(\eta, s) - sM(\eta, 0) - M_z(\eta, 0).
$$

(12)

Since, the droplets do not penetrate the ground, from (10e), the last term becomes zero. Then, we take Laplace transform for (12) w.r.t. $\eta$ obtaining

$$
q \tilde{M}^{(z,\eta)}(q, s) - \tilde{M}^{(z)}(0, s) = \frac{s^2 \tilde{M}^{(z,\eta)}(q, s) - s\tilde{M}^{(\eta)}(q, 0)}{s^2 - q}.
$$

(13)

By taking Laplace of (10b) we obtain

$$
\tilde{M}^{(z)}(0, s) = Qe^{-sH},
$$

which is plugged in (13) obtaining

$$
\tilde{M}^{(z,\eta)}(q, s) = \frac{s\tilde{M}^{(\eta)}(q, 0)}{s^2 - q} - \frac{Qe^{-sH}}{s^2 - q}.
$$

(14)

Then, by taking the inverse Laplace transform of (14) w.r.t $s$, we find

$$
\tilde{M}^{(\eta)}(q, z) = \tilde{M}^{(\eta)}(q, 0) \cosh(\sqrt{q}z) - \frac{Q}{\sqrt{q}} \sinh(\sqrt{q}(z - H)).
$$

(15)

Now, we use the boundary condition (10d) to obtain

$$
\tilde{M}^{(\eta)}(q, 0) = \frac{Qe^{\sqrt{q}(z-H)}}{\sqrt{q}e^{\sqrt{q}z}} = \frac{Q}{\sqrt{q}} e^{-\sqrt{q}H},
$$

which can be plugged in (15) obtaining the following simplified expression after expanding the hyperbolic functions as sum of exponentials,

$$
\tilde{M}^{(\eta)}(q, z) = \frac{Q}{2\sqrt{q}} (e^{-\sqrt{q}(z-H)} + e^{-\sqrt{q}(z+H)}).
$$

Then, we take the inverse Laplace transform w.r.t $q$ obtaining

$$
M(\eta, z) = A + B
$$

where $A$ is expressed as

$$
A = \frac{1}{2\pi} \int_{-\infty}^{\infty} \frac{Q}{2\sqrt{q}} e^{-\sqrt{q}(z-H)} e^{q\eta} dq,
$$

and $B$ is found from

$$
B = \frac{1}{2\pi} \int_{-\infty}^{\infty} \frac{Q}{2\sqrt{q}} e^{-\sqrt{q}(z+H)} e^{q\eta} dq.
$$

At this stage, we solve $A$ and $B$ by making suitable changes of variables, which simplify $M(\eta, z)$ as

$$
M(\eta, z) = \frac{Q}{\sqrt{2\pi} \eta} \left( e^{-\frac{(z-H)^2}{4\eta}} + e^{-\frac{(z+H)^2}{4\eta}} \right).
$$

(16)
Secondly, we consider the second set of equations (11a)-(11d) to obtain \( N(\eta, y) \). The Laplace transform of (11a) w.r.t. \( y \) is expressed as
\[
\tilde{N}_{\eta}^{(y)}(\eta, r) = r^2 \tilde{N}_{\eta}^{(y)}(\eta, r) - rN(\eta, 0) - N_{\eta}(\eta, 0).
\]
Again we take Laplace transform w.r.t. \( \eta \). Since, Laplace transform of \( \delta \) is equal to 1, Laplace transform of (11b) results in \( \tilde{N}_{\eta}^{(y)}(0, r) = 1 \). Plugging it and rearranging the expression finally results in,
\[
\tilde{N}_{\eta}^{(y, \eta)}(q, r) = \frac{rd_1}{r^2 - q} - \frac{d_2}{r^2 - q}
\]
where \( d_1 = \tilde{N}_{\eta}^{(y)}(q, 0) \) and \( d_2 = 1 - \tilde{N}_{\eta}^{(y)}(q, 0) \). Then, by taking inverse Laplace transform w.r.t. \( r \) we obtain
\[
\tilde{N}_{\eta}^{(y, \eta)}(q, y) = d_1 \cosh(\sqrt{q}y) - d_2 \sinh(\sqrt{q}y).
\]
For further simplification, we expand the hyperbolic functions as sum of exponentials, evaluate it at boundary point and compare with transform of (11d). These steps result in the following expression,
\[
\tilde{N}_{\eta}^{(y, \eta)}(q, +\infty) = \lim_{y \to \infty} (d_1 e^{\sqrt{q}y} - d_2 \frac{1}{\sqrt{q}} e^{\sqrt{q}y}) = 0
\]
which can be substituted in (18) obtaining
\[
\tilde{N}_{\eta}^{(y, \eta)}(q, y) = d_2 \frac{e^{\sqrt{q}y}}{\sqrt{q}}.
\]
Similarly, we use the strategy we followed before for \( \tilde{M}_{\eta}^{(y)}(q, z) \) and take inverse Laplace of \( \tilde{N}_{\eta}^{(y, \eta)}(q, y) \) obtaining,
\[
N(\eta, y) = d_2 \frac{e^{-y^2/4\eta}}{\sqrt{\pi \eta}}.
\]
To find \( d_2 \), we use (11b) that gives
\[
\delta(y) = \lim_{\eta \to 0} d_2 \frac{1}{\sqrt{\pi \eta}} e^{-y^2/4\eta}.
\]
Then, by using the definition of delta as a limit of Gaussian,
\[
\delta(y) = \lim_{x \to 0} \frac{1}{\sqrt{2\pi x^2}} e^{-x^2/4}.
\]
Now, we comparing (21) and (22) and find
\[
d_2 = \frac{1}{\sqrt{2}}.
\]
Fig. 3: Concentration of virus for source present at $\vec{r} = [0, 0, 177]$.

Therefore, $N(\eta, y)$ turns out to be,

$$N(\eta, y) = \frac{1}{\sqrt{2\pi\eta}} e^{-\frac{y^2}{4\eta}}. \tag{23}$$

Finally, by inserting (16) and (23) in (9), we find the solution of (4) as

$$C(\eta, y, z) = \frac{Q}{2\pi\eta} e^{-\frac{y^2}{4\eta}} \left( e^{-\frac{(z-H)^2}{4\eta}} + e^{-\frac{(z+H)^2}{4\eta}} \right). \tag{24}$$

To visualize the spread of aerosols, a contour plot is presented in Fig. 3. The source is located at a certain height at origin which can be seen as the point of highest concentration. Moving away from the source results in a drop in concentration, however, this change is not constant. In fact, it is like a cone with its vertex at the source spreading in the direction of wind. Analyzing the expression derived above, it can be observed that the expression is in fact product of two normal curves whose variance changes with downwind distance. This trend can be more clearly visualized in Fig. 4 where increase in downwind distance increases the spread of individual contours in the $y-z$ plane. Also this spread is more significant up till a certain point along the $x$-axis after which the overall or mean concentration itself is too low to be sensed or detected.
Thus, it can also be concluded that on average the concentration drops as we move away from the source, however the trend is not linear.

C. Molecular Receiver

We propose a detection mechanism that could be leveraged to distinguish between healthy and infected person. Once, the infected person has released certain amount of pathogens into the atmosphere, and they have passed through the molecular channel, the receiver acts as an absorbing surface that absorbs most of the pathogen-laden droplets. The architecture of molecular receiver is shown in Fig. 5. The details of three major blocks are presented below.

1) Aerosol Sampler: Several techniques have been developed for collection of suspended air particles. Aerosol sampler is the front end of our receiver which controls the sampling rate of air. Although there are several other techniques, the sampler proposed in this receiver architecture is
Fig. 6: Electrostatic air sampler.

based on the principle of electrostatic precipitation which is not only commercially available but also allows sampling of particles with sizes as small as 2-100nm. [26]. The sampler sensitivity in terms of sampling nano-sized particles is quiet significant since, the droplet sizes are of the order of few micrometers and the diameter of virus and bacteria, in general can be of the order of nanometers.

The architecture of the electrostatic air sampler is depicted in Fig. 6. The two main components of the sampler are ionizer and charged electrode. The ionizer induces negative charge on air particles that pass then through the next chamber and collect on the positively charged electrode after repelling by the outer negatively charged boundaries. The performance of sampler is quantified through it’s collection efficiency. As reported in [27], collection efficiency of 80–90% is achievable with commercial electrostatic aerosol samplers. For the rest of paper, we denote sampler efficiency by \( \xi \).

2) Biosensor: Biosensors are sensing devices that translate molecular events into processable information [28], [29]. They usually consist of a recognition layer followed by transducer that converts the recognized signal into a processable form [30]. The physical change that the bio-recognition layer undergoes on contact with target bodies is quantified. The recognition layer is connected to a transducer which converts the behavior or the variation in recognition layer into processable information. Based on the varying property which is being measured, biosensors are
classified into three types, electrical, mechanical and optical.

In the electrical biosensors, a change in current, voltage, or conductance is observed when a binding event takes place in the recognition layer. On the other hand, in optical sensors, the optical properties of the recognition layer are altered when it comes in the presence of target cells. As for the mechanical biosensors, they consist of nanomechanical systems that are capable of detecting the forces, motions, mechanical properties and masses, which emerge in biomolecular interactions [31].

In this work, we consider electrical biosensors due to their high sensitivity and selectivity [32]. There are two basic types of electrical biosensors, which are known as biocatalytic and affinity based. In biocatalytic sensors, the presence of a virus or a target specie induces enzymes (already present on recognition layer) to produce a certain chemical substance whose concentration is then measured in order to obtain information about the presence of target. On the other hand, affinity based sensors consist of virus or target-specific antibodies placed on the recognition element. In the presence of target, a binding event between target and antibody takes place which is translated to variation in some electrical property(current, voltage, conductance, etc.). Field effect transistors (FETs) are the most commonly used affinity-based electrical biosensors. The amplification property of FETs permits that a small change in voltage at the gate induces a large current change in source-drain channel yielding a highly sensitive biosensor [33].

The Silicon NanoWire (Si-NW) FET is transistor with Si-NW is placed between the source and the drain terminals over the FET substrate. The virus is detected with the help of antibody receptors that are placed on the Si-NW as shown on Fig. 7. When the FET is placed in an antigen-rich solution, the antigens come into contact with the antibody receptors and a binding event takes place. The binding events effect the source-drain conductance channel resulting in accumulation or depletion of electrons just like gate voltage. Thus, the binding events are translated to current change across the source-drain channels by producing a change in the FET conductance. The inherent amplification property of FETs allows for even small number of binding events to produce measurable current making it a highly sensitive sensor [34]–[36]. It was shown in [34], that the presence of a virus resulted in a dramatic change in source-drain current. In [35], the presence of influenza A virus results in discrete changes in conductance while no change in conductance occurs in presence of other viruses such as adenovirus, which demonstrates the high selectivity of the sensor. In [36], an air sampler was integrated with FET and it was shown that discrete conductance changes were observed when sensor was exposed
Fig. 7: Si-NW FET

to aerosols and the change was proportional to the aerosol concentration. The setup was able to detect in real-time and the whole process of sampling, sensing and detection occurred in less than 2 minutes.

3) Processing and Detection: The most important factor while designing the processing and detection block is the input signal model and noise. As explained in [37], binding noise and flicker noise are dominant in MC receivers.

- **Binding noise**: The probabilistic binding events between virus and receptors existing at the FET biosensor result in a binding noise. A detailed modeling of the binding noise is discussed in [38], [39]. A Markovian approach is adopted to model the dynamics of biosensor and derive closed form expressions for settling time and noise power spectral density (PSD). Since, we are interested in analyzing the system in the steady state, where we wait for a longer period than the settling time before measuring the output signal, the captured virus
concentration is given by \[39\],
\[
C_{ss} = N \frac{P_a}{P_a + K P_d} = N \gamma \tag{25}
\]
where \(N\) is the total number of antigens, \(P_a\), \(P_d\), and \(K\) are the association probability, dissociation probability and number of possible states, respectively.

- **Flicker Noise**: This noise is known also as \(1/f\) noise, where it is dominant at low frequencies and results from semiconductor channel imperfections. Flicker noise can be modeled as Gaussian \([40], [41]\) and is independent of the virus concentration because it solely depends on the transistor characteristics.

Moreover, we can have interference noise that results from other biological entities which might interfere with the binding process of virus and the corresponding antibody receptor \([37]\). However, since we assume the room is perfectly sanitized before the donor enters, the interference noise is negligible and is ignored. Therefore, the final expression for the received concentration incorporating the noise effects can be written as,
\[
C_r = \eta \gamma C_{mean} + n \tag{26}
\]
where, \(\eta\) represents aerosol sampler efficiency, \(\gamma\) is a fraction representing the probabilistic binding process, \(n\) is additive noise that incorporates the effect of flicker, thermal noise and other residual noise and is modeled as Gaussian with mean zero and variance \(N_0^2\). \(C_{mean}\) is average concentration of virus particles that are present in the receiver chamber and is given by,
\[
C_{mean} = \int \int \int_{V_{rx}} \frac{Q}{2 u \pi \eta} e^{-\frac{z^2}{4(\eta - \eta_0)}} (e^{-\frac{(z-H)^2}{4(\eta - \eta_0)}} + e^{-\frac{(z+H)^2}{4(\eta - \eta_0)}}) dx dy dz \tag{27}
\]
where \(V_{rx}\) represents receiver volume. This receiver could be a 1-D array of biosensors, a sphere or some other appropriate surface with sufficient number of receptors. Depending upon the receiver geometry and receptor/biosensor density, closed form expressions for average received concentration of pathogen may be derived. This aspect could be explored further in future.

In the detection process, \(C_{mean}\) is compared with a pre-determined threshold, \(C_{th}\), through maximum posterior probability rule to determine whether the person is infected or not. Let \(I\) and \(H\) represent the infected and healthy person, thus the decision is made according to following rule,
\[
Pr(I|C_r) \leq_{I} \Pr(H|C_r).
\]
Then, by applying Bayes’ rule and assuming that the event of person being infected or healthy is equally likely, we obtain the following expression,

\[ \Pr(C_r|I) \leq \Pr(C_r|H) \]

Now, from (26), we can expand the above the expression as,

\[ \frac{1}{\sqrt{2\pi N_o}} e^{-\frac{(C_r - \gamma \xi C_{\text{mean}})^2}{2N_o^2}} \leq \frac{1}{\sqrt{2\pi N_o}} e^{-\frac{(C_r)^2}{2N_o^2}} \]

Rearranging the terms on both sides results in the following inequality,

\[ C_r \leq \frac{\gamma \xi C_{\text{mean}}}{2} \] (28)

Thus, the maximum likelihood threshold value should be equal to,

\[ C_{\text{th}} = \frac{\gamma \xi C_{\text{mean}}}{2} \] (29)

For further insights, we derive the probability of missed detection \( P_{\text{md}} \) as follows,

\[ P_{\text{md}} = P(C_r \leq C_{\text{th}}|I) \] (30)

Again from (26) we obtain,

\[ P_{\text{md}} = \int_{-\infty}^{C_{\text{th}}} \frac{1}{\sqrt{2\pi N_o}} e^{-\frac{(C_r - \gamma \xi C_{\text{mean}})^2}{2N_o^2}} \]

Through change of variables, we get the final expression for probability of missed detection,

\[ P_{\text{md}} = Q\left(\frac{\gamma \xi C_{\text{mean}}}{\sqrt{2\gamma \xi C_{\text{mean}}} N_o}\right) \] (31)

From (31) and (29), it can be observed that the probability of missed detection not only depends on the average received concentration of pathogens but also on the sampler efficiency on which is taken into account while incorporating the threshold value.

IV. NUMERICAL RESULTS

In this section, we analyze the performance of the proposed system numerically by studying the miss-detection probability. To this end, we use a simulation scenario with the parameters listed in Table I, unless otherwise specified. It must be noted that the receiver is placed in-line with the source in the \( y - z \) plane as assumed in Fig. 3. Specifically, the receiver is located at \( d_x \) distance along downwind direction was a sphere of radius \( r_d \) centered at \( \vec{u}_s = [d_x, 0, H] \). The received mean concentration was calculated using (27). Our assumption of perfectly sanitized
indoor environment prior to beginning of experiment justifies our use of probability of missed detection (31) as an evaluation function for the proposed setup. Although there is still a margin for false positives due to sensors’ electronics, but it should be quiet small given the sensors output signal is dependent on the binding event which would occur only in presence of viral aerosols. Thus, we focus on probability of missed detection only which not only provides a measure to quantify the performance but also reflects the impact of different parameters such as downwind distance and noise.

In the first numerical example, we study the effect of $Q$ on the virus detection, which is highly affected by the virus concentration and the breathing rate. For this purpose, we study the $P_{\text{md}}$ versus the distance between the infected human and the detection, i.e., $d_x$, in Fig. 8. In general, the detection is highly affected by the distance where $P_{\text{md}}$ increases as the distance increases. The impact of $Q$ is dominant in relativity small distances due to the q-function behavior of the miss detection probability in (31). Therefore, it is recommended to have a movable detectors that can be close to the possible infected human and/or increase $Q$ if possible. Although having mobile detector is possible but controlling $Q$ is certainly challenging. One way to do so is to increase the breathing rate by some suitable exercises, which can be applied to improve the detection process. For example, if we can triple $Q$ for 1 meter distance, $P_{\text{md}}$ rate drops by as large as 40 dB.

In the second numerical example, we study the impact of turbulence on the detection process. To this end, we plot $P_{\text{md}}$ versus the distance for different turbulence variance in Fig. 9. First, we observe similar effect of the distance on $P_{\text{md}}$ for different turbulence variances in

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean Wind Speed $U$</td>
<td>15 cm/sec</td>
</tr>
<tr>
<td>rms turbulent velocity along y axis, $u_y$</td>
<td>3 cm/sec</td>
</tr>
<tr>
<td>rms turbulent velocity along z axis, $u_z$</td>
<td>3 cm/sec</td>
</tr>
<tr>
<td>Human Height, $H$</td>
<td>177 cm</td>
</tr>
<tr>
<td>Sampler Efficiency, $\eta$</td>
<td>80%</td>
</tr>
<tr>
<td>Binding Efficiency of Receiver, $\gamma$</td>
<td>60%</td>
</tr>
<tr>
<td>Radius of spherical receiver $r_d$</td>
<td>5 cm</td>
</tr>
<tr>
<td>Flow rate, $Q$,</td>
<td>50 droplets/sec</td>
</tr>
</tbody>
</table>
crosswind directions. In addition, the turbulence can severely degrade the detection probability performance even at short distances from the detection. At short distances, as the turbulence variance increases, the virus disperses in directions away from the detector area, which worsens the performance of $P_{md}$.

Finally, we present a Monte Carlo simulation of the system to study the $P_{md}$ for different distances between the infected human and the detector. The effect of different parameters like wind velocity, crosswind turbulence, flow rate, ..., etc, is captured in the signal-to-noise (SNR) term that is defined as,

$$\text{SNR} = \frac{|\eta \gamma C_{\text{mean}}|^2}{N_0^2}.$$ 

The received signal is generated using (27) and (26) and is compared then with a threshold computed from (29). If the received signal is above the threshold, the person is termed as infected otherwise it corresponds to an error. As mentioned in Section III-B, where initial and boundary conditions are stated, the diffusivity coefficients are isotropic and depend on
Fig. 9: Effect of rms turbulent velocity along crosswind directions on $P_{md}$ versus the distance between the infected human and the detector.

the downwind distance. The dispersion parameters depend strongly on the atmospheric physical characteristics, and can be empirically estimated by different approaches in the literature [42]. With the assumptions of negligible molecular diffusion and short downwind distances allow us to model dispersion parameters as a linear function of downwind distance [42], [43]. In this example, we assume low wind conditions ($U \leq 3 \text{ m/s}$) and model the dispersion parameters as [43] [42],

$$K_y(x) = \frac{u_y d_x}{U}$$

$$K_z(x) = \frac{u_z d_x}{U}.$$

Fig. 10 shows the average performance of $P_{md}$ over 1000 independent scenarios for a specific distances between the transmitter (infected human) and the receiver (detector) considering different SNR values. It can be observed that the performance of the proposed systems improves with increasing SNR for different distances. Moreover, It can be observed that as the distance
increases, the error probability increases and the difference is more significant at higher SNRs. For example, around 10 dB, there is a drop of more than 10 dB in missed detection rate, when distance is halved. For fixed wind conditions, the error rate can be improved by increasing the sampler efficiency or decreasing the distance because one has no control over the viral concentration emitted by infected human or the flicker noise.

It can be concluded from the above results that the trend for missed detection against downwind distance, flow rate, SNR, and source concentration is non-linear. The drop in performance with distance is sharp until a certain range after which the curve is almost flat. Thus, for further analysis, the distance range can be divided into a two sectors, a near-source and distant low concentration region. Moreover, higher concentration and lower turbulent velocity implies a lower error probability, a close receiver location can guarantee improved results.

Fig. 10: Probability of miss-detection vs SNR for different downwind distance.
V. CONCLUSION

The paper defined a new research dimension in MC, which is viral aerosol transmission, spread mechanism and detection. The mathematical modeling of aerosol channel provides insights into the dynamics of virus spread and guides to study ways to detect it. Applying artificial airflow overcomes the slowness of diffusion based spread and allows the detection of viruses, thus it is a key enabler for the viral detection system. The simulation results show that the miss detection is controlled by the distance, virus flow rate, turbulence, receiver binding efficiency and others. The proposed mathematical problem was studied using steady state analysis of virus transmission and detection due to breathing. However, the future studies should include coughing and sneezing as other sources to be be incorporated in the system modeling. In addition, the transient analysis is important to explore different features such as the memory channel behavior. Moreover, it is imperative to optimize the receiver(s) location and study multiple sources scenarios. Finally, this work can also be extended in the context of predicting the occurrences of pandemics and taking preparatory measures.

REFERENCES


