Webapp – Simple Explanation

https://zechlau14.github.io/airborne-transmission-webapp/

version 0

Abstract

This webapp aims to help users understand the risk of indoors airborne virus transmission, and the effects of the room conditions and the occupant behaviour on that risk. The app uses the efficient airborne transmission model in [1] that assumes the viral particles are 'advected by airflow, diffused due to turbulence, emitted by infected people, removed due to ventilation, and removed due to ventilation, inactivation of the virus and gravitational settling.' It assumes that the occupants in the room maintain social distancing so there is no risk of short-range transmission. Users can change parameters such as the room dimensions, occupant position and activity, ventilation settings, event duration, and other advance parameters.

1 Intended use and main assumptions

Airborne viral transmission occurs when infectious viral particles are carried by the respiratory aerosols produced by an infectious person.[2] When a susceptible person breathes in these aerosols, there is a risk of being infected by the virus.

As these respiratory aerosols are small, they follow the recirculating air currents in the room. And if the ventilation is poor, they can accumulate, further increasing the risk of airborne viral transmission. Using the model presented in [1], this webapp estimates the risk of infection throughout the room from airborne transmission due to accumulation of infectious viral particles in a clean room from a single infectious person with specific inputs from the user.

As other viral transmission routes are not accounted for, the user should take into account that there are additional risks of infection in addition to the estimate produced by this webapp. Therefore, the results from this webapp should only be used as a way to understand how different behaviours and interventions affect the risk of airborne viral transmission, and should not be used as a definitive or absolute evaluation of risk.

2 Using the app

2.1 Model Inputs

2.1.1 Basic Parameters

In **Room dimensions**, the user can specify the dimensions of a rectangular room (in metres), or select from one of three presets. To set the floor area of the room, the user may also drag the bottom right corner of the **Dynamic 2D-room representation**.

Then in **Infectious person**, the user can input the coordinates of the infectious person in the room, the amount of talking being done by the infectious person and the type of mask worn by the infectious person. Alternatively, the user can also drag the avatar of the infectious person in the **Dynamic 2D-room representation** to set the position of the infectious person.

Similarly, in **Susceptible person**, the user can input the coordinates of the susceptible person in the room, the activity of the susceptible person and the type of mask worn by the susceptible person. Once again, the avatar in the **Dynamic 2D-room representation** may be dragged to set the position of the susceptible person.

For **Ventilation**, the user can set the ventilation rate in terms of *air changes per hour* (ACH). One ACH means that in one hour a volume of air equal to the volume of the room (defined by the user in the Room dimensions input) has been pumped into the room by the air-conditioning unit. For users who are uncertain of the ACH of the room, preset values that correspond to the recommendations by the American Society of Heating, Refrigeration and Air-Conditioning Engineers (ASHRAE) have been provided.[3, 4] The user can also set the speed of air pumped in by the air-conditioning unit.

Finally, in **Event** the user can set the duration of the event. Checking the **add a break** box, allows the user to introduce a break during the event that starts and ends at a time of the user's choosing. During the break, the webapp assumes that all occupants *have left* the room and the air-conditioning unit has been *left on*.

2.1.2 Advanced Parameters

Clicking the **Advanced Options** button allows the user access to the advanced parameters considered by the model.

The first group of advanced parameters are those relating to the distribution of respiratory droplets produced: the 'emission rate for breathing' and the 'gravitational settling rate'. The emission rate is the average number of respiratory droplets produced while a person breathes, and the gravitational settling rate is the average speed for a respiratory droplet to fall to the ground from a height of one metre. There is currently no agreement in the literature about these values, for example see [5, 6, 7, 8].

The second group of advanced parameters are those relating to the properties of the virus studied: the 'viral load', 'viral deactivation rate' and the 'median infectious dose'. The viral load is the number density of viral particles in the person's respiratory fluids, usually measured by swabbing the nose or back of the throat of an infectious person. The viral deactivation rate is related to how long the virus remains infectious while in the air. And the median infectious dose is the average number of virus particles that a susceptible person has inhaled to become infected. The defaults assume a virus about as infectious as the SARS-CoV-2 virus.[9, 10, 11]

Finally, the user can change up the step sizes, Δx, Δy and Δt used in the computation of the model. Making these larger will decrease the webapp's run time, but at the cost of accuracy. However, making these inputs smaller yields diminishing returns. The authors believe that the default settings chosen present a happy compromise between speed and accuracy, but the user is welcome to try choices of their own.

2.2 Model Outputs

2.2.1 Base Results

When the user clicks the **Run** button, the webapp calculates then returns the average infection risk from airborne transmission throughout the room. In the **Output message**, the user can change the number of occupants in the room to obtain the average number of people that are likely to be infected by this event.

The webapp also returns a contour plot of the floor area of the room. The contours show the infection risk throughout the room, assuming that the infectious person does not move during the event, save for exiting the room during a break and then returning to the same position.

2.2.2 Explore More Results

On clicking the **Explore more** button, the user is given the option to obtain different outputs from the same set of inputs. These options are

1. the time-evolution of the concentration and infection risk for the susceptible person that the user has positioned in the room,
2. a contour plot of the airborne viral concentration throughout the room at the end of the event.
3. the time-evolution of the spatially-averaged airborne viral concentration, and
4. the time-evolution of the spatially-averaged infection risk.

3 Scientific Basis

The full scientific basis of this webapp is given in detail in [1]. Here we summarise the main parts and note any additions made to improve the usability of the webapp.

3.1 Governing Equation

We assume that 'advected by airflow, diffused due to turbulence, emitted by infected people, removed due to ventilation, and removed due to ventilation, inactivation of the virus and gravitational settling.'[1] Therefore, the governing equation that the model is an advection–diffusion–reaction equation

$$\frac{\partial C}{\partial t} + \nabla \cdot (vC) - \nabla \cdot (\nabla K \nabla C) = R\delta(x - x_0)\delta(y - y_0) - (\lambda + \beta + \sigma)C, \tag{1}$$

where C is the concentration of the viral particles (particles/m^3), v is the airflow velocity (m/s), K (m^2/s) is the turbulent diffusion coefficient, R is the rate of viral particle emission (particles/s), (x_0, y_0) is the coordinates of the infectious person, λ is the ventilation rate (s^{-1}), β is the viral deactivation rate (s^{-1}) and σ is the gravitational settling rate (s^{-1}).

We assume there is no viral particles in the room initially, ie.

$$C(x, y, 0) = 0. \tag{2}$$

We model the recirculating air loop in the room as a set of periodic boundary conditions:

$$C(0, y, t) = C(2l, y, t), \tag{3}$$

$$\frac{\partial}{\partial x}C(0, y, t) = \frac{\partial}{\partial x}C(2l, y, t), \tag{4}$$

where l is the length of the room. And we apply Neumann boundary conditions to the other pair of walls

$$\frac{\partial}{\partial y}C(x, 0, t) = \frac{\partial}{\partial y}C(x, w, t), \tag{5}$$

where w is the width of the room.

3.2 Exhalation of viral particles

The rate of viral particle emission, R is given by

$$R = \begin{cases} \mu(1 - \eta_{\text{inf}})\{(1 - \rho_{\text{inf}})R_{\text{breathing}} + \rho_{\text{inf}}R_{\text{talking}}\}, & \text{if } \mu < 1 \\ (1 - \eta_{\text{inf}})\{(1 - \rho_{\text{inf}})R_{\text{breathing}} + \rho_{\text{inf}}R_{\text{talking}}\}, & \text{if } \mu \geq 1 \end{cases} \tag{6}$$

where ρ_{inf} is the fraction of time the infectious person spends talking, η_{inf} is the efficiency of the mask worn by the infectious person, $R_{\text{breathing}}$ and R_{talking} (particles/s) are the respiratory aerosol emission rate for the respective activities, and μ is the number of viral copies per respiratory aerosol.

The user can directly input η_{inf} and ρ_{inf} in the basic parameters, and $R_{\text{breathing}}$ in the advance parameters. The preset η_{inf} values provided in the webapp were taken from [12, 13]. It is important to note that these values can vary in reality depending on the manufacturing quality of the mask, especially since many cloth masks are made by amateurs, and how well the mask is worn. The placeholder value for $R_{\text{breathing}}$ was taken from [6].

On the other hand, R_{talking} and μ are calculated by the webapp from the user's inputs through the following formulae:[6]

$$R_{\text{talking}} \approx 10R_{\text{breathing}}, \tag{7}$$

and [14, 15]

$$\mu = \frac{\pi}{6}d_p^3 c_v, \tag{8}$$

where c_v is the viral load of the virus (viral copies/ml) which the user can control in the advance parameters, and d_p is the average diameter of the respiratory particles, which is 5 μm.[16] We've taken placeholder value of c_v is taken from [17].

3.3 Removals

Following [18, 19], we've assumed that ventilation, gravitational settling, and biological deactivation are first order removals. The user can directly input the rates for each of these removal mechanisms into the webapp. As mentioned in section 2.1.1, the preset values for the ventilation settings, λ, are taken from [3, 4]. While the placeholder values for β and σ are taken from [9] and [14] respectively.

3.4 Movement of Viral particles

The movement of the viral particles in the air is controlled by advection and turbulent diffusion. The viral particles are carried by advection by the air flow from the air-conditioning unit, which is controlled by the user through the **airflow velocity** input. The presets for this are taken from [20].

On the other hand, the turbulent diffusion coefficient K is calculated by the webapp from the user's inputs, assuming the single air-conditioning unit, by [21]

$$K = c_k V \lambda (2 c_\epsilon V)^{-1/3}, \tag{9}$$

where c_k is the von Karman constant, c_ϵ is the constant of proportionality in Taylor's Dissipation Law, and V is the volume of the room calculated from the user's inputs in **Room dimensions**.

3.5 Dose of viral particles inhaled

The dose of viral particles inhaled by a susceptible person, d, is given by [22, 23, 24]

$$d(x, y, t) = (1 - \eta_{\text{sus}}) \int_0^t \rho_{\text{sus}}\ C(x, y, t')\ \mathrm{d}t', \tag{10}$$

where η_{sus} is the efficiency of the mask worn by the susceptible person and ρ_{sus} is the respiratory volume rate of the susceptible person (m^3/s). The user can control η_{sus} and ρ_{sus} directly in the **Susceptible person** inputs. The preset values for these parameters are taken from [12, 25] and [26] respectively.

3.6 Infection risk

Finally, we assume an exponential probability density function for a susceptible person being infected from airborne transmission as a function of the dose of viral aerosols inhaled, d, [11, 22]

$$P(d) = 1 - e^{-Id}, \tag{11}$$

where I is a conversion factor that is related to the median infectious dose, d_m, by

$$\frac{1}{2} = \begin{cases} 1 - \exp\left(-I d_m\right), & \text{if } \mu \leq 1 \\ 1 - \exp\left(-\frac{I d_m}{\mu}\right), & \text{if } \mu > 1. \end{cases} \tag{12}$$

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