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A USER-FRIENDLY TOOL TO COMPUTE INFECTION PROBABILITY OF SARS-COV-2 INDOOR: THE USER GUIDE AND ITS APPLICATION IN MEDICAL PRACTICE

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After some initial hesitancy at the beginning of the COVID-19 pandemic, the academic community agreed that the infection process is mostly airborne and generally associated with closed environments. Therefore, assessing the indoor infection probability is mandatory to contain the spread of the disease, especially in those environments, like school classrooms, hospital wards or public transportation, with higher risk of overcrowding. For this reason, we developed a software tool in Python to compute infection probability and determine those mechanisms that contribute to reduce its diffusion in closed settings. In this paper, we will briefly illustrate the model we used and focus our attention on the description of the main features of the software and give some examples of how it can be used in the clinical practice to predict the spread of the disease in the rooms of a generic ward, optimize room occupancy or drive healthcare workers' activity schedule. Finally, some limitations and further implementations of our work will be reported.

Keywords: SARS-CoV-2; infection probability; software tool.

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1. Introduction

Since the World Health Organization declared the COVID-19 outbreak a pandemic on $11th$ $11th$ March 2020,¹ SARS-CoV-2 caused the death of 6.610.329 people around the world, 179.985 of them in Italy only.[2](#page-13-1)

Several studies demonstrated that it behaves like other airborne viruses such as MERS-CoV (Middle East respiratory syndrome coronavirus infection) and measles or mycobacteria such as tuberculosis.[3](#page-13-2) It means that viral copies discharged by the infectors, through cough and sneeze, remain suspended in the air on dust particles, respiratory and water droplets and might be inhaled by exposed subjects.

The transmission of SARS-CoV-2 can occur in both outdoor and indoor settings,[4](#page-13-3) but the risk of transmission indoor is higher^{[5](#page-13-4)} especially in small, crowded, and poor ventilated spaces like school classrooms, hospital wards and public transportation.^{[6](#page-13-5),[7](#page-13-6),[8](#page-13-7)} Some passive methods might be very effective to prevent diffusion, like adequate ventilation, 9 use of personal protection equipment and social distancing; these are, along with massive vaccination, 10 the key to contain infections. Since newer strains of the virus are emerging and undermining vaccine effectiveness, the requirement of booster injection and updated versions of the vaccine is rising.^{[11](#page-14-0)} The synthesis of new and effective drugs is difficult and time demanding, then it must be associated with other countermeasures. These are important, especially in the period of transition towards a post-pandemic era, to return safely to our daily activities; indeed ventilation, room occupancy and other factors can be optimized to reduce infection probability in those, potentially dangerous, environments.

Different models to compute infection probability for COVID-19 have been used in several studies, starting from the Wells-Riley model for airborne pathogens^{[12](#page-14-1)} to numerical simulations.^{[6](#page-13-5)} The aim of our study is to propose a model based on Wells-Riley's, but adapted to the specificities of SARS-CoV-2, and to identify those features that can contribute to spread reduction. Even though the transmission through fomites is possible and studies demonstrated that surface stability for COVID-19 is higher compared to other analogous viruses, 13 we considered airborne transmission as the main diffusion route, basing on current literature.^{[14](#page-14-3)}

The main purpose is to obtain an agile and flexible model to perform quick, but reliable, evaluations. Our model has been used to develop a software tool in Python. The software is meant to be used also by those who are less familiar with mathematical modeling and has been distributed to the staff of the Prevention and Protection in Workplaces Service of the University Hospital of Trieste for their evaluations and it is continuously updated.

1.1. Code availability

The source code in Python is available on GitHub: [https://github.com/](https://github.com/benedettasantoro22/covid-19-evaluation-tool) [benedettasantoro22/covid-19-evaluation-tool](https://github.com/benedettasantoro22/covid-19-evaluation-tool).

2. Methods

2.1. The mathematical model

2.1.1. The probabilistic model for infection probability

As mentioned in the Introduction, we started to build our model from that proposed by Riley.[12](#page-14-1) The starting point is assuming that the air inside the room is mixed due to air drafts and ventilation (mixing hypothesis), then viruses emitted by the infectors uniformly distribute in the room in a time shorter than any other characteristic times of the system; it means that distribution time is shorter than the viral natural decay time in air and any other decay due to removal mechanisms (see below). From that, the probability that one susceptible subject is infected does not depend on the distance from the infectors since each individual might inhale the same quantity of contaminated air.

In the original model, the room is treated like a box of a certain volume (V) occupied by a number I of infectors and S of susceptible individuals; viral copies are removed from the room air due to ventilation. We added other elements that contribute to remove the virus from the environment: the effect of relative humidity (RH) , 15 15 15 which influences the stability of the droplets in the air, the presence of HEPA (High Efficiency Particulate Air) filters in the ventilation system, 16 the effectiveness of ultraviolet radiation to destroy the viral RNA.^{[17](#page-14-6)} We called λ_{vent} , λ_{RH} , λ_{HEPA} , and λ_{UV} the decay constants (in units h⁻¹) associated to each removal mechanism; see Section [2.2.2](#page-4-0) and Table [A1](#page-8-0) for details. Moreover, we considered that masks contribute to reduce the number of viral copies emitted by infectors of a factor $(1 - \alpha)$, where α is the outward protection efficiency of the mask and, analogously, reduce the number of viruses inhaled by susceptible occupants by a factor $(1 - \beta)$, where β is the inward protection efficiency. In a perfectly filtering mask $\alpha = \beta = 1$ (100% efficiency), while the constants vanish if the occupants do not wear masks.

At last, we called r (quanta/h) and p (m^3/h) the quanta of virus^{[12](#page-14-1)} emitted per unit time and the pulmonary ventilation of an adult.^{[18](#page-14-7)} respectively. The r parameter varies according to the activity and the contagiousness of the infector, see Section [2.2.4](#page-5-0) and Table [A2](#page-10-0) in the Appendix for further details.

Then the mean number of infections I occurring in a room occupied, continuously, by the subjects for a time t , is given by:

$$
\bar{I} = (1 - \alpha) (1 - \beta) IS \frac{rp}{\sum_{i} \lambda_i V} t \tag{1}
$$

where $i = \{vent, HEPA, RH, UV\}$ and $(1 - \alpha)r$ is the fraction of viruses that passes through the mask of the infectors per unit time and $(1 - \beta)$ p is the fraction of contaminated air inhaled by the exposed individuals. Furthermore, we assumed that infectors continuously emit droplets while in the room.

By assuming a Poissonian statistics, the probability of no infection and of at least one infection are, respectively:

$$
P(\text{no infection}) = e^{-\bar{I}}
$$
 $P(\text{at least one infection}) = 1 - e^{-\bar{I}}$ (2)

2.1.2. The viral concentration

The viral concentration in the room can be calculated by considering two contributions: a positive term due to the emission of viral copies by infectors and a negative one given by both reducing factors and inhalation from susceptible occupants. This is formalized into the following differential equation:

$$
\frac{dC}{dt}\left(t\right) = \left(1 - \alpha\right)\frac{rI}{V} - \sum_{i} \left(\lambda_i + \frac{\left(1 - \beta\right)p}{V}\right)C\tag{3}
$$

where C [quanta/m³] is the viral concentration, while the other parameters are the same reported previously. The contribution p/V can be omitted since, in standard conditions, we have $V \gg p$.

The equation above has then the solution:

$$
C(t) = C_0 \exp\left(-\sum_{i} \lambda_i t\right) + (1 - \alpha) \frac{rI}{\sum_{i} \lambda_i V} \left(1 - \exp\left(-\sum_{i} \lambda_i t\right)\right) \tag{4}
$$

where C_0 is the initial concentration of viruses in the room.

In the Figure [1,](#page-4-1) two possible profiles for the viral concentration are shown, one for $C_0 = 0$ and one for $C_0 \neq 0$. The value of the concentration saturates when the positive and negative contributions are the same; then the saturation concentration C_{sat} is the value that corresponds to a vanishing derivative:

$$
C_{sat} = (1 - \alpha) \frac{rI}{\sum_{i} \lambda_i V} \tag{5}
$$

In the tool, C_0 has been set to zero by default, and it corresponds to the initial occupation of the room. This choice does not affect the evaluation of the infection probability in a stationary condition, which depends on C_{sat} only. Indeed, from Equation [1](#page-2-0) the mean number of infections is: $\overline{I} = (1 - \beta)SpC_{sat}t$.

From the Equation [4](#page-3-0) it is also possible to estimate the minimum waiting time before entering a room after the infectors left, with minimum risk; indeed, by considering $r = 0$ and a concentration of 1% with respect to the concentration of the occupied room as the optimal one, the minimum time t_{min} is given by:

$$
t_{min} = -\frac{\ln(0.01)}{\sum_{i} \lambda_i} \tag{6}
$$

2.2. The Software Tool

The model described in the previous section has been implemented in a Graphical User Interface (GUI) written in programming language Python; the source file has been compiled to obtain a standalone executable file compatible with Windows machines. The software is characterized by different tabs which guide the user from the input of the initial parameters to the final evaluation of the infection probability; it is possible to navigate through windows or with the menu on the top left part of the screen or with the buttons.

Fig. 1. Plot of the viral concentration profile for a 100 m^3 room with 5 infectors, 40% RH and 2 air exchanges/hour ventilation; the solid line refers to an initial concentration of 0.05 quanta/ $m³$, while the dashed one to 0 quanta/ m^3 .

2.2.1. User's information

The first window after the homepage records the user's information. It is possible to insert the user identification (name and surname), the name of the Structure, the Department, and the Room number/name where the infection occurred, or it is likely to occur. It is not mandatory to fill this part, because calculations can be performed regardless, but since the tool is meant to be used in the clinical practice, it is still good practice to track all the actions done. For this reason, information provided in this tab is used to fill a logbook file (see Section [2.2.6\)](#page-6-0).

2.2.2. Room parameters

To continue with the evaluation, it is necessary to input the details of the room: surface and height, ventilation, relative humidity, the permanence time and indicate if the room is equipped with HEPA filters. In our case, we derived surface and height of the room we wanted to analyze from the planimetry provided by the Prevention and Protection Department (PPD) as well as the mechanical ventilation (λ_{vent}) . It is possible to choose between three levels of relative humidity (21%, 40% or 70%) from a drop-out menu, each of them associated with a λ_{RH} , while the tool automatically sets a mean solar intensity and the corresponding λ_{UV} . See Table [A1](#page-8-0) in the Appendix for the numerical values of λ_{RH} and λ_{UV} .

The software considers that both infectors and susceptible individuals enter the room at the same time, then the permanence time is the same for I and S .

At last, it is possible to indicate if the room is equipped with HEPA filters by selecting the checkbox on the bottom of the window. If it is checked, λ_{HEPA} is set to 99.97% of λ_{vent} , where this percentage corresponds to the efficiency of the filters, as reported in Ref. [16,](#page-14-5) otherwise is null.

2.2.3. Occupants

In the following tab, the user inputs the number of infectors and susceptible individuals, category of susceptible occupants and the type of the masks worn. It is possible to select between different categories; we decided to insert some groups of healthcare workers, as required by PPD experts, but this information is useful just for descriptive reasons and does not influence the evaluation, but it might contribute to modify the permanence time (e.g., assistant nurses spent more time with the patients than nurses).

To simplify the model, infectors and exposed subject are supposed to wear the same personal protection equipment (PPE), respectively. The checkbox must be selected to allow the software to enter the information about masks effectiveness. We considered two types of personal protection equipment: surgical masks and FFP2 respirators; for the inward and outward efficiency we selected the lowest values indicated in Ref. [19](#page-14-8) and reported them in Table [A1.](#page-8-0)

The number of susceptible individuals can be omitted (see below).

2.2.4. Occupants' activities

In the same window, the occupants' activities are selected; users are guided in this choice; indeed they can open a pop-up window, by pressing the button with the question mark, which shows a table, re-adjusted by Ref. [20](#page-14-9) with three breathing activities (breathing, coughing and speaking loudly), four intensities (at rest, low, medium, heavy) and three levels of contagiousness of the infectors (low, medium, high). To guide the user's choice, we decided to group the values of r in this table in three categories, each associated with a color code, for increasing risk: yellow for r less than or equal to 300 quanta/h, orange for r between 300 and 600 quanta/h and red for r greater than 600 quanta/h. The activity and the shedders' contagiousness can be selected from the two drop-out menus in the software tab. The numerical values for r are collected in Table [A2](#page-10-0) in the Appendix.

2.2.5. Results

The last window is dedicated to the evaluation results. A canvas can be filled with the profile of the viral concentration, calculated through Equation [4;](#page-3-0) the plot can be erased by clicking on the "RESET" button. Concentration plot can be exported to image, or in any preferred file format, by right-clicking on the canvas and selecting the "Export" entrance from the menu. If the canvas is not cleared and some parameters are changed in the previous windows, the new viral concentration will be shown in the same canvas and axes automatically re-scaled.

The "SAVE" button allows the user to save the evaluation results, referred to the last parameters inserted, in a text file. This file contains a summary of the user's information and parameters with the calculations performed according to the equations reported in previous sections for the infection probability, the viral concen-

tration in the room and the saturation concentration. Moreover, the software discloses some suggestions to keep the diffusion under acceptable levels: if the product $S \cdot P$ (at least one infection), is greater than the original number of infectors, the tool will calculate the minimum ventilation and the maximum resident time, by fixing all other parameters:

$$
\begin{cases}\n\lambda_{vent}^{min} = \frac{b \ S \ t}{\ln\left(\frac{S}{S-1}\right)} - (\lambda_{RH} + \lambda_{HEPA} + \lambda_{UV}) \\
t_{max} = \frac{\sum_{i} \lambda_{i}}{b \ S} \ln\left(\frac{S}{S-1}\right) \\
b = (1-\alpha)(1-\beta) I\frac{rp}{V}\n\end{cases}
$$
\n(7)

As mentioned in the Section [2.2.3,](#page-5-1) if the number of susceptible individuals is omitted, the software computes the maximum number of people allowed to keep the infection probability below 10%:

$$
S_{max} = -\ln(0.9) \frac{\sum_{i} \lambda_i}{bt} \tag{8}
$$

 S_{max} is automatically computed by the tool if the probability is higher than 10%.

2.2.6. Additional output files

Along with the evaluation file, the tool produces a logbook file, like that shown in Figure [2,](#page-6-1) and a folder with the profiles of the probability for at least one infection, like those described in the following sections.

l loabook - Blocco note di Windows.
File Modifica Formato Visualizza ?
The GUI version is that of 21/10/2022, quanta emission rates are collected in: https://doi.org/10.1177/1420326X211039544
27/10/2022 16:21:52--Santoro: Hospital of Trieste -- Room 19 C:/Users/bened/ROOT/DOTTORATO/APP/APP-ENG/dist/evaluation.txt
The GUI version is that of 21/10/2022, quanta emission rates are collected in: https://doi.org/10.1177/1420326X211039544 27/10/2022 16:22:58--Larese: Hospital of Trieste -- Meeting room C:/Users/bened/ROOT/DOTTORATO/APP/APP-ENG/dist/evaluation.txt
The GUI version is that of 21/10/2022, quanta emission rates are collected in: https://doi.org/10.1177/1420326X211039544
23/11/2022 16:13:33--Milotti: Hospital of Trieste -- Emergency Unit C:/Users/bened/ROOT/DOTTORATO/APP/APP-ENG/dist/ARTICOLO/ventilation.txt
The GUI version is that of 21/10/2022, quanta emission rates are collected in: https://doi.org/10.1177/1420326X211039544
23/11/2022 16:13:43--Santoro: Hospital of Trieste -- Emergency Unit C:/Users/bened/ROOT/DOTTORATO/APP/APP-ENG/dist/ARTICOLO/ventilation.txt
The GUI version is that of 21/10/2022, quanta emission rates are collected in: https://doi.org/10.1177/1420326X211039544
23/11/2022 16:13:54--Larese: Hospital of Trieste -- Emergency Unit C:/Users/bened/ROOT/DOTTORATO/APP/APP-ENG/dist/ARTICOLO/ventilation.txt
The GUI version is that of 21/10/2022, quanta emission rates are collected in: https://doi.org/10.1177/1420326X211039544
24/11/2022 15:05:24--Milotti: Hospital of Trieste -- Emergency Unit C:/Users/bened/ROOT/DOTTORATO/APP/APP-ENG/dist/evaluation.txt
The GUI version is that of 21/10/2022, quanta emission rates are collected in: https://doi.org/10.1177/1420326X211039544
24/11/2022 15:05:38--Santoro: Hospital of Trieste -- Emergency Unit C:/Users/bened/ROOT/DOTTORATO/APP/APP-ENG/dist/ARTICOLO/mask.txt
The GUI version is that of 21/10/2022, quanta emission rates are collected in: https://doi.org/10.1177/1420326X211039544
24/11/2022 15:08:50--Larese: Hospital of Trieste -- Emergency Unit C:/Users/bened/ROOT/DOTTORATO/APP/APP-ENG/dist/ARTICOLO/mask.txt
The GUI version is that of 21/10/2022, quanta emission rates are collected in: https://doi.org/10.1177/1420326X211039544
24/11/2022 15:44:20--Milotti: Hospital of Trieste -- Emergency Unit C:/Users/bened/ROOT/DOTTORATO/APP/APP-ENG/dist/ARTICOLO/mask.txt

Fig. 2. An example of logbook file produced by the software: each entry contains the GUI version, the reference for the quanta emission rates, user's surname and the location of the infection event and the path for the evaluation file.

3. Results

In this section, we will show some results of the calculations we performed with the software to highlight the effect of the passive mechanisms to contain the spread of the disease.

We set the infection event in a generic room with volume $V = 89.70 \,\mathrm{m}^3$ with a mean ventilation of 3 air exchanges per hour. The volume has been obtained by averaging the volumes of the rooms of the Emergency Medicine Unit at the Hospital of Trieste, while the value of the mechanical ventilation has been provided by the PPD.

3.1. The Effect of Ventilation

We analyzed the effect of ventilation in reducing the infection probability. We considered a medium shedder patient, heavily coughing, sharing the room for 2 h with other two patients, see Table [A2](#page-10-0) for the value of r in this situation.

Then we obtained three concentration profiles by setting λ_{vent} to 3, 4.5 and 6 air exc./h, respectively. Figure [3](#page-7-0) shows that with a higher ventilation, we obtain a lower final concentration. The same conclusion can be deduced from the infection probability profiles in Figure [4.](#page-8-1)

In Table [1](#page-8-0) we collected the results for the three analyzed scenarios: the infection probability diminishes for higher ventilation because C_{sat} decreases (Equation [5](#page-3-1)) for the expression); moreover, the minimum waiting time t_{min} (Equation [6](#page-3-2) and Table [1\)](#page-8-0) is reduced. We decided to report the maximum viral concentration C_{max} that is reached in the room instead of C_{sat} , even though they slightly differ from each other. The tool calculated $S_{max} = 1$ for all the simulated scenarios.

Fig. 3. Plot of the viral concentration in the room for three different ventilation: the upper, middle and lower curves refer to 3, 4.5 and 6 air exchanges/h, respectively.

Table 1. Results of the simulations for three different values of the room ventilation.

λ_{vent} $\left[\arctan \frac{\pi x}{\pi} \right]$	P (no infection) [%]	$P(\text{at least one infection})$ [%]	C_{max} [quanta/m ³]	t_{min} [h]	\mathfrak{D}_{max}
	66.20	33.80	0.21	0.40	
4.5	69.70	30.30	0.19	0.40	
	72.60	27.40	0.17	0.30	

Fig. 4. Infection probability profile for: a) $\lambda_{vent} = 3$ air exchanges per hour; b) $\lambda_{vent} = 4.5$ air exchanges per hour; c) $\lambda_{vent} = 6$ air exchanges per hour.

3.2. The Effect of Mask Wearing

We repeated the simulation with the same room described at the beginning of Section [3](#page-7-1) and we tested the effect of the mask wearing in reducing the infection probability.

In our scenarios, there were one infected patient and two susceptible healthcare

workers performing an aerosol generating procedures (AGP) for a permanence time of half an hour.

In the three scenarios, exposed individuals wear: no mask, a surgical and a FFP2 mask, respectively; the viral concentration profile is sketched in Figure [5.](#page-9-0)

Studies show that AGP, like intubation and tracheotomy, which were performed during the pandemic on positive tested patients, are not associated with an increased risk of transmission.[21](#page-14-10) Nevertheless, we decided to select the heaviest activity, the highest level and the maximum contagiousness of the infector for these simulations (r corresponds to the value in the last table enter in Table [A1\)](#page-8-0), in order to obtain a more conservative evaluation, knowing that the results are just an upper limit.

From results reported in Table [2](#page-10-0) and the infection probability plots in Figure [6,](#page-10-1) it is possible to assess that the infection probability for susceptible individuals is reduced as well as the minimum ventilation while the maximum resident time increased, according to changes in the mask wearing (no mask, surgical, FFP2).

Then the tool estimated $S_{max} = 1$ for the last scenario we analyzed and zero for the others.

The value of t_{min} is equal to 0.4 h as in the first row of Table [1](#page-8-0) because it only depends on the values of the removal factors (Equation [6\)](#page-3-2) that we kept constant in these simulations.

The values of t_{max} and λ_{vent}^{min} for the last scenario are not reported, because $S \cdot P$ is less than the original number of infectors.

Fig. 5. Plot of the viral concentration in the room with an infectious patient and two healthcare workers during an AGP.

Table 2. Results of the simulations we performed by varying mask type for susceptible individuals.

mask	P (no infection) 1%]	$P(\text{at least one infection})$ 1%]	C_{max} [quanta/m ³]	t_{max} ſhl	λ_{vent}^{min} $\left[\arctan\exp\left(\frac{h}{h}\right)\right]$
no	22.90	77.10	3.04	0.2	15
surgical	47.10	52.90	3.04	0.5	
FFP2	86.30	13.70	3.04		

Fig. 6. Infection probability profiles for the three reported scenarios in the main text: a) susceptible healthcare workers do not wear masks during the AGP; b)-c) the susceptible individuals wear surgical masks and FFP2 respirators, respectively.

4. Discussion and Conclusions

Our study aimed to determine a risk prediction model for SARS-CoV-2; the proposed model can be applied to every pathogen with the same transmission route by re-scaling the parameters according to the disease considered.

Compared to Wells-Riley model, we added the shielding effect of personal protection equipment (different for every type of adopted mask) by introducing the factors α and β , we used the values of infection quanta specific for COVID-19 and introduced three decay constants for relative humidity, HEPA filtering effectiveness and solar illumination.

Since results of studies about the effects of vaccination in reducing the probability of transmission are still controversial, $22,23$ $22,23$ $22,23$ we decided to neglect this contribution in our model for a more conservative evaluation.

The model has been implemented in a user-friendly tool for the calculation. Simulations showed that higher ventilation and masks might reduce significantly the infection probability for exposed subjects; the value of λ^{min}_{vent} provided by the software could be useful to estimate the correct forced ventilation in potentially dangerous Hospital Department or in quarantine rooms; furthermore, t_{max} and S_{max} might be used to optimize the exposure time of healthcare staff dealing with infected patients in order to reduce the risk of their contamination and the chance to spread the virus among healthy patients and workers.

Moreover, it can be useful to evaluate mitigation procedures in other setting like classrooms and offices.

Our work has some assumptions that we plan to make less stringent in the future: it is based on a stationary model based on the mixing hypothesis, the values of the parameters refer to the first variant of the virus, then some evaluation might be over (under)-estimated.

Author Contributions

Conceptualization, Larese, Milotti; Methodology, Milotti; Software, Santoro, Writing - original draft, Santoro, Writing - review & editing, Larese, Milotti, Santoro.

Ethical Compliance

Not applicable

Conflicts of Interest

There are no conflicts to declare.

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Appendix

Tables

In Table [A1,](#page-8-0) we collect the values, descriptions, symbols, and bibliographic references of the parameters used for the calculations performed with the software tool.

In Table [A2,](#page-10-0) we report the possible values of the quanta emission rate (r) for three activities, four activity levels and three level of contagiousness of the infector(s); the table is re-adjusted from Ref. [20.](#page-14-9)

For the table with the color code we mentioned in the Section [2.2.4,](#page-5-0) see the documentation of the GUI available on GitHub at the following link: [https://github.com/benedettasantoro22/covid-19-evaluation-tool/](https://github.com/benedettasantoro22/covid-19-evaluation-tool/blob/main/code/INSTRUCTIONS.md) [blob/main/code/INSTRUCTIONS.md](https://github.com/benedettasantoro22/covid-19-evaluation-tool/blob/main/code/INSTRUCTIONS.md).

Table A1. Summary of all the parameters used in the text, their symbols, values and the corresponding references to current literature.

Table A2. Values of the quanta emission rate (in quanta/hour) for different activities and activity levels.

List of acronyms

We report a list of the acronyms we used in the main text:

- RH Relative Humidity;
- HEPA High Efficiency Particulate Air filters;
- UV Ultraviolet radiation;
- GUI Graphical User Interface;
- **PPD** Prevention and Protection Department;
- **PPE** Personal Protection Equipment;
- AGP Aerosol Generating Procedures.

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