REHVA
Federation of European Heating, Ventilation and Air Conditioning Associations

REHVA COVID-19 Multi-room and Recirculation Calculator – Technical Manual

A tool for HVAC systems operational strategy assessment for reducing infection risk in existing and newly designed buildings

Introduction

COVID-19 pandemic is today an unresolved medical problem and any possible measure that may lower SARS-CoV2 virus propagation has to be applied. While the medical research area is still gaining knowledge on its transmission and the severity of illness it causes, there is not unanimous consensus on the airborne infection route. Starting from this today, even more recognised possibility, the engineering research area is working to produce guidelines focusing on how to reopen and safely use buildings after the lockdown, providing advice on specific components, buildings/space types, and suggesting mitigation measures [1].

If airborne viral emission and diffusion are assumed to be important, there are several design and operational measures that can be undertaken for reducing the airborne infection risk in closed spaces as buildings:

- ventilation rates should be increased as much as compatible with comfort and energy issue;
- indoor air and extracted air should not be recirculated;
- individuals should avoid staying directly in the flow of air from another person;
- the number of people sharing the same indoor environment should be minimised, and last resort,
- people working/studying/etc. in a common space should correctly wear protective facial masks.

Effects on virus spread of all these measures are not easily quantifiable, but for some of them some simple modelling can help to understand their relative effectiveness. For this reason, a simplified tool has been developed to assess comparatively effectiveness and potential application of such of actions on both existing and new building and HVAC systems.

Tool background

The tool is based on the standard airborne disease transmission Wells-Riley model, i.e. quanta based and full mix hypothesis behind, described in [2] and [3]. It extends the single room model to a Multi-rooms Model with possible air recirculation among rooms, through centralised HVAC system and via air transfer to common service area (corridor, toilettes and staircases) where air extraction to outside is performed via dedicated exhaust air ductwork. The model is a dynamic model, i.e. the time dependent problem is solved.

It is possible to partially remove the full-mix hypothesis using the ventilation Contaminant Removal Effectiveness, ϵ_r, which depends on the chosen air distribution system. In the tool it is possible to modify the recirculation ratio from 1 to 0 and eventually to add an HEPA filter or equivalent virus removal/inactivation equipment (UV-C, etc.) on the return air lo lower as much as possible the virus spread via air recirculation. The model also accounts for "virus losses" in the HVAC system (deposition in ducts, in AHU and natural decay when contaminated air moves through such components), using the same approached used for rooms but in steady state approximation, i.e. using virus removal coefficients as done for general spaces.

Splitting the ductwork in supply and return branches, which can have significant different virus concentrations, and using a volume weighting factor to account for the different pathways different virus concentrations have to go through before to reach the AHU or to reach each served spaces, under Quasi Steady State Hypothesis the **concentration balance equation on the return ductwork** can be rewritten for each branch i as:

$$C_{ETA,i}(t) = C_i(t) - \lambda_{Rd,d,i} \cdot \frac{V_{V;Rd,i}}{q_{V;ETA,i}} \cdot C_{avg;i}(t) \tag{1}$$

where

$C_{ETA,i}$ is virus concentration in extracted air at the end of specific ductwork branch from Room i to AHU, in [quanta/m^3];

$C_{avg;i}$ is average virus concentration in this ductwork branch air volume, [quanta/m^3];

$\lambda_{Rd,d,i}$ duct virus removal coefficient for ductwork serving Room i, [h^{-1}];

$V_{Rd,i}$ volume of return ductwork serving Room i, in [m^3];

$q_{V;ETA,i}$ extracted volume air flow from Room i, in [m^3/h].

with

$$\lambda_{Rd,d,i} = \lambda_{R,d,i} + \kappa_{R,i} + \lambda_{R,ad,i} \tag{2}$$

$\lambda_{R,d,i}$ virus removal coefficient by deposition on surfaces of ductwork serving Room i, [h^{-1}];

$\kappa_{R,i}$ virus decay coefficient of ductwork serving Room i, [h^{-1}];

$\lambda_{R,ad,i}$ virus removal coefficient by additional measurements of ductwork serving Room i, [h^{-1}];

Assuming linear approximation

$$C_{avg;i}(t) \cong \frac{C_{ETA,i}(t) + C_i(t)}{2} \quad ; \quad \alpha_{R,i} = \frac{V_{Rd,i}}{q_{V;ETA,i}} \tag{3}$$

it is

$$C_{ETA,i}(t) = \left(\frac{1 - 0.5\,\lambda_{Rd,d,i} \cdot \alpha_{R,i}}{1 + 0.5\,\lambda_{Rd,d,i} \cdot \alpha_{R,i}}\right) \cdot C_i(t) = \beta_{R,i} \cdot C_i(t) \tag{4}$$

with

$\alpha_{R,i}$ dimensional removal factor for return branch i, in [h];

$\beta_{R,i}$ dimensionless removal factor for return branch i, [-] defined as $\beta_{R,i} = \frac{1-0.5\,\lambda_{Rd,d,i}\cdot\alpha_{R,i}}{1+0.5\,\lambda_{Rd,d,i}\cdot\alpha_{R,i}}$.

Air Handling Unit is modeled using same approach after mass conservation balance is applied to the system described by figure 1, where an air dumper is controlling the recirculation ratio (RF).

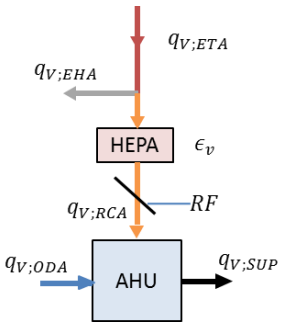

Figure 1 Recirculation managed by AHU with removal/deactivation device on the return duct after exhaust air expulsion.

The input to the removal/deactivation device, identified as HEPA filter in figure 1, is the weighted virus concentration in the extracted ait from each room as

$$C_{ETA}(t) = \sum_{i=1}^{N} C_{ETA,i}(t) \cdot \frac{q_{V;ETA,i}}{q_{V;ETA}} = \sum_{i=1}^{N} \beta_{R,i} \cdot C_i(t) \cdot \frac{q_{V;ETA,i}}{q_{V;ETA}} \quad (5)$$

Thus, the recirculated air virus concentration before mixing with outdoor ventilation air is:

$$C_{RCA}(t) = (1 - \epsilon_v) \cdot C_{ETA}(t) \quad (6)$$

where ϵ_v is the removal/deactivation device efficiency, [-], and the supply air virus concentration is given by:

$$C_{UTA-in}(t) = C_{ODA}(t) \cdot (1 - RF) + C_{RCA}(t) \cdot RF \quad (7)$$

where

$C_{ODA}(t)$ virus concentration in outdoor air, in [q/m^3], usually null;

$RF = q_{V;RCA}/q_{V;SUP}$ UTA recirculation factor, in [-];

Thus, under Quasi Steady State Hypothesis, the virus concentration balance over the AHU as black box is written as for the ductworks as:

$$C_{SUP}(t) = \left(\frac{1 - 0.5\,\lambda_{UTA} \cdot \alpha_{UTA}}{1 + 0.5\,\lambda_{UTA} \cdot \alpha_{UTA}}\right) C_{UTA-in}(t) = \beta_{UTA} \cdot C_{UTA-in}(t) \quad (8)$$

where coefficients λ_{UTA}, $\alpha_{UTA}$and β_{UTA} have the same meaning as expressed before for the return ducts.

Under Quasi Steady State Hypothesis the concentration delivered by each supply ductwork branch i can be written as for the return ductwork as:

$$C_{SUP,i}(t) = \left(\frac{1 - 0.5\,\lambda_{Sd,d,i} \cdot \alpha_{S,i}}{1 + 0.5\,\lambda_{Sd,d,i} \cdot \alpha_{S,i}}\right) \cdot C_{SUP}(t) = \beta_{S,i} \cdot C_{SUP}(t) \quad (9)$$

where

$\lambda_{Sd,d,i}$ duct virus removal coefficient for ductwork supplying Room i, [h^{-1}];

Combining equation from (1) to (8), assuming null the virus concentration in the outdoor air, the virus concentration in the supply air to each room can be written as function of the virus concentration in each room:

$$C_{SUP,i}(t) = \beta_{S,i} \cdot \beta_{UTA} \cdot RF \cdot (1 - \epsilon_v) \cdot \sum_{k=1}^{N} \beta_{R,k} \cdot C_k(t) \cdot \frac{q_{V;ETA,k}}{q_{V;ETA}} \quad (10)$$

where the dimensionless virus removal factors $\beta_{S,i}$, β_{UTA} and $\beta_{R,k}$ account for virus removal due to deposition and decay in the ductworks and AHU, while ϵ_v is the efficiency of the virus removal/inactivation unit.

For the **generic Room i, the concentration balance in full mix hypothesis** is:

$$\frac{dC_i(t)}{dt} = \dot{C}_{s,i}(t) + \gamma_i C_{SUP,i}(t) - \lambda_i C_i(t) \quad (11)$$

where

$\dot{C}_{s,i}$ virus concentration source in Room i, in [q/(h m^3)],

γ_i virus supply coefficient in Room i due to recirculation, [h^{-1}].

λ_i virus total removal coefficient in Room i, [h^{-1}].

To account for specific flow pattern due to air distribution system typology and thus partially remove the full mix hypothesis, the virus supply coefficient γ_i is defined as:

$$\gamma_i = q_{V;SUP,i} \cdot \epsilon_{r,i} / V_i \quad (12)$$

where

$q_{V;SUP,i}$ supply air volume flow rate to Room i, in [m^3/h];

$\epsilon_{r,i}$ ventilation Contaminant Removal Effectiveness Room i, (=1 for full mix), [-];

V_i volume of Room i, in [m^3].

To account for facial mask effect on virus spread by the infected person, the virus concentration source is defined as

$$\dot{C}_{s,i} = \left(1 - \epsilon_{IPFM,i}\right) \cdot IP_i \cdot e_i / V_i \quad (13)$$

where

e_i virus emission rate per person in Room i, in [q/(h pers)];

IP_i number of infected people in Room i, in [pers]

$\epsilon_{IPFM,i}$ facial mask efficiency for infected person in Room i, $[-]$.

Instead, the effect of facial masks worn by susceptible people is taken into account when calculating the infection risk probability using the Wells-Riley model, i.e.:

$$R\%_i = \left(1 - e^{-(1-\epsilon_{SPFM,i})\cdot IR_i \cdot t_{ex,i} \cdot C_{avg,i}}\right) \cdot 100 \tag{14}$$

where

$\epsilon_{SPFM,i}$ facial mask efficiency for susceptible people in Room i, $[-]$;

IR_i present people breathing rate in Room, in [m^3/h];

$t_{ex,i}$ exposure time (given space occupancy time interval) in Room, in [h]

$C_{avg,i}$ average virus concentration in the given space over the occupancy time interval, in [q/m^3].

The average number of potentially infected people is then given in each room by

$$NIP_i = \frac{R\%_i}{100}(NP_i - IP_i) \tag{14}$$

where

NP_i number of people in Room i, [pers];

IP_i number of infected people in Room i, in [pers].

Combining equation (10) with equation (11) it is possible to write for each room $\boldsymbol{i}$ an ordinary differential equation like

$$\frac{dC_i(t)}{dt} = \sum_{j=1}^{N-1} a_{i,j} \cdot C_j(t) + a_{i,i} \cdot C_i(t) + s_i(t) \tag{15}$$

which can be approximated by an algebraic equation substituting the time derivative with a forward finite difference obtaining

$$C_i^{\tau+1} = \left(1 + \Delta t \cdot a_{i,i}\right) \cdot C_i^{\tau} + \sum_{j=1}^{N-1} \Delta t \cdot a_{i,j} \cdot C_j^{\tau} + \Delta t \cdot s_i^{\tau} \tag{16}$$

where

Δt is the discretization time interval, in [h];

$a_{i,j}$ coupling coefficients, in [h^{-1}];

s_i^{τ} virus source term, in [q/(h m^3)];

τ integer time index ($t = \tau \cdot \Delta t$), [-].

Equation (16) represents a set of N equations that can be easily solved using matrix notation as

$$\{C_i\}^{\tau+1} = \left[b_{i,j}\right] \cdot \{C_i\}^{\tau} + \{\Delta t\, s_i\}^{\tau} \tag{17}$$

where

$$\begin{aligned} b_{i,i} &= 1 + \Delta t \cdot a_{i,i} \\ b_{i,j} &= \Delta t \cdot a_{i,j} \quad \forall\, i \neq j \end{aligned} \tag{18}$$

NOTE: to have a fast-to-solve problem fixed air flow rates over the whole calculation day are assumed; this assumption implicates constant coefficient for the matrix equation (17), but does not change the model structure, which can account for variable flows calculation (if air flow time schedule are provided as input) just updating the matrix coefficient each time step.

System layout and limitations

To have a relatively easy and fast to use tool some limitation have been applied such as:

- constant ventilation air flow rate during the whole day;
- fixed building plan layout typology to allow fast data input and calculations (see Figure 2 System layoutFigure 2);
- rooms number is unlimited (memory space is just sized to manage 100 rooms, but can be expanded according to the available computer memory), while there is only one corridor, one toilette room and one staircase compartment;
- extraction-only systems are possible in toilets and staircase only;
- transferred air through the corridor is automatically calculated, if any exists due to extraction in toilets and/or in staircase compartments;
- virus source (infected person) can be placed in any place and can be more than one, each with its specific virus strength.

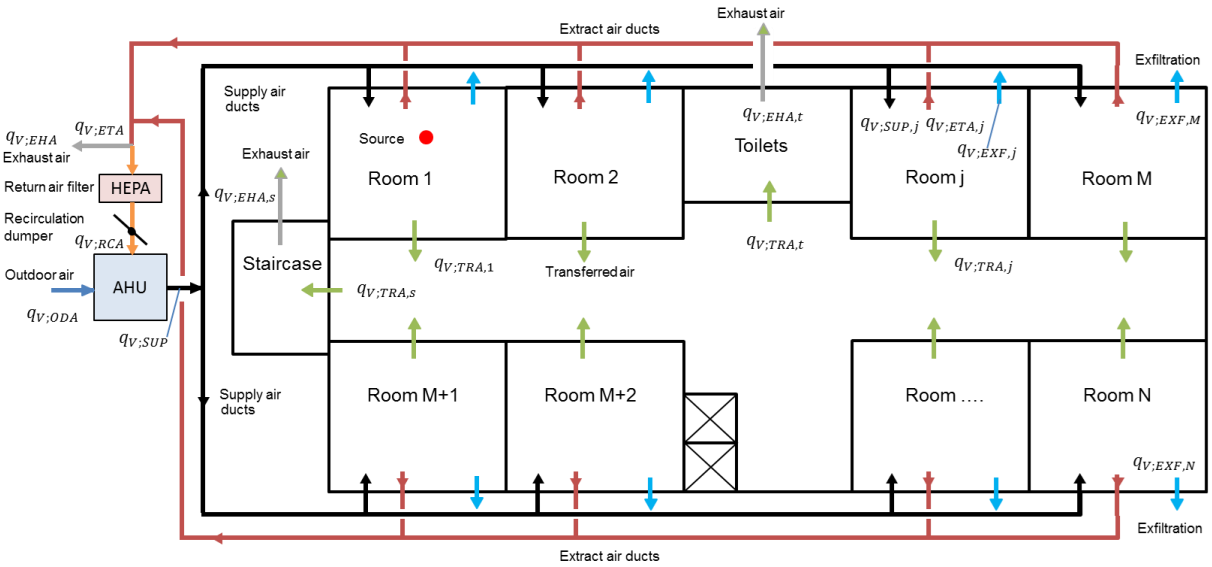

Figure 2 System layout

The basic assumption to use the tool is that all supply and extracted air flow rate to/from each room are known and the extracted flow rate is provided as a fraction of the supply one. These parameters are usually provided in the system design masterplan.

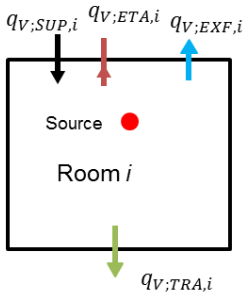

Figure 3 Air mass balance in Room i

To avoid to solve an air flow network, a simplified approach is then used to calculate transferred air flows, which are allowed only between rooms and corridor, and corridor to toilets and/or staircase if any exhaust air extraction is in place there. The basic assumption is that any room is always in pressurized state, i.e. only exfiltration and transferred air flows are allowed (Figure 3). An air mass balance on the whole system is then performed to calculate transferred air flows assuring air mass conservation consistency.

Input checks are employed as well as mass balance check to avoid that some inconsistent input is producing inconsistent result.

An occupancy schedule can be specified only with to time slots inside the building operational time in a day (the tool calculates for one day only), but it can be different in any room.

Tool output

As result of the tool calculation the following data are available in the main sheet of the Excel workbook ("Multi-cal" tab):

- average virus concentration in each room, corridor, toilettes and staircase, over the working day, in quanta/m^3;
- individual infection risk over the day in each of those spaces calculated with the Wells-Riley model, in [%];
- average number of potentially infected people in each room, corridor, toilettes and staircase, over the working day;
- virus air to surface deposition over the day in each space, on AHU surfaces, on HEPA or equivalent virus removal/inactivation equipment (V-C, etc.), on supply and return ductworks, in quanta.

The virus concentration time evolution in each space is reported (using a printout time interval, which can be greater than the integration time interval) in a second sheet called "Concentrations", while air to surface virus deposition time history is available in a third sheet called "Depositions".

In the main sheet diagrams, see Figure 4, are available for:

- virus concentration time history in each space;
- virus air to surface deposition time history in each space;
- individual infection risk in each space histogram;
- average number of potentially infected people in each room histogram.

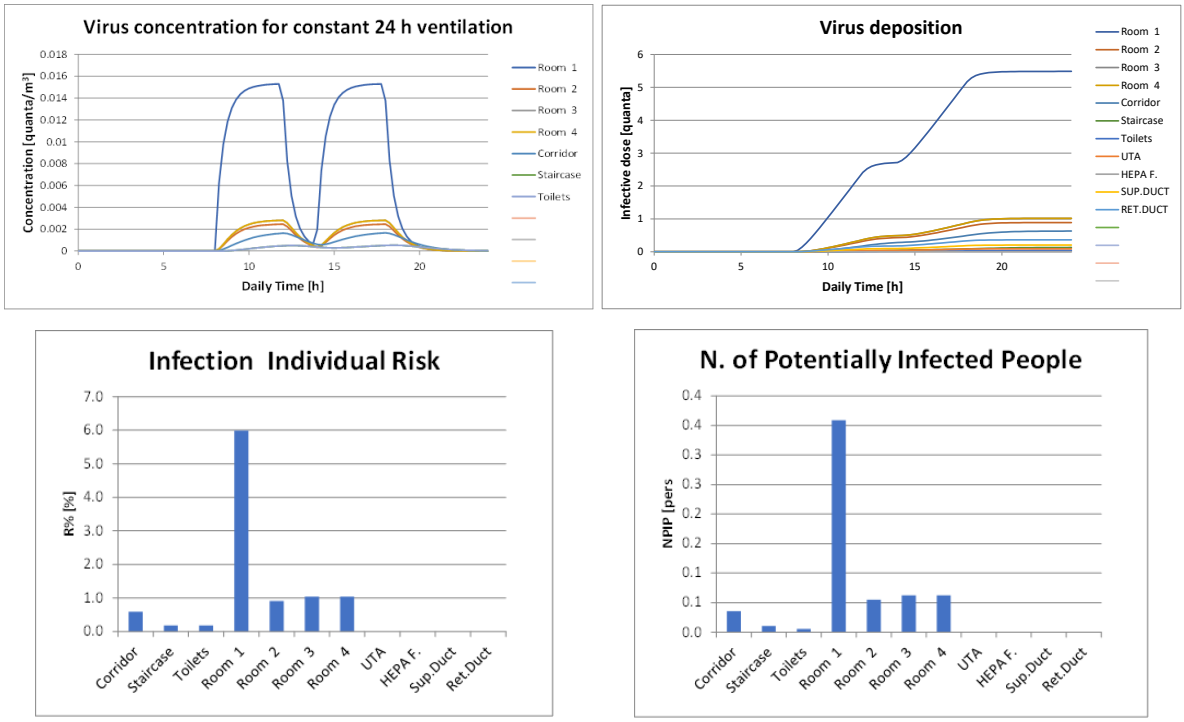

Figure 4 Tool graphic output.

Use, Limitations and Uncertainties

The tool was developed with the Sars-CoV-2 virus in mind and the underlying estimates for source strengths (quanta values) are based on studies that solely examined the 2019 version of the virus and not any latest, more contagious SARS-CoV-2 variants (i.e. in the UK, South-Africa, Brazil etc.). Therefore, any subsequent research on the topic has not been considered for its development and update. Its application and calculation results should be interpreted considering this limitation.

Currently, the tool is using the infection risk probability function from Wells-Riley model to assess the infection risk, but it is physically based (i.e. mass balance based) and can easily be updated with different infection risk probability functions or just by using virus particles concentration instead of quanta values to give a relative picture of different proposed actions.

The tool is developed under MS Excel using VBA (Visual Basic for Applications) programming language. It is simple enough to use and fast to execute for a comparative COVID-19 infection risk analysis for a standard building floor and the most common air distribution layouts – something that compromises its flexibility as it can't be used for any type of application.

Input values and assumptions

Although SARS-CoV-2 quanta/h emission values include some uncertainties, it is already possible to calculate infection risk estimates and conduct comparisons on the effect of ventilation and room parameters. These limitations and uncertainties mean that rather than predicting an absolute infection risk, the calculation is capable of comparing the relative effectiveness of solutions and ventilation strategies to support the most appropriate choice. Therefore, the tool provides just an **indication** of risk.

The model results strongly depend on the input parameters and their uncertainty reflect on the result itself. Thus, this tool is intended to be used by experts only, who know the meaning of each input value and their impact on the results.

Some very sensible and specific COVID-19 input parameters are provided in drop-down lists, such as the virus emission rate per person, susceptible people breathing rates, etc. Even though these parameters have been taken from the most updated scientific sources (as reported in the disclaimer), their selection is under the user's responsibility.

Full mixing hypothesis creates another uncertainty because, in large and high-ceiling rooms, the virus concentration is not necessarily equal all over the room volume.

Results

The generated results are sensitive to quanta emission rates which can vary over a large range. The uncertainty of these values is high. Also, there are likely to be super spreaders that are less frequent but may have higher emission rates. This makes absolute probabilities of infection uncertain, and it is better to look at the order-of-magnitude. The relative effect of control measures may be better understood from this calculation, given the current state of knowledge.

Calculated probability of infection is a statistical value that applies for a large group of individuals, but differences in individual risk may be significant depending upon the individual's personal health situation and susceptibility.

These limitations and uncertainties mean that rather than predicting an absolute infection risk, the calculation is capable of comparing the relative effectiveness of solutions and ventilation strategies

to support the most appropriate choice. The calculation model can show which strategy offers the lowest load for non-infected persons and provides just an indication of risk. The model can be applied to show low and high-risk rooms in existing buildings, which is very useful in the risk assessment of how buildings should be used during the outbreak.

Tool availability

This tool has been produced with the intention to give to any socially responsible HVAC engineer a simple and fast to use engineering “weapon” in fighting against COVID-19 pandemic. For this reason, this tool will be freely available after the evaluation of REHVA COVID-19 Task Force.

Download the REHVA COVID-19 Multi-room and Recirculation Calculator at REHVA’s website: https://www.rehva.eu/activities/covid-19-guidance

Feedback

If you are specialist in the issues addressed in this document and you have remarks or suggestions for improvements, feel free to contact us via livio.mazzarella@polimi.it. Please, mention **"Multi-room and Recirculation Calculator"** as subject when you email us.

Colophon

This document was prepared by Prof. Livio Mazzarella, Milan Polytechnic University (livio.mazzarella@polimi.it), with the support of the REHVA COVID-19 Task Force. Members of this expert group are:

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Acknowledgement

This work has been carried out during my mandate as AiCARR expert in the COVID-19 REHVA Task Force, the work of which was stimulus for developing the model. For this reason, I would like to acknowledge all REHVA COVID-19 Task Force participants and AiCARR for this opportunity.

Prof. Livio Mazzarella

Disclaimer

This model is our best scientific estimate, based on the information currently available. It is provided in the hope that it will be useful to others in providing and applying more efficient virus removal options during this pandemic.

It must be used ONLY for comparative infection risk analysis related to possible improvements on both ventilation solutions for new buildings/systems and retrofit and operational strategies for existing buildings/systems under pandemic condition.

The model result strongly depends on the input parameters and their uncertainty reflect on the result itself. Thus, this tool is intended to be used by EXPERTS ONLY, who know the meaning of each input and their impact on the results.

It is an ongoing work and may therefore contain defects or "bugs" inherent to this type of software development. In case some mistakes or deficiencies are found, please write to: livio.mazzarella@polimi.it .

The individual developers and REHVA will in no event be liable for any direct or indirect, material or moral, damages of any kind, arising out of the use of the tool.

References

[1] REHVA COVI-19 Task Force, 2020, REHVA COVID-19 guidance document, August 3, 2020, Brussels, https://www.rehva.eu/activities/covid-19-guidance/rehva-covid-19-guidance

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