

# Risk mapping of respiratory viral transmission and disease severity using individual and environmental health parameters: A scoping review and protocol analysis

Rebecca Niese<sup>a,\*</sup>, Dominique van der Vlist<sup>b</sup>, Mark Verhagen<sup>b,c</sup>, Noortje de Haan<sup>b</sup>,  
Melissa Stunnenberg<sup>a</sup>, Fábio Serafim<sup>a</sup>, Mirjam Kretzschmar<sup>a,d</sup>, Annemieke van der Wal<sup>a</sup>,  
Lucie Vermeulen<sup>a</sup>, Aletta Tholen<sup>a</sup>, Ana Maria de Roda Husman<sup>a,e</sup>

<sup>a</sup> Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), PO Box 1, 3720 BA, Bilthoven, the Netherlands

<sup>b</sup> Amsterdam Health & Technology Institute, Paasheuvelweg 25, 1105 BP, Amsterdam, the Netherlands

<sup>c</sup> Leverhulme Centre for Demographic Science, University of Oxford, 42-42 Park End St, OX1 1JD, Oxford, United Kingdom

<sup>d</sup> Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht (UMCU), Utrecht University, PO Box 85500, 3508 GA, Utrecht, the Netherlands

<sup>e</sup> Utrecht University (UU), PO Box 80125, 3508 TC, Utrecht, the Netherlands

## ARTICLE INFO

### Keywords:

SARS-CoV-2

Influenza

Review

Transmission

Disease severity

Risk map

## ABSTRACT

Due to the impact respiratory viruses have on human health, a lot of data has been collected and visualised in tools such as dashboards that provide retrospective insights into the course of an epidemic or pandemic. Two well-known respiratory viruses, influenza virus and SARS-CoV-2, are the causative agents of influenza and COVID-19, respectively. A scoping review was performed using Embase including data from January 2000 until April 2021 to identify individual and environmental health parameters that affect transmission of influenza virus and SARS-CoV-2, as well as disease severity (morbidity (hospitalisation) and mortality) of influenza and COVID-19. Summary data was extracted from published articles. A total of 2280 unique articles were identified by the search, 484 articles were analysed, and 149 articles were included. The information of included articles was combined with data from Dutch databases to create prospective interactive maps that visualise risk areas in the Netherlands on health region, municipality, and neighbourhood-level. Included health parameters are contacts per day, mixing patterns, household composition, presence of certain indoor public spaces, urbanity, meteorological values, average income, age, ethnicity, comorbidity, sex, and smoking habits. The impact and input of these parameters are adjustable by users allowing a fit-for-purpose approach. These maps can be used to corroborate local policy decisions in times of health crisis, or in pandemic preparedness plans, serving as an instant visualisation tool of risk areas in the country. Despite limitations caused by data unavailability, simplification steps, and lack of validation, these interactive maps provide an important basis that can be elaborated on by further research that integrates both individual and environmental parameters.

## 1. Introduction

Of all the infectious diseases worldwide, lower respiratory tract infections causing pneumonia and bronchitis result in the greatest disease burden of all, posing the fourth most common cause of death globally as well as the largest proportion of all infectious disease hospitalisations [1]. Respiratory viruses have been shown to be very effective as they can readily adapt genetically, do not adhere to geographical borders, are

regularly found to be zoonotic, are often very transmissible, and can therefore cause a pandemic [1]. As healthcare improves, the population ages, increasing the number of individuals with immunocompromising conditions who are most at risk of these diseases [2].

In the 21st century, the world has seen a rapid spread of multiple types of respiratory viruses both in humans and in animals, including Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and influenza viruses [3]. SARS-CoV-2, the causative agent of Coronavirus

\* Corresponding author at: Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), PO Box 1, 3720, BA, Bilthoven, the Netherlands.

E-mail address: [rebecca.niese@rivm.nl](mailto:rebecca.niese@rivm.nl) (R. Niese).

<https://doi.org/10.1016/j.onehlt.2024.100741>

Received 24 August 2023; Accepted 21 April 2024

Available online 23 April 2024

2352-7714/© 2024 The Authors. Published by Elsevier B.V. This is an open access article under the CC BY-NC license (<http://creativecommons.org/licenses/by-nc/4.0/>).

Disease 2019 (COVID-19), is the most recent example of such a virus that caused a pandemic, starting in December 2019, and still ongoing at the time of writing. This virus was originally found in Wuhan, China, but it has since spread to all countries globally including the Netherlands. It has caused a total of approximately 8.6 million official cases in the Netherlands by January 3rd 2023, as well as almost 23,000 official deaths [4].

Individual (such as age) and environmental (such as urbanity) parameters are often presented as two separate insights influencing transmission or disease severity of respiratory virus infections: an upcoming new Dutch environmental law (“de Omgevingswet”) shows that governance is increasingly focusing on the environment, providing a very politically relevant opportunity to propose an integrated approach that includes both individual and environmental parameters [5]. Also, in the context of pandemic preparedness, a tool to integrate and visualise transmission and disease severity risk could be helpful. It is crucial that policymakers stay informed with the most recent developments in terms of academic research on the topic and that this information is presented in an actionable way. Unfortunately, research is often dispersed across academic journals and requires time, effort, and specialist knowledge to dissect and interpret. In addition, research insights can be challenging to translate into concrete actions for policymakers. Also, in rapidly evolving crises, new information is added to the existing knowledge base frequently, quickly outdated reviews. In addition to these challenges, a lot of information is visualised in dashboards of retrospective nature and rarely cover all possible health parameters that could have an impact on transmission or disease severity.

The aim of this study was to investigate whether it is possible to create prospective interactive maps of risk areas of the Netherlands by combining national population data with scientific data on individual and environmental parameters that affect transmission of influenza virus and/or SARS-CoV-2 and their disease severity.

1.1. Methodology

1.1.1. Search strategy

A scoping review was performed. Articles were searched in Embase on parameters influencing three outcome measures 1/ transmission risk, 2/ morbidity risk and 3/ mortality risk of influenza virus (influenza) and SARS-CoV-2 (COVID-19). The results of Cevik et al. served as inspiration for health parameter search terms [6]. These were combined with search terms related to influenza virus and/or SARS-CoV-2 and with search terms on the selected outcome measures. Search terms included influenza, SARS-CoV-2, COVID-19, living environment, socio-economic status, host factors such as age and comorbidities, and contact pattern. No study authors were contacted, no grey literature was included, no articles were translated, and no unpublished articles were included. Where possible, data was collected from cohort studies resulting in summary estimates. The full search terms and strategy can be found in the Supplementary data, paragraphs A5 (search terms) and A4 (literature search).

1.1.2. Selection criteria

Selection criteria for the study are:

- Published in an English, peer-reviewed journal, published between January 2000 and April 2021.
- Offered quantitative evidence on transmission, morbidity, or mortality expressed in Relative Risk (RR), Odds Ratio (OR), Hazard Ratio (HR), percentages (%), contact rates, or associations.
- Pertained to results from Western countries, countries with a comparable Gini index to the Netherlands (−5 to +5) [7].
- Excluded case studies as they did not provide comparative data

1.1.3. Review protocol

The review follows the protocol of Preferred Reporting Items for

Systematic Reviews and Meta-Analyses (PRISMA) [8]. After the literature search in Embase, all articles were downloaded and duplicates were removed in EndNote20 [9]. Subsequently, relevant literature was selected based on a title and abstract screening by two researchers (RN and FS) independently. Then, a full-text screening of the selected articles was conducted by two researchers (RN and MS) independently. Conflicts were resolved through mutual discussion. Relevant data identified during the full-text screening was extracted. Included articles were subdivided into Cevik’s four categories 1/ Contact Pattern, 2/ Living Environment, 3/ Socio-Economic Status, and 4/ Host Factor [6]. Within these categories, recurring themes were identified as possible health parameters. Findings that were reported in at least three retrieved articles were included. When findings were inconsistent, the outcome of most articles was adhered to. No bias risk analysis, sensitivity analysis or variability assessment was performed.

1.2. Outcome measures

The following outcome measures were used in the scoping review:

- ‘Transmission’ was defined as the occurrence of a positive test, secondary attack rate, or as cases in studies that clearly specified not intending hospitalisation or mortality.
- ‘Disease severity’ was defined as the occurrence of either:
  - o ‘Morbidity’: occurrence of admission to the hospital or Intensive Care Unit.
  - o ‘Mortality’: occurrence of death.

1.2.1. Risk map creation after scoping review

To create risk maps, environmental or population data on each parameter was collected for the Dutch setting from the Dutch Central Bureau of Statistics (CBS) (microdata and Statline), the Royal Dutch Meteorology Institute (KNMI), and the Dutch National Institute for Public Health and the Environment (RIVM) databases [10–12]. The data source level was investigated to see whether modification of the data was required. Then, all included parameters were further divided into concrete mutually exclusive and exhaustive risk groups (e.g., smokers and non-smokers). The collected data was used to assign every individual to their associated risk group for each parameter. If direct data was not available, proxy data was used that resembled the direct data as much as possible (e.g., individual-level medicine use data as a proxy for presence of comorbidities). Based on the risk group assignment of individuals, an average area risk score was calculated for each parameter, ranging between 1 (low risk) and 5 (high risk). In addition, an overall area risk score was calculated by averaging the area’s risk scores for all parameters. All risk scores were provided on three levels: health region, municipality, and neighbourhood level. The process is visualised in Fig. 1. Risk scores were given for transmission and for disease severity

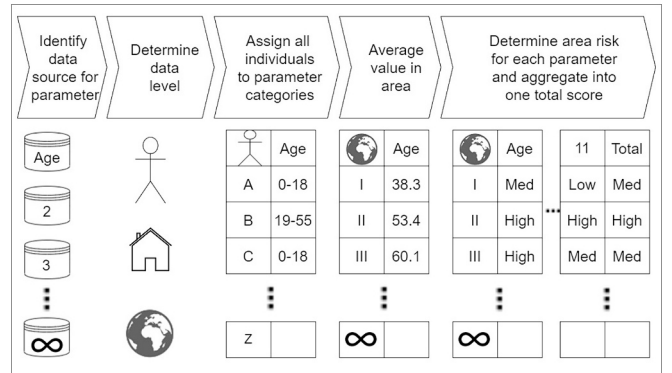


Fig. 1. This figure illustrates the process of data collection for each parameter.

separately.

Insights for transmission and for disease severity were visualised in two interactive maps using the open source packaging of R programming language, Version 4.2.2, Auckland, NZ, [13] and uploaded to a private online test location pending validation (available upon request). The website includes three main features: a map of the Netherlands on transmission risk, a map of the Netherlands on disease severity risk, and an information hub. The latter presents information from the supplementary data as well as more elaborate information surrounding the interpretation of the risk scores for each health parameter. The risk scores shown in the two maps are determined by overlaying the results of each relevant parameter and can be observed for three different aggregation levels: health region, municipality, and neighbourhood level.

Interviews with potential end-users were organised, both in workshops and through individual meetings. Main topics of discussion were implementation of the maps into current dashboards and implementation of features in the map to ensure a fit-for-purpose approach. Recommendations of these end-users were implemented into the maps.

## 2. Results

A PRISMA flow diagram was created of the scoping review (Fig. 2). 2795 articles were retrieved from Embase. After removing duplicates, a total of 2280 articles were included for title and abstract screening. Selection criteria excluded a further 1838 articles. Based on the

suggestions from other authors, 21 articles were added to the categories living environment and contact patterns, subsequently resulting in 463 articles selected for full-text screening. The full-text screening phase resulted in the exclusion of a further 272 articles. A total of 191 articles were included after full-text screening. A further 42 articles were placed aside because they discussed the impact of non-pharmaceutical interventions (NPIs) which was deemed outside the scope of the project. Therefore, 149 articles were included as the underpinning of the dashboard.

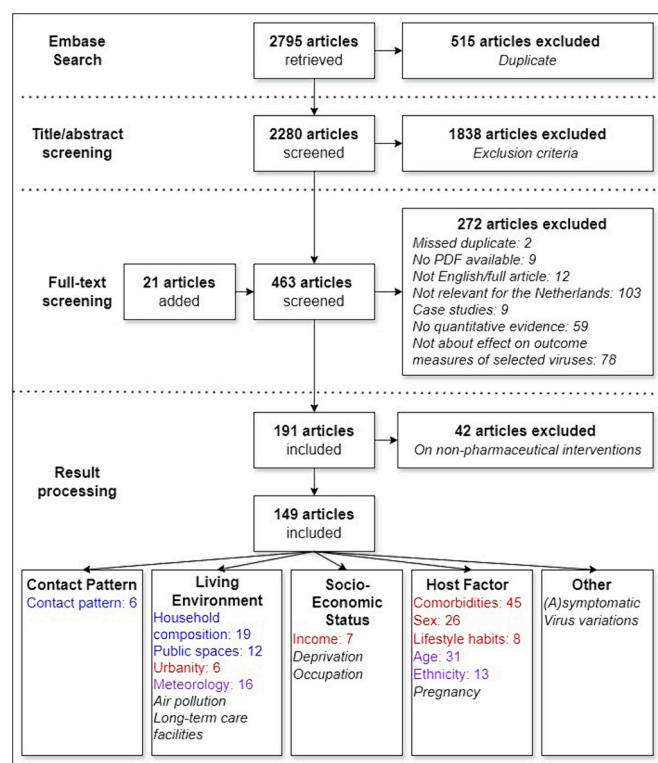
Eleven health parameters indicated an effect on risk of transmission, morbidity or mortality of SARS-CoV-2 (COVID-19) or influenza virus (influenza) (Fig. 2). A brief summary for each category is provided below. Full results, including those from excluded parameters, can be found in the supplementary data, paragraphs A1.1–A1.4.

The contact pattern category includes all parameters on human-human interactions. The scoping review showed that the number and direction of contacts each day was dependent on age. To investigate the effects of contact patterns on transmission of influenza virus and SARS-CoV-2, the study by Mossong et al. was of high importance [15]. This study provided elaborate information on European contact behaviour. A website was provided that allowed the selection of specific data [16]. Children aged 10–14 years engaged in the highest number of contacts per day and adults aged 70+ years engaged in the least. Individuals mainly contacted individuals within their age group. This assortative pattern was most pronounced in those aged 5–24 years, and least pronounced in those aged 55–69 years. Additionally, children (10–14 years) tended to mix with adults in the 30–39 years age range regularly, as did these middle-aged adults with the elderly (>70 years) [15]. This implies that age influences the amount and direction of contacts which in turn affects transmission risk.

The living environment category includes parameters on indoor environments as well as outdoor environments and urbanity. Households with two or more members were at higher risk of transmission than those with one member where virus transmission within the household is not possible. However, increasing the household size to beyond three members did not show a significant increase in transmission risk [17–19]. Instead, the age and relationship of the members within the household were more important, with children usually increasing the risk of transmission [17,18,20–22] and partners increasing the risk even more than children, likely due to their close interaction with each other [6,19,22–24]. Indoor public spaces could also form a transmission risk. Locations that increased transmission risk included religious locations and work conferences/workplaces [24–26]. Lastly, meteorological factors could affect the risk of transmission. Air temperature was found to be negatively correlated to SARS-CoV-2 and influenza virus transmission [27]. Factors in the living environment that were found to be related to disease severity were urbanity and meteorologic factors. The average hospitalisation rate of COVID-19 [28] and influenza [29] was much higher in the most urban or densely populated areas compared to the most rural areas. Air temperature was negatively correlated with mortality risk [27].

For the category Socioeconomic status (SES), income was associated with influenza hospitalisation risks. More hospitalisations were found in relatively poor neighbourhoods compared to relatively rich neighbourhoods [29–31]. Large income inequality in an area was also associated with an increase in the number of COVID-19 deaths [32]. These outcomes show that income of individuals affects the risk of disease severity.

The host factor category includes all parameters on the individual level, such as age, ethnicity, comorbidities, sex (binary, assigned at birth), and smoking habits. Transmission (incidence) of influenza virus decreased with age, peaking between 5 and 19 years of age [21,33–35]. Transmission of SARS-CoV-2 likely showed an opposite pattern, increasing with age [23,36]. Also, ethnic minorities were associated with an increased incidence of influenza and COVID-19 compared to Caucasians [29,37,38].



**Fig. 2.** The PRISMA flow diagram of the scoping review. Many articles reported on multiple parameters, so the total amount of articles appears to exceed 149. Eleven health parameters were included, with those in blue affecting transmission, red affecting disease severity, and purple affecting both. Seven health parameters are shown in italics and were excluded, either because their information was not supported by at least three articles (four parameters: presence of long-term care facilities, deprivation level of an area, occupation level of an area, presence of pregnant women), because they could not be visualised geographically (two parameters: being (a)symptomatic, variations within and between viruses) or because they were too complex to visualise statically (one parameter: air pollution [14]). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Hospitalisation risk due to influenza likely showed a bimodal age pattern, with the largest peak occurring in the highest age group [34,35,39–43], and a secondary peak in the youngest age group [39–41]. For COVID-19, increase of hospitalisation risk with age was observed [36,44,45]. Influenza [34,42,46] and COVID-19 [36,44,47] mortality risk increased with age. Also, ethnic minority groups like blacks in the American context were associated with increased hospitalisation rates [30,31,37,48] and mortality [37,38,43] risk of both influenza and COVID-19. Additionally, the following comorbidities were associated with increased hospitalisation rates or mortality: diabetes [37,44–46,48–60], hypertension [37,44,45,47–59,61–63], cardiovascular disease (CVD) [42,44,45,48–51,53–65], obesity [37,44,47,48,52,57], chronic kidney disease (CKD) [42,44,46,49–55,58], cancer [33,42,44,46,51–53,55,56,58,60], chronic obstructive pulmonary disease (COPD) [42,44,50,51,53,54,59,61,64], cerebrovascular disease [45,51,53,59,60,65], and respiratory disease [40,45,48,51,58,60,64]. More detailed information can be found in the Supplementary data, paragraph A1.4.1 and fig. A1. Men were at higher risk of influenza [30,31,33,41,43] and COVID-19 [36,42,48,49,51,61,66,67] hospitalisation than women. They were also at higher risk of mortality due to influenza [46] or COVID-19 [36,44,47,51,60,65–67]. Lastly, influenza and COVID-19 hospitalisation risk increased with smoking [33,48,50]. These results show that age, ethnicity, comorbidities, sex, and smoking all affect disease severity of influenza and COVID-19.

Then, each parameter was assigned risk groups and (proxy) data sources were identified to geographically visualise the distribution of these risk groups in each area. Where possible, five risk groups were identified per categorical parameter (0 = low risk, 4 = high risk). The

input for both risk maps has been provided in Table 1. Fig. 3 shows the example workflow of the resulting risk map tool.

Table 1a illustrates the process of assigning individuals a comparable risk metric that could be used to aggregate transmission risk measures at the spatial level. When variables were categorical (categ.), ordinal mapping was done (higher categories reflect higher risks). When variables were continuous (contin.), individuals were assigned a value that ensures higher values reflect higher risk. Lastly, when variables were already aggregated at a regional level, individuals in the region were assigned the regional risk value. In general, risk measures were assigned to individuals and aggregated from the individual to the spatial level.

Table 1b illustrates this process for the disease severity map.

The third feature of the private test location is a knowledge hub where the underlying information from the scoping review is presented for each parameter separately. This hub features the elaborate version of the findings for each of the four categories as presented in the Supplementary material, paragraphs A1.1–A1.4. Fig. A2 shows what the hub looks like when in use.

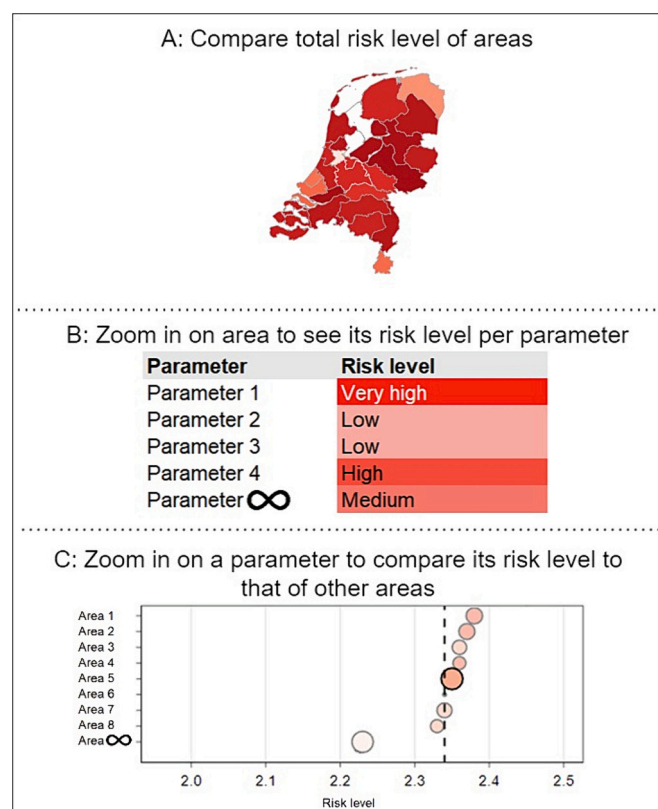
Potential end-users are epidemiologists working in various regions, regional epidemiological consultants, regional physician consultants, health and environment consultants working at various municipal health services, research institutions, universities, the ministry of health, and the pandemic and disaster preparedness centre. Interviews with these potential groups revealed the desire to be able to alter settings for the maps and to have the map validated. Users can adjust the weight of the effect of parameters to visualise the need for or impact of policy strategies targeted at (a) specific parameter(s) in an area. The risk group settings provided in table 1 can be adjusted as well, which can be useful to predict risk areas of a hypothetical ‘respiratory virus disease X’ with different characteristics than influenza virus and SARS-CoV-2. None of the potential end-users saw possibilities of adding the interactive maps to an existing system prior to validation.

### 3. Discussion

This study identified eleven parameters that either affected transmission or disease severity or both: contacts per day, mixing patterns, household composition, presence of certain indoor public spaces, urbanity, meteorological values, average income, age, ethnicity, comorbidity, sex, and smoking habits. Each of these parameters has been well-documented in literature by at least three separate studies, and in themselves are therefore not new. However, the overview of all these different parameters together is new, as none of the retrieved articles investigated all retrieved parameters at once.

In addition, the maps developed in this project provide an innovative way to combine and visualise information on individual and environmental parameters based on scientific knowledge, stimulating scientists to take their review findings to the next level. The general framework that was conceived in this study can be used by other countries to develop their own maps and dashboard. Once validated, the maps provide an opportunity to be used in dashboards with detailed information that can be altered by users to create a unique fit-for-purpose approach. Due to their prospective and quick nature, they can be used in pandemic preparedness strategy plans as well.

Despite plenty of strengths, the current interactive maps and the framework to develop them contain limitations as well. The interactive maps rely on results from a scoping review, which is a type of review to quickly determine what is known about a topic, but there is no qualitative assessment of included studies. Therefore, scoping reviews do not provide conclusive quantitative data, rather discover trends and directions of effects. This is the reason behind the simplification of research findings, only incorporating information that was presented in three or more scientific articles, ignoring study quality. Another limitation is that the current maps are static. A time component was not incorporated into the maps, so elements such as seasonality and mobility were not incorporated. Also, combining different types of information



**Fig. 3.** Example workflow of the online risk map tool. The top panel (A) shows the geographic distribution of overall risk for areas in The Netherlands. The middle panel (B) shows a table detailing the various risk parameters underlying the overall risk score for a selected area. The bottom panel (C) shows the distribution of the selected parameter across all areas, with the selected area highlighted.



**Table 1a**  
Dashboard input for transmission map.

Parameter	Virus	Risk categories	Aggregation level	Data type	Data source
Contacts pattern	Both	Higher number of contacts per day increased risk	Individual	Contin.	POLYMOD matrix & CBS microdata 'age' <sup>8,13</sup>
Household composition	Both	0: Single-person households – lowest risk	Household	Categ.	CBS Microdata <sup>8</sup>
Household composition	Both	1: Multi-person households (no children or partners) – low risk	Household	Categ.	CBS Microdata <sup>8</sup>
Household composition	Both	2: Multi-person households with at least one child and no partners – high risk	Household	Categ.	CBS Microdata <sup>8</sup>
Household composition	Both	3: Multi-person households (including partners) – highest risk	Household	Categ.	CBS Microdata <sup>8</sup>
Indoor public spaces	Both	Higher number of communal buildings (non-residential) increases risk	Regional	Contin.	Statline <sup>8</sup>
Meteorology	Both	Lower temperature increases risk	Regional	Contin.	KNMI <sup>9</sup>
Age	Influenza virus	0: 20–24 – lowest risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	Influenza virus	1: 40+ – low risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	Influenza virus	2: 0–4 or 25–39 – high risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	Influenza virus	3: 5–19 – highest risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	SARS-CoV-2	0: 0–20 – lowest risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	SARS-CoV-2	1: 21–64 – low risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	SARS-CoV-2	2: 65–69 – high risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	SARS-CoV-2	3: 70+ – highest risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Ethnicity	Both	0: Native Dutch – low risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Ethnicity	Both	1: Migrant background (proxy for ethnic minorities) – high risk	Individual	Categ.	CBS Microdata <sup>8</sup>

**Table 1b**  
Dashboard input for disease severity map.

Parameter	Disease	Risk categories	Aggregation level	Data type	Data source
Urbanity	Both	Higher number of addresses per km <sup>2</sup> increases risk	Regional	Contin.	Statline <sup>8</sup>
Meteorology	Both	Lower temperature increases risk	Regional	Contin.	KNMI <sup>9</sup>
Income	Both	More people in the area living below poverty line increases risk (earning <120% of the social minimum in the Netherlands)	Individual	Contin.	CBS Microdata <sup>8</sup>
Age	Influenza	0: 5–19 – lowest risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	Influenza	1: 20–39 – low risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	Influenza	2: 40–54 – medium risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	Influenza	3: 0–4 – high risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	Influenza	4: 55+ – highest risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	COVID-19	0: 0–17 – lowest risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	COVID-19	1: 18–29 – low risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	COVID-19	2: 30–64 – medium risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	COVID-19	3: 65–84 – high risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Age	COVID-19	4: 85+ – highest risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Ethnicity	Both	0: Native – low risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Ethnicity	Both	1: Migrant background (proxy for ethnic minorities) – high risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Comorbidities	Both	0: No comorbidities – low risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Comorbidities	Both	1: One comorbidity (amongst selected comorbidities) – medium risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Comorbidities	Both	2: More than one comorbidity (amongst selected comorbidities) – high risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Sex	Both	0: Female – low risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Sex	Both	1: Male – high risk	Individual	Categ.	CBS Microdata <sup>8</sup>
Smoking	Both	More smokers increases risk	Regional	Contin.	RIVM <sup>107</sup>

has proven difficult, as comparison groups, case definitions and viruses or virus strains under investigation varied wildly, and research findings were presented in many different units. Therefore, two simplification steps were implemented. Firstly, all findings were simplified into a semi-quantitative direction of effect (positive or negative effect). Secondly, each parameter contributes equally to the area's total risk score. This falsely assumes that each health parameter is independent and contributes equally, even though some are likely strongly correlated such as age and comorbidities. It was deemed impossible to include possible correlations between parameters because none of the retrieved articles performed a multivariable regression on all parameters at once. Also, new parameters may be identified in the future, or some parameters may be disabled by end-users, each requiring new multivariable regressions to be performed.

Also, some health parameters that were incorporated in the maps were represented by indirect proxies due to data unavailability, such as ethnicity. Such proxy-use can lead to false conclusions but was unavoidable while the direct data was unavailable.

Lastly, the maps had a very strict Dutch boundary. International travel to and from the Netherlands is a big risk factor for transmission (after all, this is how the COVID-19 pandemic started). This was outside the scope of the current project.

Cevik et al. reviewed the effect of health parameters on SARS-CoV-2 transmission and their four categories were used as the foundation of the search terms for this scoping review [6]. However, they focus on transmission risk of individuals, whereas this study attempts to provide not only transmission risk but also disease severity risk and provides information on regional level as opposed to individual level. Verhagen et al. have created maps similar to the disease severity map in this study for the United Kingdom, where COVID-19 hospitalisation pressure was taken as the outcome measure and individual as well as environmental health parameters were incorporated [68]. They found that the health parameters age, social deprivation, population density and ethnicity affected this risk. Each of these parameters was found in the current study as well, but due to the more elaborate search in this study by also including transmission risk, even more parameters were identified here. Another study that attempted to create a risk map (of COVID-19 transmission) was the Australian work of Zachreson et al. where mobility data was used to predict where most new SARS-CoV-2 infections would occur [69]. These examples show prospective risk mapping is being done for COVID-19, but combining it with influenza, as well as combining transmission and disease severity, additionally combining individual and environmental parameters, and visualising the results on the regional, municipality, and neighbourhood level, provides a new integrated approach for respiratory virus risk indication.

Further research into the field of pandemic preparedness should incorporate individual and environmental parameters, rather than studying one or two health parameters at a time. This allows for better judgement of correlations between the health parameters that were identified here using regression models. In addition to more integrated scientific knowledge, further elaboration of available health data is needed so health parameters can be visualised more directly. Also, more scientific data needs to be collected on parameters that did not make it into the map. Lastly, the maps presented in this study can be further improved by adding a dynamic factor, an international factor, and the effect of non-pharmaceutical interventions. Validation needs to occur too.

#### 4. Conclusion

The scoping review provided valuable information on both individual and environmental health parameters as input for prospective interactive maps on transmission of influenza virus and SARS-CoV-2, as well as on disease severity of influenza and COVID-19. While its pragmatic and integrated approach comes with limitations and simplifications, these maps provide a valuable basis of information in light of

pandemic preparedness. They enable the visualisation of the potential risk of virus transmission and disease severity upon respiratory viral infection in a specific area even before the start of an outbreak. Settings are adjustable, making the maps exceptionally suitable for their purpose. Providing the general framework for such an approach allows for the use of this approach by other countries as well. Further research on integrated approaches such as the one presented here should be considered. Also, the presented interactive maps should be further updated with other parameters and later validated so they provide reliable options for informing policy. Nevertheless, these first versions of the interactive maps provide a solid foundation for risk visualisation in the Netherlands, exemplifying how an integrated spatial approach can lead to an overarching overview of risks using population data. Further research will have to validate whether the interactive maps provide actionable insights for professionals at local and national level to make integrated policy decisions in times of health crises.

#### Contributors

RN was involved in the investigation, data curation, writing of the original draft, reviewing and editing of the manuscript, visualisation, and project administration. DvdV was involved in software, data curation, and writing of the original draft. MV was involved in software, writing of the original draft, and visualisation. NdH was involved in the investigation and writing of the original draft. MS was involved in the investigation. FS was involved in the conceptualisation, methodology, and investigation. MK was involved in the supervision and provided expert opinion where needed. AvdW was involved in the conceptualisation, methodology, supervision, and project administration. LV was involved the supervision and project administration. AT was involved in the conceptualisation, methodology, supervision, project administration, and funding acquisition. AMRH was involved in the conceptualisation, methodology, supervision, project administration, reviewing and editing of the manuscript, and funding acquisition. All authors provided feedback on the analysed data and on the report. Everyone had full access to all the data in the study and had final responsibility for the decision to submit for publication.

#### Data sharing

Data collected for the study will be made available to others on the information webpage (Knowledge hub) of the online test location as well as in the Supplementary data paragraphs A1.1-A1.4.

#### Declaration of competing interest

The authors declare no competing interests. The funder of the study had no role in study design, data collection, data analysis, data interpretation, or writing of the report.

#### Data availability

Data will be made available on request.

#### Acknowledgements

Funding was provided by the Dutch Ministry of Health, Welfare and Sports (VWS) under Programme 19 research into COVID-19 (project number: V/190027/22/OM). The authors would like to thank the Ministry for their financial support, as well as Brigit Staatsen, Laurens Zwakhals, Miranda Mesman, Gijs Klous, Job Spijker and Henriëtte Giesbers for their continuous feedback throughout the project.

#### Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.oneh.2024.100741>.

[org/10.1016/j.onehlt.2024.100741](https://doi.org/10.1016/j.onehlt.2024.100741).

## References

- [1] R.L. Hodinka, Respiratory RNA Viruses, *Microbiol Spectr* 4 (2016) 4, <https://doi.org/10.1128/9781555819040.ch11>.
- [2] K.C. Carroll, Laboratory diagnosis of lower respiratory tract infections: controversy and conundrums, *J. Clin. Microbiol.* 40 (9) (2002) 3115–3120, <https://doi.org/10.1128/jcm.40.9.3115-3120.2002>.
- [3] J.A. Al-Tawfiq, A. Zumla, P. Gautret, et al., Surveillance for emerging respiratory viruses, *Lancet Infect. Dis.* 14 (10) (2014) 992–1000, [https://doi.org/10.1016/S1473-3099\(14\)70840-0](https://doi.org/10.1016/S1473-3099(14)70840-0).
- [4] RIVM. Current information about COVID-19 <https://www.rivm.nl/en/coronavirus-covid-19/current-information2023> [01-08-2023].
- [5] RIVM. Omgevingswet <https://www.rijksoverheid.nl/onderwerpen/omgevingswet> [07-03-2024].
- [6] M. Cevik, J.L. Marcus, C. Buckee, T.C. Smith, Severe acute Respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission dynamics should inform policy, *Clin. Infect. Dis.* 73 (Suppl. 2) (2021), <https://doi.org/10.1093/cid/ciaa1442>. S170–S6.
- [7] T.W. Factbook, Gini index coefficient – distribution of family income, <https://www.cia.gov/the-world-factbook/field/gini-index-coefficient-distribution-of-family-income/country-comparison: CIA.gov, 2022> (10-10-2022).
- [8] D. Moher, L. Shamseer, M. Clarke, D. Ghersi, A. Liberati, M. Petticrew, P. Shekelle, L.A. Stewart, Preferred reporting items for systematic review and Meta-analysis protocols (PRISMA-P) 2015 statement, *Syst. Rev.* 4 (1) (2015) 1, <https://doi.org/10.1186/2046-4053-4-1>.
- [9] EndNote 20 ed. Philadelphia, PA: Clarivate; 2013.
- [10] CBS. The Netherlands. CCBotSt. <https://www.cbs.nl/2022> [02–01–2022].
- [11] KNMI. Maand- en jaarwaarden <https://www.knmi.nl/nederland-nu/klimatologie/maandgegevens2022> [03–01–2023].
- [12] RIVM. Gezondheid per buurt, wijk en gemeente 2020 <https://www.rivm.nl/media/smap/2022> [02-01-2022].
- [13] R Core Team, RStudio Version 4.2.2. <http://www.rstudio.com/>.
- [14] Veldhoven-van der Meer S. Onderzoek luchtkwaliteit, veehouderij en COVID-19 en consultatie algemene regels industriële emissies. In: Management MolaW, editor. [https://www.tweedekamer.nl/kamerstukken/brieven\\_regering/detail?id=202121077&did=2021D240482020](https://www.tweedekamer.nl/kamerstukken/brieven_regering/detail?id=202121077&did=2021D240482020) [10-05-2022].
- [15] J. Mossong, N. Hens, M. Jit, et al., Social contacts and mixing patterns relevant to the spread of infectious diseases, *PLoS Med.* 5 (3) (2008) e74, <https://doi.org/10.1371/journal.pmed.0050074>.
- [16] Social Contact Rates (SOCRATES) Data Tool. <http://www.socialcontactdata.org/socrates/2023> [03-01-2023].
- [17] J.G. Petrie, S.E. Ohmit, B.J. Cowling, et al., Influenza transmission in a cohort of households with children: 2010–2011, *PLoS One* 8 (9) (2013), <https://doi.org/10.1371/journal.pone.0075339>.
- [18] H. Nishiura, H. Oshitani, Household transmission of influenza (H1N1)-2009 in Japan: age-specificity and reduction of household transmission risk by Zanamivir treatment, *J. Int. Med. Res.* 39 (2) (2011) 619–628, <https://doi.org/10.1177/147323001103900231>.
- [19] Z.J. Madewell, Y. Yang, I.M. Longini Jr., M.E. Halloran, N.E. Dean, Household transmission of SARS-CoV-2: a systematic review and Meta-analysis, *JAMA Netw. Open* 3 (12) (2020) e2031756, <https://doi.org/10.1001/jamanetworkopen.2020.31756>.
- [20] C. Viboud, P.Y. Boëlle, S. Cauchemez, et al., Risk factors of influenza transmission in households, *Br. J. Gen. Pract.* 54 (506) (2004) 684–689, <https://pubmed.ncbi.nlm.nih.gov/15353055/>.
- [21] R. Savage, M. Whelan, I. Johnson, et al., Assessing secondary attack rates among household contacts at the beginning of the influenza a (H1N1) pandemic in Ontario, Canada, April–June 2009: a prospective, observational study, *BMC Public Health* 11 (2011) 234, <https://doi.org/10.1186/1471-2458-11-234>.
- [22] L. Chaw, W.C. Koh, S.A. Jamaludin, L. Naing, M.F. Alikhan, J. Wong, Analysis of SARS-CoV-2 transmission in different settings, *Brunei. Emerg Infect Dis* 26 (11) (2020) 2598–2606, <https://doi.org/10.3201/eid2611.202263>.
- [23] E. Goldstein, M. Lipsitch, M. Cevik, On the effect of age on the transmission of SARS-CoV-2 in households, schools, and the community. \*, *J Infect Dis* 223 (3) (2021) 362–369, <https://doi.org/10.1093/infdis/jiaa691>.
- [24] M.M. Sugg, T.J. Spaulding, S.J. Lane, et al., Mapping community-level determinants of COVID-19 transmission in nursing homes: a multi-scale approach, *Sci. Total Environ.* (2021) 752, <https://doi.org/10.1371/journal.pone.0240205>.
- [25] Q.J. Leclerc, N.M. Fuller, L.E. Knight, Group CC-W, S. Funk, G.M. Knight, What settings have been linked to SARS-CoV-2 transmission clusters? *Wellcome Open Res* 5 (2020) 83, <https://doi.org/10.12688/wellcomeopenres.15889.2>.
- [26] W.C. Koh, L. Naing, L. Chaw, et al., What do we know about SARS-CoV-2 transmission? A systematic review and meta-analysis of the secondary attack rate and associated risk factors, *PLoS One* 15 (10) (2020), <https://doi.org/10.1371/journal.pone.0240205>.
- [27] D. Paraskevis, E.G. Kostaki, N. Alygizakis, et al., A review of the impact of weather and climate variables to COVID-19: in the absence of public health measures high temperatures cannot probably mitigate outbreaks, *Sci. Total Environ.* (2021) 768, <https://doi.org/10.1016/j.scitotenv.2020.144578>.
- [28] D.F. Cuadros, Y. Xiao, Z. Mukandavire, et al., Spatiotemporal transmission dynamics of the COVID-19 pandemic and its impact on critical healthcare capacity, *Health Place* (2020) 64, <https://doi.org/10.1016/j.healthplace.2020.102404>.
- [29] C. Sloan, R. Chandrasekhar, E. Mitchel, W. Schaffner, M.L. Lindegren, Socioeconomic disparities and influenza hospitalizations, Tennessee, USA, *Emerg Inf Dis* 21 (9) (2015) 1602–1610, <https://doi.org/10.3201/eid2109.141861>.
- [30] K. Tam, K. Yousey-Hindes, J.L. Hadler, Influenza-related hospitalization of adults associated with low census tract socioeconomic status and female sex in New Haven County, Connecticut, 2007–2011, *Influenza Other Respi. Viruses* 8 (3) (2014) 274–281, <https://doi.org/10.1111/irv.12231>.
- [31] K.M. Yousey-Hindes, J.L. Hadler, Neighborhood socioeconomic status and influenza hospitalizations among children: New Haven County, Connecticut, 2003–2010, *Am. J. Public Health* 101 (9) (2011) 1785–1789, <https://doi.org/10.2105/AJPH.2011.300224>.
- [32] J. Wildman, COVID-19 and income inequality in OECD countries, *Eur. J. Health Econ.* 22 (3) (2021) 455–462, <https://doi.org/10.1007/s10198-021-01266-4>.
- [33] N.J. Dharan, L.Z. Sokolow, P.Y. Cheng, et al., Child, household, and caregiver characteristics associated with hospitalization for influenza among children 6–59 months of age: an emerging infections program study, *Pediatr Inf Dis J* 33 (6) (2014), <https://doi.org/10.1097/INF.0000000000000283> e141–e50.
- [34] A. Steens, S. Waaijenborg, P.F.M. Teunis, et al., Age-dependent patterns of infection and severity explaining the low impact of 2009 influenza a (H1N1): evidence from serial serologic surveys in the Netherlands, *Am. J. Epidemiol.* 174 (11) (2011) 1307–1315, <https://doi.org/10.1093/aje/kwr245>.
- [35] A.J.X. Zhang, To KKW, H. Tse, et al., High incidence of severe influenza among individuals over 50 years of age, *CVI* 18 (11) (2011) 1918–1924, <https://doi.org/10.1128/05357-11>.
- [36] B.G. Pijls, S. Jolani, A. Atherley, et al., Demographic risk factors for COVID-19 infection, severity, ICU admission and death: a meta-analysis of 59 studies, *BMJ Open* 11 (1) (2021), <https://doi.org/10.1136/bmjopen-2020-046460>.
- [37] J. Allotey, E. Stallings, M. Bonet, et al., Clinical manifestations, risk factors, and maternal and perinatal outcomes of coronavirus disease 2019 in pregnancy: living systematic review and meta-analysis, *BMJ* (2020) 370, <https://doi.org/10.1136/bmj.m3320>.
- [38] K.T. Mills, E. Peacock, J. Chen, et al., Experiences and beliefs of low-income patients with hypertension in Louisiana and Mississippi during the covid-19 pandemic, *J. Am. Heart Assoc.* 10 (3) (2021) 1–13, <https://doi.org/10.1161/JAHA.120.018510>.
- [39] S. Paine, G.N. Mercer, P.M. Kelly, et al., Transmissibility of 2009 pandemic influenza A(H1N1) in New Zealand: effective reproduction number and influence of age, ethnicity and importations, *Euro Surveill.* 15 (24) (2010). <https://europepmc.org/article/MED/20576236>.
- [40] A. Jules, C.G. Grijalva, Y. Zhu, et al., Estimating age-specific influenza-related hospitalization rates during the pandemic (H1N1) 2009 in Davidson co, TN. *Influenza Other Respir Viruses* 6 (3) (2012) e63–e71, <https://doi.org/10.1111/j.1750-2659.2012.00343.x>.
- [41] E.J. Crichton, S.J. Elliott, R. Moineddin, P. Kanaroglou, R.E.G. Upshur, An exploratory spatial analysis of pneumonia and influenza hospitalizations in Ontario by age and gender, *Epidemiol* 135 (2) (2007) 253–261, <https://doi.org/10.1017/S095026880600690X>.
- [42] F. Aziz, F. Aberer, O. Moser, et al., Impact of comorbidities on mortality in hospitalized influenza patients with diabetes – Analysis of the Austrian Health Insurance, *Diabetes Res. Clin. Pract.* (2021) 174, <https://doi.org/10.1016/j.diabres.2021.108758>.
- [43] P. Moyo, A.R. Zullo, K.W. McConeghy, et al., Risk factors for pneumonia and influenza hospitalizations in long-term care facility residents: a retrospective cohort study, *BMC geriatr* 20 (1) (2020) 47, <https://doi.org/10.1186/s12877-020-1457-8>.
- [44] M. Shankar, K.R. Nishanth, SARS-coronavirus disease 19 and comorbidities- a systematic review, *JCDR* 14 (12) (2020) OE01–OE6, <https://doi.org/10.7860/JCDR/2020/45988.14373>.
- [45] S. Cheng, Y. Zhao, F. Wang, Y. Chen, A.C. Kaminga, H. Xu, Comorbidities' potential impacts on severe and non-severe patients with COVID-19: a systematic review and meta-analysis, *J. Med.* 100 (12) (2021) e24971, <https://doi.org/10.1097/MD.00000000000024971>.
- [46] T.M. Quandelacy, C. Viboud, V. Charu, M. Lipsitch, E. Goldstein, Age- and sex-related risk factors for influenza-associated mortality in the United States between 1997–2007, *Am J Epidemiol* 179 (2) (2014) 157–167, <https://doi.org/10.1093/aje/kwt235>.
- [47] P. Shah, J. Owens, J. Franklin, et al., Demographics, comorbidities and outcomes in hospitalized Covid-19 patients in rural Southwest Georgia, *Ann. Med.* (2020) 1–7, <https://doi.org/10.1080/07853890.2020.1791356>.
- [48] C. Lassale, B. Gaye, M. Hamer, C.R. Gale, G.D. Batty, Ethnic disparities in hospitalisation for COVID-19 in England: the role of socioeconomic factors, mental health, and inflammatory and pro-inflammatory factors in a community-based cohort study, *Brain Behav.* 88 (2020) 44–49, <https://doi.org/10.1016/j.bbi.2020.05.074>.
- [49] M. Fathi, K. Vakili, F. Sayehmiri, et al., The prognostic value of comorbidity for the severity of COVID-19: a systematic review and meta-analysis study, *PLoS One* 16 (2021), <https://doi.org/10.1371/journal.pone.0246190>.
- [50] S. Khateri, H. Mohammadi, R. Khateri, Y. Moradi, The prevalence of underlying diseases and comorbidities in COVID-19 patients; an updated systematic review and Meta-analysis, *AAEM* 8 (1) (2020) 1–17, <https://doi.org/10.22037/aaem.v8i1.807>.
- [51] X. Fang, S. Li, H. Yu, et al., Epidemiological, comorbidity factors with severity and prognosis of COVID-19: a systematic review and meta-analysis, *J. Aging Res.* 12 (13) (2020) 12493–12503, <https://doi.org/10.18632/aging.103579>.

- [52] W.H. Ng, T. Tipih, N.A. Makoah, et al., Comorbidities in SARS-CoV-2 patients: a systematic review and meta-analysis, *mBio* 12 (1) (2021) 1–12, <https://doi.org/10.1128/mBio.03647-20>.
- [53] T. Yin, Y. Li, Y. Ying, Z. Luo, Prevalence of comorbidity in Chinese patients with COVID-19: systematic review and meta-analysis of risk factors, *BMC Infect* 21 (1) (2021), <https://doi.org/10.1186/s12879-021-05915-0>.
- [54] K. Nandy, A. Salunke, S.K. Pathak, et al., Coronavirus disease (COVID-19): a systematic review and meta-analysis to evaluate the impact of various comorbidities on serious events, *Diabetes Metab. Syndr.* 14 (5) (2020) 1017–1025, <https://doi.org/10.1016/j.dsx.2020.06.064>.
- [55] P. Ssentongo, A.E. Ssentongo, E.S. Heilbrunn, D.M. Ba, V.M. Chinchilli, Association of cardiovascular disease and 10 other pre-existing comorbidities with COVID-19 mortality: a systematic review and meta-analysis, *PloS One* (2020) 15, <https://doi.org/10.1371/journal.pone.0238215>.
- [56] S. Bae, S.R. Kim, M.N. Kim, W.J. Shim, S.M. Park, Impact of cardiovascular disease and risk factors on fatal outcomes in patients with COVID-19 according to age: a systematic review and meta-analysis, *HEART* (2020), <https://doi.org/10.1136/heartjnl-2020-317901>.
- [57] D. Müller-Wieland, N. Marx, M. Dreher, K. Fritzen, O. Schnell, COVID-19 and cardiovascular comorbidities, *Exp. Clin. Endocrinol. Diabetes* (2020), <https://doi.org/10.1055/a-1269-1405>.
- [58] A.E. Mesas, I. Caverro-Redondo, C. Álvarez-Bueno, et al., Predictors of in-hospital COVID-19 mortality: a comprehensive systematic review and meta-analysis exploring differences by age, sex and health conditions, *PloS One* (2020) 15, <https://doi.org/10.1371/journal.pone.0241742>.
- [59] B. Wang, R. Li, Z. Lu, Y. Huang, Does comorbidity increase the risk of patients with COVID-19: evidence from meta-analysis, *J. Aging Res.* 12 (7) (2020) 6049–6057, <https://doi.org/10.18632/aging.103000>.
- [60] D.C. Thompson, M.G. Barbu, C. Beiu, et al., The impact of COVID-19 pandemic on long-term care facilities worldwide: an overview on international issues, *Biomed. Res. Int.* (2020), <https://doi.org/10.1155/2020/8870249>.
- [61] V. Jain, J.M. Yuan, Predictive symptoms and comorbidities for severe COVID-19 and intensive care unit admission: a systematic review and meta-analysis, *Int. J. Public Health* 65 (5) (2020) 533–546, <https://doi.org/10.1007/s00038-020-01390-7>.
- [62] M.B. Naeini, M. Sahebi, F. Nikbakht, et al., A meta-meta-analysis: evaluation of meta-analyses published in the effectiveness of cardiovascular comorbidities on the severity of COVID-19, *Obes* (2021) 22, <https://doi.org/10.1016/j.obmed.2021.100323>.
- [63] J. Yang, Y. Zheng, X. Gou, et al., Prevalence of comorbidities and its effects in coronavirus disease 2019 patients: a systematic review and meta-analysis, *Int. J. Infect. Dis.* 94 (2020) 91–95, <https://doi.org/10.1016/j.ijid.2020.03.017>.
- [64] Hoang T, Anh TTT. Comparison of comorbidities in relation to critical conditions among coronavirus disease 2019 patients: a network meta-analysis. *Infect Chemother* 2021;53. doi:<https://doi.org/10.3947/IC.2020.0136>.
- [65] U. Patel, P. Malik, M.S. Usman, et al., Age-adjusted risk factors associated with mortality and mechanical ventilation utilization amongst COVID-19 hospitalizations—a systematic review and Meta-analysis, *SN Compr Clin Med* 2 (10) (2020) 1740–1749, <https://doi.org/10.1007/s42399-020-00476-w>.
- [66] E. Klang, S. Soffer, G. Nadkarni, et al., Sex differences in age and comorbidities for COVID-19 mortality in urban new York City, *SN Compr Clin Med* 2 (9) (2020) 1319–1322, <https://doi.org/10.1007/s42399-020-00430-w>.
- [67] J. O'Brien, K.Y. Du, C. Peng, Incidence, clinical features, and outcomes of COVID-19 in Canada: impact of sex and age, *J. Ovarian Res.* 13 (1) (2020), <https://doi.org/10.1186/s13048-020-00734-4>.
- [68] M.D. Verhagen, D.M. Brazel, J.B. Dowd, I. Kashnitsky, M.C. Mills, Forecasting spatial, socioeconomic and demographic variation in COVID-19 health care demand in England and Wales, *BMC Med.* 18 (1) (2020) 203, <https://doi.org/10.1186/s12916-020-01646-2>.
- [69] C. Zachreson, L. Mitchell, M.J. Lydeamore, N. Rebuli, M. Tomko, N. Geard, Risk mapping for COVID-19 outbreaks in Australia using mobility data, *J. R. Soc. Interface* 18 (174) (2021), <https://doi.org/10.1098/rsif.2020.0657>.