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EsteR – A Digital Toolkit for COVID-19 Decision Support in Local Health Authorities

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Abstract. In Germany, the current COVID-19 cases are managed and reported by the local health authorities. The workload of their employees during the pandemic is high, especially in periods of high infection numbers. In this work a decision support toolkit for local health authorities is introduced. A demonstrator web application was developed with the R Shiny framework and is publicly accessible online. It contains five separate tools based on statistical models for specific use cases and corresponding questions of COVID-19 cases and their contacts. The underlying statistical methods have been implemented in a new open-source R package. The toolkit has the potential to support local health authorities' employees in their daily work. A simulated-based validation of the statistical models and a usability evaluation of the demonstrator application in a user study will be carried out in the future.

Keywords. COVID-19, Quarantine, Decision Support Techniques, Public Health, Statistical Models

1. Introduction

The current COVID-19 pandemic is a huge burden for the 378 local health authorities in Germany, which are responsible for managing the COVID-19 cases. Their work includes contacting and informing infected persons to isolate themselves. The local health authorities have to trace contacts of infected persons, record incoming test results from laboratories and order quarantine. In addition, outbreak events must be investigated with special attention. The overall workload of health authorities due to the COVID-19 pandemic is so high that they temporarily prioritize their work towards managing the pandemic [1]. In periods of high infection rates, the local health authorities were not able to trace back contacts of infected persons [2].

Decision support systems can streamline and simplify such processes. For example, in clinics, such tools are already used for diagnosis, triage and prognosis, as well as personalized support for treatment decisions and automated tools for monitoring [3,4]. Moreover, models for predicting the number of COVID-19 infections have been

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proposed [5], which allow governments to adapt their regulations to control the pandemic. Network models can be used to analyze the effect of different social distancing scenarios on the spread of COVID 19 [6] and strategies to prevent a second wave [7]. Furthermore, tools for personal usage have been developed, e.g., a COVID-19 aerosol transmission risk calculator [8] to estimate the infection risk for indoor meetings and the microCOVID calculator [9] which allows to assess the infection risk for specific situations or for the whole day.

To the best of our knowledge, there are no tools for the guidance of quarantine and isolation orders at the local level. Most of the local health authorities use SurvNet [10], which is a reporting management software developed and released by the Robert-Koch Institute (RKI), and/or SORMAS [11], which is a system for epidemic management. Both software applications allow the management of COVID-19 cases and contacts, but up to now do not include decision support tools or statistical models.

The aim of our project is to support the local health authorities with a decision support web application based on statistical modeling. For this purpose, statistical models have been developed for certain use cases, which are described in section 2. Afterwards, the resulting R package smidm is described, and the web application is illustrated and discussed in section 3 and 4. Finally, the paper ends with section 5 containing conclusions and future work.

2. Methods

In cooperation with the local health authority Berlin-Reinickendorf different use cases and questions were determined. For these problems, tools based on statistical models were developed as decision support. Each tool of the application is explained in more detail.

2.1. Infection period

In this use case, the most likely time point of infection of one or more infected persons is visualized. In a systematic review and meta-analysis in [12] the reported pooled mean and median of the COVID-19 incubation period were 6.3 and 5.4 days, respectively. The most widely used distributions for parametrization of the incubation period were normal and log-normal, but the reported mean and median are not equal. Thus, it was decided to use a log-normal distribution. The needed parameters were directly calculated from the reported mean and median as 1.69 for the mean parameter and 0.55 for the standard deviation parameter. Based on the symptom onset date, the probability of infection in the days before symptom onset is shown in this tool, as well as the high-density regions [13] for 80% and 95%.

Beside one infected person, the tool allows to examine the infection period of several infected persons. Then, the user has to enter all symptom onset dates, and how many persons had their symptom onset on each date. Based on this input, a mixture density $p_{inf}(t)$ is created

$$p_{inf}(t) = \sum_{i=1}^{n_p} w_i \cdot p_{inf_i}(t), \quad w_i = \frac{n_i}{n}, \tag{1}$$

where n is the number of infected persons, n_p is the number of symptom onset dates and $p_{inf_i}(t)$ is the density and n_i the number of persons for the i-th symptom onset date. The resulting mixture density is again a probability density and gives an overview of the possible infection periods of all considered infected persons.

2.2. Illness period

A person infected with COVID-19 is considered and the question is when the infected contacts will show first symptoms. Zhang et al [14] estimated gamma distribution parameters for the serial interval between symptom onsets of infected persons and the symptom onset of infected contacts as 2.39 for the shape and 0.48 for the rate parameter. For our tool, those gamma parameters were used and based on the symptom onset of the infected person the probability of symptom onsets of the infected contacts is displayed together with the 80% and 95% high-density regions.

Furthermore, the tool allows to show the probabilities of symptom onset for the second and third generation of contacts. These probabilities are determined by a convolution of the probability density function of the previous generation with the probability density function for infecting the next generation of contacts. Thereby, the assumption is made that the infection transmissions are independent from contact generation to generation. For gamma distributions, a convolution of two gamma distribution equals the summation of their first parameters, so for each contact generation the model has the gamma distribution

$$p_{ill_g}(t) \sim \Gamma\,(g \cdot \alpha, \beta) \tag{2}$$

where α, β are the shape and the rate parameter for probability distribution, when the infected contacts of an infected person show first symptoms, and g is the considered generation.

In the demonstrator app the probability distributions and their 80% and 95% high-density regions [13] for the first, second and third generation are calculated, and the user can select which one should be shown.

2.3. Infectious period

With this tool, the potentially infectious period can be calculated for an infected person. In literature, an analysis of COVID-19 viral shedding and transmissibility was reported and a gamma distribution for infectious period of cases/patients was estimated based on the symptom onset date [15]. The authors provided an R script from which the shape parameter can be calculated as 20.52 and the rate parameter as 1.60 Based on that, this gamma distribution as well as the 80% and 95% high-density regions [13] are displayed to show when an infected person with symptoms is and was most likely infectious based on the symptom onset date.

For infected persons without symptoms, the period during which the person has to be considered as infectious is calculated according to the regulations of the Robert Koch-Institute (RKI) [16] and visualized. Based on the entered earliest infection date and date of positive testing, the calculated period is visualized on a timeline.

2.4. Infection Spread

The following situation is considered: a group of people has met at a certain event and some of them started to show symptoms in the first days after the event. Assuming that their symptoms are due to an infection at the specific event, the tool gives a worst-case prediction for how many people of the group are expected to be infected and to show symptoms in the following days.

First, two predictions for the total number of symptomatic infections in the group are done: The lognormal density for the incubation time described in 2.1 is used to calculate the percentage of all symptomatic infections to occur up to the last day with an observed illness. Based on the total number of observed illnesses so far, the expected total number of symptomatic infections inside the given group is then determined. In the other approach, the results from Davies et al. [17] are used, who studied the age-dependency of the transmission of COVID-19. For low, medium and high risk the reported 2.5% quantile, mean and 97.5% quantile of the infection rate were averaged over different age groups and multiplied by the corresponding age-specific mean symptom rate (Table 1). The product gives a literature-based prognosis of the setting-specific rate of symptomatic infections inside the group, independent of already observed infections. An absolute value of predicted symptomatic infections is calculated by multiplying this rate with the total group size.

Table 1. Age group-specific infection and symptom rates among infected persons calculated from Extended Data Fig. 4, p. 1218 in [17].

Age Group	**Low risk infection rate**	**Medium risk infection rate**	**High risk infection rate**	**Symptom rate**
<20	0.26	0.39	0.55	0.25
20-59	0.63	0.81	0.97	0.38
>59	0.63	0.81	0.95	0.66
mixed	0.54	0.71	0.85	0.41

To estimate the worst-case prediction, the maximum of the two predicted numbers of total symptomatic infections is used and split up according to the incubation time density mentioned above to estimate how many people will show symptoms on each of the following days after the last observed illness.

2.5. Risk assessment for group quarantine

In this use case, the following situation is considered: A group met and at least one person was infected. After the contact event, tests (e.g., polymerase chain reaction PCR tests) were performed by part of the group and all test results were negative. With the tool, the probability that no one was infected and that no further cases will occur can be calculated.

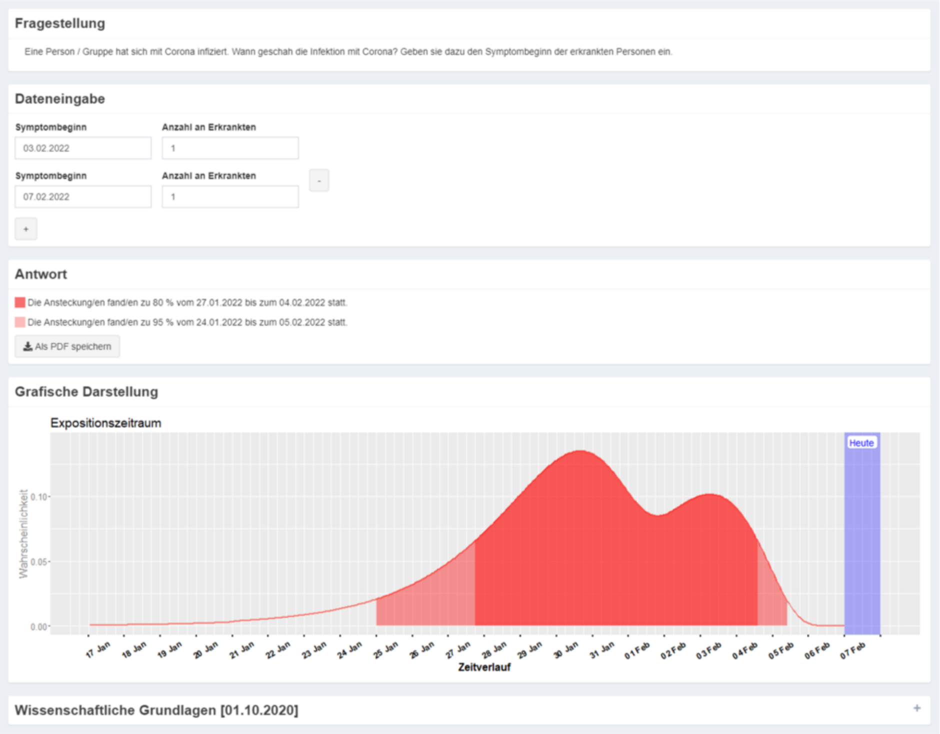
The statistical model used for this tool as well as all necessary parameters are described in [18] and has been specified for certain situations such as school classes or children daycare centers, which are the most common use cases in local health authorities. Beside PCR tests, antigen tests can be considered, which have been used more frequently since the beginning of 2021.

3. Results

3.1. R package smidm

All functions needed for the statistical models of each tool were developed in R [19] and have been bundled in the package *statistical modelling for infectious disease management* (smidm). The functions for visualization are not part of the package but are shown in the vignettes. The package smidm is available on Fraunhofer Git repository (https://gitlab.cc-asp.fraunhofer.de/ester/smidm/) for other R users and is published under the BSD-3 license.

3.2. Demonstrator web application



Fragestellung

Eine Person / Gruppe hat sich mit Corona infiziert. Wann geschah die Infektion mit Corona? Geben sie dazu den Symptombeginn der erkrankten Personen ein.

Dateneingabe

Symptombeginn: 03.02.2022
Anzahl an Erkrankten: 1
Symptombeginn: 07.02.2022
Anzahl an Erkrankten: 1

Antwort

🟥 Die Ansteckung/en fand/en zu 80 % vom 27.01.2022 bis zum 04.02.2022 statt.
🟥 Die Ansteckung/en fand/en zu 95 % vom 24.01.2022 bis zum 05.02.2022 statt.

Wissenschaftliche Grundlagen [01.10.2020]

Figure 1. Screenshot of the web application showing the infection period tab for two persons with symptoms onset on 03. and 07. February 2022.

The web application was developed with the R shiny framework [20] and uses the statistical model functions of the smidm package. The demonstrator web application can be accessed at https://ester.fraunhofer.de/. On the starting page, the users get an overview of all existing tools, and whether they apply to single infected persons or to group situations. All tools have the same, consistent structure and layout: the considered situation and question is described, the necessary inputs can be entered, and the answer is given as a text output and a corresponding visualization is shown if applicable. At the bottom, the tool lists the used scientific literature.

The web application has been introduced to employees of the local health authority Berlin-Reinickendorf to detect misunderstandings and to enhance the usability. In the process, the demonstrator was briefly introduced and then given to the employees. They used it for their purposes and shared their feedback with us. This allowed us to conclude how employees use the tools, whether the interface is usable for them, and where usability can be further improved in the application. The results were then used to simplify and restructure the tools and the web application.

A screenshot of the resulting web application showing the infection period tab for two infected persons with symptom onset date on 3. and 7. February 2022 is shown in Figure 1. The considered situation and question of the tab is described briefly and precisely in the first section. The symptom onset dates can be entered with the built-in calendar, further dates can be added and unneeded entries can be removed. Based on the entered inputs, the results are immediately and automatically calculated. In this tab, the text answer simultaneously serves as a legend for the 80% and 95% intervals in the plotted graphs.

4. Discussion

The developed web application can support the daily work of employees at local health authorities, but the benefit of our demonstrator application is limited, because it presumably cannot help overloaded personnel and will not be used by them. Furthermore, the statistical models were developed for specific use cases, where we assumed only information, which typically available for employees at the local health authorities. When cases are reported, no information about the transmission dynamic are available, e.g., whether a super spreading event took place. Hence, our models give a generic view of the transmission dynamics. Until now, no full evaluation of the statistical models has been done and it is not clear how much the employees benefit from using the web application in their daily work. For this purpose, we plan to conduct different simulation studies for validating each statistical model. In addition, a usability study for evaluating the benefit of using the web application for the employees in the local health authorities will be conducted.

Furthermore, parameters from the most recent literature search are currently used in the statistical models of the toolkit. They will be replaced over time by the results of an ongoing systematic review and meta-analysis within the project [21]. However, the used information can get outdated when new corona variants become established and then have to be updated. Currently, the package bundles the statistical models for the several COVID-19 use cases. In the future, further models for other infectious diseases, which have the potential to help the local health authorities in certain situations, could be developed and added to the package.

5. Conclusion

We introduced a decision support application for local health authorities. It contains several tools based on statistical models for different use cases of COVID-19 cases and their contacts. The web application as well as the package smidm including the statistical models are or will available on the internet. The developed web application has the potential to support the daily work of employees at local health authorities. In future work, the usage of our decision support application by employees will be evaluated and the used statistical models will be validated with simulation studies.

Declarations

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Conflict of Interest: The authors declare that there is no conflict of interest.

Contributions of the authors: SJ and RA wrote the first version of the manuscript. SJ, RA, LK, JS, BG and MW revised the manuscript. LK, RA and SJ reviewed the literature. SJ and RA developed the statistical models and the web application. MW supervised the research. All authors have approved the manuscript as submitted and accept responsibility for the scientific integrity of the work.

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