Dear editors,

We would like to express our gratitude for the thorough review of our manuscript titled "Modeling Geographic Vaccination Strategies for COVID-19 in Norway". We appreciate the valuable feedback provided by the reviewers, which has greatly contributed to the improvement of our work.

In response to the insightful comments, we have diligently revised the manuscript to address each concern and enhance the overall quality of our research. Below is a detailed summary of the review comments and the corresponding changes made.

Thank you for the opportunity to revise and resubmit our manuscript. We look forward to your feedback and appreciate your time and consideration.

Sincerely, Louis Yat Hin Chan Department of Method Development and Analytics, Norwegian Institute of Public Health, Oslo, Norway imlouischan@gmail.com Reviewer #1:

The authors provide a clear and well written account of the modeling efforts conducted by the Norwegian Institute of Public Health to evaluate different allocation strategies for COVID-19 vaccines and guide policy making. Methodology is well grounded, with good integration between modeling efforts and calibration using good quality data, the sources of which are (almost) all clearly documented.

## Response: We appreciate the reviewer's feedback and have made revisions. Please find below our point-to-point responses.

I only have two big concerns regarding the work (outlined in points 3 and 4 below), but I believe they should not impede publication as long as they are properly addressed. Points 1 and 2 outline minor improvements.

1) I commend the authors for the good quality of the text and figures, and my only request in this front is to please use the appropriate command for starting quotations: the first mark is flipped as in line 202 and in the Acknowledgments section; please check if I missed other uses. It also would be nice (but not essential) if Fig 1 followed the color scheme for ABM used in Fig 6, since all the other figures are tastefully colored.

## • We have corrected the two quotations.

We vaccinate individuals who are not infected at the time of vaccination and assume that the vaccines are <u>"leaky"</u> (leaky", meaning that the vaccine effect of both the first 217

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## 8 Acknowledgments

The project was funded by the Research Council of Norway "."COVID-19 in Norway: A real-time analytical pipeline for preparedness, planning and response during the COVID-19 pandemic in Norway"." grant number 312721. The mobility data was collected and provided by Telenor Norway.



• We have updated Fig 1 with the same colors as Fig 6.

2) The social settings for contacts between agents need to be clarified in two instances:2.1) The "Community setting" for contacts is not properly defined as it is first mentioned;

• We have added a sentence to define "community" while it is first mentioned in Section 4.2.1.

The community contacts refer to interactions that take place outside of the 124 household, school, university, or workplace, and may include activities such as taking 125 public transportation, grocery shopping, and socializing with friends. These contacts 126 are modeled as random processes based on following a negative binomial distribution 127 to represent super-spreading events [45] and taking into consideration the age of 128 potential contacts and physical distance between cells. Relative contact rates among 129 different age groups are also considered, with the highest contact rate observed among 130 those aged 20 to 29 years according to the unpublished social contact studiestaken into 131 account based on the social contact study survey 11. To reflect real-world mobility 132 patterns, we employ a heavy-tailed distribution function based on mobility data from 133 the largest telecommunication company in Norway, Telenor [12, 34]. This function 134 results in a greater likelihood of short-distance transmission compared to long-distance 135 transmission. 136

2.2) In paragraph between lines 287 and 291, please cite source and give a brief account of the methodology that led to the proportions of infections in each of the settings explored. Moreover, the Community social setting is not listed here and you only mention "other settings"; are these "other settings" the definition for the Community setting that was missing as it was first mentioned?

• We have added a citation showing that the data were collected by Norwegian Surveillance System for Communicable Diseases (MSIS).

The IBM was additionally calibrated to fit the proportions of the four transmission 303 routes based on information provided by general practitioners regarding likely 304 transmissions and collected by Norwegian Surveillance System for Communicable 305 Diseases (MSIS) [37]. The data collected from general practitioners about the likely 306 transmission revealed that 45.1%, 9.9%, 6.238.6%, 9.9%, and 38.66.2% of cases from 307 January to July 2021 were infected within households, workplaces, schools, and other 308 settings, respectively. community, workplaces, and schools, respectively. We used these 309 proportions to establish specific weights for scaling the transmission rate in each 310 setting. 311

• We have replaced the "other settings" by "community" to be consistent throughout the entire article.

January to July 2021 were infected within households, workplaces, schools, and other settings, community, workplaces, and schools, respectively. 308

3) The authors mention that contacts are modeled based on an unpublished social contact studies (105-106).

3.1) Later on, they explain that contact are uniformly distributed for agents within household, schools, universities and workplaces, which leaves only the Community setting (which was already vague) to follow any heterogeneous contact structure. I therefore find the statements in lines (105-106) misleading as it implies data integration of observed contact patterns to a greater degree than actually performed. Again, in lines 506 and 507, the authors mention that heterogeneous contact structure was employed in all four contact settings; this clashes with their explanation that contacts were uniformly distributed in the This needs to be addressed!

## • We have added the explanation of contacts within households, schools, universities, and workplaces in Section 4.2.1.

Contacts within specific households, schools, universities, and workplaces are 137 uniformly distributed among all individuals belonging to those institutions. The 138 **IBM's structure** assumed to mix randomly. Individuals are assigned to specific 139 households and establishments based on age-structured census data, with middle-aged 140 individuals more likely to reside with their spouse and children, and the elderly often 141 living in pairs or alone. Younger individuals are assigned to schools, while adults are 142 more likely to be in workplaces. Hence, contacts within households and occupations 143 are assumed age-dependent without using an explicit contact matrix, as in the case of 144 community contacts. The IBM was originally developed to study the transmission 145 dynamics of MRSA in Norway [1] and has been adapted to model COVID-19 146 transmission, as presented in this paper. A main difference is that the current version 147 does not include hospital settings, and healthcare workers are assumed to have the 148 same contact patterns as other occupational groups. 149

3.2) Contact structured is a fundamental element of ABM, and therefore cannot be obscured. Please, address

- if there are valid reasons for this data to remain unpublished;

- if it will be published soon and give enough information for us and the readers to be able to find it later on;

- or include reasonable summary of these studies and their results in the SI (if it was already done and I missed it, please cite the appropriate section of the SI in your original lines).

• We have added the citation. The social contact study was recently published on medRxiv [https://doi.org/10.1101/2023.11.18.23298731].

Appendix. Moreover, we rely on unpublished social contact studies a social contact studies a social contact studies a social contact patterns 105 106

4) The approach to contact modeling was quite limiting, mainly because

4.1.1) if does not account for heterogeneities in the contact venues employed (different types of workplaces can have very different contact structures with terrible consequences for disease propagation like in accounts of meat processing plants in various countries);

• We did not model heterogeneous contact patterns in "workplaces" in the ABM. This was due to the lack of available data that could inform such a level of granularity. We acknowledge this limitation, recognizing that our model assumes the same pattern for all types of interactions among colleagues.

4.1.2) it does not account for multiplicity of roles of a contact venue; for example: where does a restaurant or supermarket place in your venue classification? It is certainly a very relevant social setting and their workers can be effective super spreaders, but at the same time this is not a "workplace" for their customers, so are they not meeting with the workers in your contact model? Then, how could the model hope to represent super-spreading events in these and any other setting? And If so, fundamental mechanism of social interaction which are very important for disease propagation and play a large role in indirect protection conferred by good

vaccination policies are not being captured at all and the true potential of ABMs is not being realized.

- In the ABM, interactions in "workplaces" pertain to transmissions between colleagues, constituting a smaller fraction, about one-tenth of all transmissions.
- On the other hand, interactions such as those between customers and workers are categorized as "community", as transmissions occur during activities like grocery shopping. More than one-third of all transmissions occur in these community interactions.
- We assumed that the number of contacts in the "community" follows a negative binomial distribution, representing potential super-spreading events. We have added this in Section 4.2.1.

transportation, grocery shopping, and socializing with friends. These contacts are modeled as random processes based on following a negative binomial distribution to represent super-spreading events [45] and taking into consideration the age of 128

4.1.3) the assignment of roles to agents (e.g. front line workers) in the ABM model is not described in its appropriated place (section 4.2.1) and only assumed in the Results section. How are these roles assigned, and are any other types of roles assigned to the agents? How do the roles affect contacts?

• In the ABM, we do not assign higher contact rates to healthcare workers; rather, we assume that individuals in these roles share the same contact patterns as others. Our model only prioritizes vaccination as a primary focus. We have added our assumption in Section 4.2.1.

Contacts within specific households, schools, universities, and workplaces are	137
uniformly distributed among all individuals belonging to those institutions. The	138
IBM's structure assumed to mix randomly. Individuals are assigned to specific	139
households and establishments based on age-structured census data, with middle-aged	140
individuals more likely to reside with their spouse and children, and the elderly often	141
living in pairs or alone. Younger individuals are assigned to schools, while adults are	142
more likely to be in workplaces. Hence, contacts within households and occupations	143
are assumed age-dependent without using an explicit contact matrix, as in the case of	144
community contacts. The IBM was originally developed to study the transmission	145
dynamics of MRSA in Norway [1] and has been adapted to model COVID-19	146
transmission, as presented in this paper. A main difference is that the current version	147
does not include hospital settings, and healthcare workers are assumed to have the	148
same contact patterns as other occupational groups.	149

4.2) I do not hope for a rework of the models to improve contact mechanics, and I believe that your primary intent of documenting the efforts for policy design during that pandemic needs to be respected. However, I would expect improvement in the discussion of the limitations of the contact model employed. These limitations and others you already mentioned are shared by most models and this is a point that the community needs to be better informed.

### • We have added this in Limitations.

rates as the general population in our models. In the IBM, we assumed a common	697
contact structure for work-related interactions based on census data. Consequently, we	698
did not distinguish healthcare workers and individuals employed in restaurants or	699
supermarkets from other occupational groups. Incorporating super-spreading events	700
was confined to community transmission, modeled by adherence to a negative	701
binomial distribution [45].	702

Despite these concerns, this is a very good work. I find that the project's methodology is very sober and responsible: the hypothesis made are clear, fit reasonably with the designed methodology and provide coherent and valuable guides for policymakers. I congratulate the authors for the work and hope they appreciate the points mentioned in a positive light, recommending this manuscript for publication after these improvements.

• Thank you very much for the comments.

Reviewer #2:

The authors study the effect of geographic prioritization of vaccination on the reduction of COVID-19 infections and severe outcomes, using two models. Their study provides valuable guidance for policy makers involved in making decisions about vaccination strategies. The paper is well written and the models are described in detail. I only have a few minor comments that need to be addressed before I can recommend the paper for publication.

# Response: We appreciate the reviewer's feedback and have made revisions. Please find below our point-to-point responses.

• Line 392: The following results shows -> ... show

• We have updated it.

outcomes, respectively, compared to the baseline strategy. The following results shows the mean values and their 95% confidence intervals (95%CIs) using  $\pm 1.96 \frac{\sigma}{\sqrt{N}}$ , 409

• Line 393: 95% confidence intervals for 1000 simulations. Can be only used if the distribution is (close to) symmetric/normal. In case of a skewed distribution, it's better to report median and IQR. Did you check whether the distribution was symmetric or skewed?

Same question for other parts of the paper where a 95% confidence interval was used.
We have confirmed the symmetry and normal distribution of RRR by visually verifying it through Q-Q (quantile-quantile) plots, where the data points align closely with a straight line.



- S1.1.4. How did you obtain the percentages 40% asymptomatic / 60% pre-symptomatic?
  - We have added a sentence with a citation. The percentage is the assumption throughout our analyses during the pandemic, and the number aligns with a systematic review [http://dx.doi.org/10.1001/jamanetworkopen.2021.37257].

symptomatic is 60%. This is the assumption throughout our analyses during the pandemic, and the 40% asymptomatic fraction aligns with findings from a systematic review 13. Symptomatic individuals may either recover or die, as shown

#### • S1.2.2. of of travelers -> of travelers

#### • We have updated it.

#### S1.2.2 Regional contact matrix

The regional contact matrix is based on mobility data from Telenor 12 aggregated to the number of movements between the specified regions. We define the contact matrix such that amount of infectiousness that "leaks" "leaks" out of a region is equal to the fraction of the population who traveled out of the region in one day. If the number of of travelers from region *i* to region *j* is  $T_{ij}$  and the population in region *i* is  $P_i$ , then the regional contact matrix is given by:

### Reviewer #3:

This paper is interesting since it presents a study of vaccine allocation based on geographic strategies, which is important regarding large countries with heterogeneous densities. Several previous studies during covid-19 times have been carried out concerning prioritisation according to age in relation to different targets (transmission/deaths/etc.) but here the publication of a method to study geographical allocation of vaccine is quite a novelty. The two presented models are quite complex and robust and should be able to well capture the presented elements. The paper is very well written, with the main article containing (almost) all the important information for a wider audience, and a very complete supplementary material describing in details the two models, the assumptions, the methodology and the detailed results. For these reasons, I recommend its publication in PLOS Computational Biology.

## Response: We appreciate the reviewer's feedback and have made revisions. Please find below our point-to-point responses.

Here are some minor comments, sometimes regarding items presented in the supplementary material that could at least be mentioned in the main document for clarity:

- L105: Little additional information should already be given here regarding the origin of the social contract matrix (before the pandemic, 2017 in Norway, only mentioned in the limitations and supplementary materials)

• We have added the citation. The social contact study was recently published on medRxiv [https://doi.org/10.1101/2023.11.18.23298731].

Appendix. Moreover, we rely on unpublished social contact studies a social contact studies a social contact studies a social contact patterns 105 to determine the heterogeneity of contact patterns 106

- L284/Fig1caption/etc.: It's is not specified in the main document how the uncertainty is generated, especially concerning estimated parameters. In the supplementary material, there is the mention of selecting the best 10 sets of parameters of a best fit method, which should be mentioned somewhere in the main text. Are the 95% confidence intervals based on those 10 sets (not so logical) ? Is it with additional stochastic realisations ?

- The uncertainty is based on a total of 1000 simulations, which are generated by 100 stochastic seeds for each of the best 10 sets. In Section 4.7, we wrote "We generated 100 realizations corresponding to the 100 stochastic seeds for each of 10 calibrated parameter sets. ".
- In Figures 1 and 6, we have updated the captions.

Fig 1. The calibrated individual-based model (IBM) and meta-population model (MPM) with data in the actual vaccination strategy. The upper and lower panels show the IBM and MPM, respectively. A and C: The time series data of all ages. The lines show the model fits with their 50 and 95% prediction intervals represented by gray colored areas based on 1000 simulations. The dots show the observed data. B and D: The age distribution of total counts. The gray Each of the 1000 colored bars show shows the counts of each from one simulation and the full bars with black borders show the mean of all simulations. The data are shown in dots with their exact numbers. During the whole period, there were 86289 confirmed cases, 2397 hospital admissions, 466 ICU admissions, and 266 deaths registered.

Fig 6. The comparison of two models for the optimal strategy for minimizing infections. A: The time series data of all ages. The lines show the model fits with their 95% prediction intervals represented by colored areas based on 1000 simulations. B: The age distribution of total counts. The black lines show the median values, and the colored areas show the 95% prediction intervals based on 1000 simulations.

- Table 1/Fig3/L558: There is a clear difference concerning optimal strategies with deaths target between the two models, with only a very short comment "likely due to slightly different population compositions" in the discussion section. Might be good to have a broader analysis here. What could be the elements that could be responsible for this difference? calibration? internal model differences? other things?

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### • We have added a part to explain the differences in Discussion.

## 6.3 Deaths

To minimize deaths, an early and geographically extended prioritization encompassing 576 21-34 municipalities comprising approximately 30% of the Norwegian population 577 (alongside approximately 10 Neutral municipalities representing approximately 20% of 578 the Norwegian population) and a more moderate level of priority, approximately 579 doubling their vaccine doses, yielded the most favorable outcomes. The optimal 580 strategies differed somewhat slightly differed between the two models, likely due to 581 slightly different population compositions. The due to variations in population 582 compositions and the geographic breakdown of the country. The IBM modeled all 356 583 municipalities, one-year age groups and different settings of transmission, while the 584 MPM was limited to a maximum of 15 geographic regions and 9 ten-year age groups. 585 These distinctions also affect the initial conditions and calibration process, resulting in 586 different outcomes in the two models. Due to the exponential increase in death 587 probabilities with age, even small changes in the elderly population led to noticeable 588 differences in the resulting strategies. The results highlight the importance of 589 determining the primary purpose of the vaccination program. In Norway, the 590 government appointed an ethics committee that concluded a vaccination program aimed 591 at minimizing the number of deaths should be chosen  $\overline{[62]}$ . As we demonstrate, this 592 leads to a significantly different optimal strategy than if the objective were to reduce 593 hospitalizations, for instance. Moreover, we anticipate that minimizing 594 disability-adjusted or quality-adjusted life year lost would also necessitate more 595 geographic prioritization, rather than solely focusing on deaths [63]. 596

- Conclusion and Discussion section: This section is one continuous block of text that is far too long. It would be more readable if it were divided into thematic subsections.

### • We have split it into 8 subsections.



- References: There is unnecessary duplication of the full bibliography, hence references in the main article only mentioned in the supplementary material. The main bibliography of the article should be reduced to the items cited.

• We have updated the bibliography in the new pdf files.