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## REJOINDER

*(Discussion on the paper by Nunes, Caetano, Antunes and Dias)*

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The authors would like to thank the commentaries from Bekker-Nielsen Dunbar and Held ([2]) and from Gomes ([3]) to their article *Statistics in times of pandemics: the role of statistical and epidemiological methods during the COVID-19 emergency*, and for sharing their experience, knowledge and work in the response to the COVID-19 epidemic.

In their commentary, Bekker-Nielsen Dunbar and Held ([2]) introduced the time-series framework of endemic-epidemic models, showing the benefit of this approach to resolve and overcome many of the challenges identified during the analysis of surveillance data and epidemic dynamics modelling. They also share their experience using Switzerland's data and present the work developed under the SUSPend project, that aims at bring knowledge on essentials components of the epidemic transmission, for its control and mitigation.

The same is revealed in the Gomes ([3]) commentary that, based on new mathematical modelling approaches, suggests that by introducing different levels of heterogeneity in the immunity or susceptibility of the population, the size of the epidemics and its conclusion can change dramatically.

Considering the four main components of infectious diseases transmission, summarised in the acronym DOTS (Duration of infectious period, Opportunities of transmission, probability of Transmission upon contact and Susceptibility), as described by Adam Kucharski from the London School of Hygiene and Tropical Medicine ([4]), it is possible to verify that, Bekker-Nielsen Dunbar and Held ([2]) and Gomes ([3]), cover, in their works, the majority of

these components. The understanding of these four components is crucial for the epidemic control and mitigation.

Gomes ([3]) describe works developed with colleagues ([1]), on the role that the heterogeneity in population susceptibility and connectivity play on the SARS-CoV-2 epidemic dynamics. They propose that by using classical mathematical disease transmission models, that assume everyone is equally susceptible, one can overestimate the Herd Immunity Threshold (HIT). Their results show that by increasing the heterogeneity of the population susceptibility, the HIT could be as low as 10%. Which means that the COVID-19 epidemic could be resolved during the 2020–21 autumn–winter season. This is an important and hopeful hypothesis, however it cannot be used as the base model for planning and decision making during the public health emergency, where it is necessary to plan for the worst and hope for the best.

The works described by Bekker-Nielsen Dunbar and Held ([2]), namely in the project SUSPend, look more deeply into the role of the Opportunities of transmission, and indirectly into the component probability of Transmission upon contact, by introducing in their models population contact matrices to model COVID-19 disease dynamics. One important feature is the possibility of modelling the changes in population contacts as a function of time, by allowing the introduction of time-dependent contact matrices. Modelling these components and measuring their impact on the disease transmission is of utmost importance, given that a relevant part of Non Pharmaceutical Interventions (NPI), recommended by Public Health Authorities, are: incentivizing social distancing, use of mask and respiratory hygiene. This pandemic has shown to us the capability of NPI, and their ability to interrupted or reduce infection transmission, given that they can be implemented at levels that do not suspend the needed social interaction and the economy.

Finally, the last component of DOTS is the Duration of infectiousness that was not directly discussed in the commentaries of Bekker-Nielsen Dunbar and Held ([2]) and Gomes ([3]). This component relates to the number of infectious individuals present in the general population, that are not isolated or in a hospital, and their infectious period. The lower the number of infectious individuals and the shorter their infectious period, results in lower transmissibility of the infection. The reduction of the transmission in this component it is in part achievable by the early identification of infection cases, its quick isolation and quarantine of the closer contacts. A group of mathematical modellers from Universidade de Trás-dos-Montes, Faculdade de Ciências e Tecnologia da Universidade NOVA de Lisboa and the Instituto Nacional de Saúde Dr. Ricardo Jorge are currently developing an age-structured SEIR model that accounts for different levels of contact tracing and symptomatic cases identification. This model is being developed under the project COVID-19 in-CTRL funded by Fundação para a Ciência e Tecnologia, under the program RESEARCH4COVID ([5]). The aim of this project is to evaluate the necessary coverage of SARS-CoV-2 symptomatic cases that need to be identified by public health teams, and the proportion of close contacts that need to be traced in order to reduce the effective reproduction number below 1.

As a final note, the authors would like to emphasize the important role that previous statistical and mathematical modelling of infectious diseases research had in the scientific response during the emergency of COVID-19. Previous developments, including open source R packages like the ones made available by R Epidemics Consortium (RECON) ([5]), or the ones described in the Bekker-Nielsen Dunbar and Held ([2]) commentary, like the surveillance R ([6, 7]) package, were of invaluable importance during all the phases of this pandemic.

In fact, it has shown the benefit of sharing knowledge and resources in the scope of enhancing the global response to current and future pandemics.

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