Monitoring Public Behavior During a Pandemic Using Surveys: Proof-of-Concept Via Epidemic Modelling

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Abstract

This brief report studies the link between behavioural changes as assessed through surveys and the time-varying reproduction number R_t (the average number of secondary infections caused by a single infected person) during the second wave of the COVID-19 pandemic in Denmark from 10-November-2020 to 01-February-2021. We find that a survey-based overall number of contacts is a good predictor for the dynamics of the second wave. We further infer that the dominant contribution comes from self-reported contacts to stranger, i.e. physically close encounters for more than 15 minutes with people that do not belong to the groups of friends, families or colleagues. Note that the report has not been peer-reviewed.

1 Introduction

Pandemic management is a balancing act. When an outbreak of infections flare up, governments and authorities need to impose restrictions and recommendations on society that are carefully calibrated to the situation. On the one hand, during the corona pandemic, such non-pharmaceutical interventions have considerable benefits by changing the dominant transmission route - close contacts between people - via the incentives and information they provide. On the other hand, these interventions have considerable costs in the form of negative externalities relating to the economy and mental health. Given this, authorities need to activate interventions that are just sufficient to control an incoming wave of infections.

This balancing act puts authorities and governments in need of information to calibrate the level of restrictions. They cannot just send out information about restrictions and recommendations. They also need to continuously receive information about the effectiveness of those restrictions and recommendations. An obvious source of information is directly related to the epidemic such as the number of infection cases, hospitalizations and deaths. Yet, without a capacity, infrastructure and public willingness for widespread testing, infection cases are difficult to monitor and changes in the public's motivation to get tested creates problems when making comparisons over time. Furthermore, there is a significant lag between the onset of

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interventions and hospitalizations and death counts, which imply that it is difficult to calibrate the interventions on the basis of such information. Consequently, researchers, authorities and governments worldwide have complemented epidemiological information with information on the direct target of the interventions: Behavior.

To quantify and monitor close contacts between people, research and public health institutions have relied heavily on proxies in the form of mobility data. This data quantifies the population's movement patterns and is unobtrusively obtained from people's smart phones and provided to researchers and governments via private companies such as Google [1]. This reliance, however, can and have raised concerns. First, it implies that pandemic management and research relies on the willingness of private companies to share information during a critical crisis. Second, citizens themselves may be concerned about privacy issues related to the sharing of phone data between companies and authorities, especially as citizens may not remember that they have consented to this sharing as part of their general acceptance of terms and services. Given the importance of public trust for successful pandemic management, such concerns - if widespread - can complicate pandemic control. Third, the data from companies such as Google, Facebook and local phone companies may not be representative of the population of interest: The entire population of the country. Rather than being invited on the basis of traditional sampling methods, people opt-in to the services of different companies and, hence, the data from any single company is likely a biased sample. Fourth, the movements of people in society as captured by mobility data is only a proxy of the quantity of interest: Actual close encounters between individuals that drive the pandemic. While the two former problems are related to reliance on private companies, the two former problems are related to the quality of the data provided by those companies. All of the problems, however, influence the ability of the authorities to effectively management an epidemic.

In this report, we therefore assess an alternative source of information about public behavior: Nationally representative surveys of the adult population. In principle, such surveys could alleviate the problems identified relating to the collection and validity of mobility data. Survey research is a centuries old low-cost methodology that can be utilized by public actors and that relies on well-established procedures for obtaining representative information on private behaviors in voluntary and anonymous ways. While the initial goal of this use of surveys is simply to calibrate the introduction of new restrictions to levels of compliance, a further promise of surveys is that they - given their voluntary dimension - can increase rather than decrease public trust. Thus, due to their voluntary nature, the use of surveys turn pandemic management into an outcome that is co-produced by authorities and citizens in collaboration and provide citizens with a channel of informing authorities about both their level of compliance but also the felt burden of restrictions and recommendations such that these can be alleviated as much as possible.

At the same time, data from surveys come with their own methodological complications. As documented by decades of research, people may not accurately report on their own behavior. Survey answers during the pandemic may be biased by, for example, self-presentational concerns and inaccurate memory. While research on survey reports of behavior during the pandemic suggests that self-presentational concerns may not affect survey estimates [6], memory biases may [4]. Even with such biases, however, surveys may be fully capable to serve as an informative monitoring tool. The key quantity to monitor is thus *changes* in *aggregate* behavior over time. Accordingly, if reporting biases are randomly distributed within the population, aggregation will provide an unbiased estimate. Even if this is not the case, changes in the survey data will still accurately reflect changes in population behavior as long as reporting biases are stable within the relevant time period.

On this basis, the purpose of the present report is to examine the degree to which survey

data provides diagnostic information about the trajectory of an unfolding epidemic. Specifically, we focus on the second wave of the corona epidemic in the fall of 2020 in Denmark. We ask whether daily representative surveys regarding the daily number of close contacts allow us to reproduce the course of this second wave.

To this end, we utilize survey data from the HOPE ("How Democracies Cope With COVID-19") research project (www.hope-project.dk). Specifically, the HOPE-project fielded an ongoing daily nationally representative survey in Denmark in mid-May 2020. The data collection continues until the end of 2021. Each day a nationally representative sample (with a daily target of N=500 complete interviews) report on their protective behavior and perceptions. Details on sampling and questions are available in [5]. In this report, we utilize survey data on the daily number of contacts, defined as being less than 2 meters away from another person for at least 15 minutes. The daily number of contacts are assessed separately for (a) family members outside the household, (b) friends and acquaintances, (c) colleagues and (d) strangers. We use data from 10-November-2020 to 01-February-2021, which is the key period of the second wave of infections with the corona-virus. By focusing on the second wave, we avoid the time period of low epidemic activity which is potentially driven by localized super-spreading events [7] rather than average contact rates.

We utilize these survey data to parametrize the time-varying reproduction number R_t as a function of the contact data. Then, we extend the semi-mechanistic Bayesian model from Flaxman et al. [3, 8] to jointly model the epidemic spreading within the five regions of Denmark and thus link the behavioural survey data to the observed number of hospitalizations and serological studies [2]. Where possible, we use partial pooling of parameters to share information across regions and thus reduce region specific biases. As a result, we determine effect sizes for each region together with a grouped effect size for all of Denmark.

In the following, we will focus on two models that differ only in the choice of predictors: We parametrize R_t with (a) the total number of contacts only or (b) four independently assumed predictors, namely, contacts to friends, family, colleagues and strangers. Both models thus assume that the epidemic during the second wave is entirely driven by the number of reported contacts. More information about the data and the modelling is available in the Appendix.

2 Results

We find that both models reproduce well the second wave of hospitalizations for all regions of Denmark (see Fig. 1 and Fig. 5 in the appendix). Hence, changes in recorded contacts plausibly translate to shifts in R_t and thus serve as an early indicator of the epidemic trajectory. Additional, region specific details can be found in the appendix (Fig. 6, 7, 8, 9, 10).

In order to quantify the effect of behavioural changes, we start from a baseline value $R_t = 1$, which corresponds roughly to our observations just before the onset of the second wave, and compare the baseline to a hypothetical increase of total contacts by 100%. Assuming that only the reported behaviour causes the second wave, we find that doubling the number of contacts leads to a three-fold increase in R_t (median: 201%; 95HPDI: $[149\%, 238\%]$; see Fig. 2b). Similarly, we find that a hypothetical reduction in overall contacts by one half would result in R_t decreasing by about one third (median: 33%; 95HPDI: $[-39\%, -26\%]$; see Fig. 2a) relative to the baseline value of $R_t = 1$. The different effect sizes with respect to an increase or decrease of contacts can be easily understood by the fact that the reproduction number is positive by definition and thus we observe a saturation effect when decreasing R_t from a relatively low baseline value of $R_t = 1$.

We also study the relative contribution of contacts to family, colleagues, friends and strangers. Despite large regional variations in some cases, we find that "contacts to strangers"
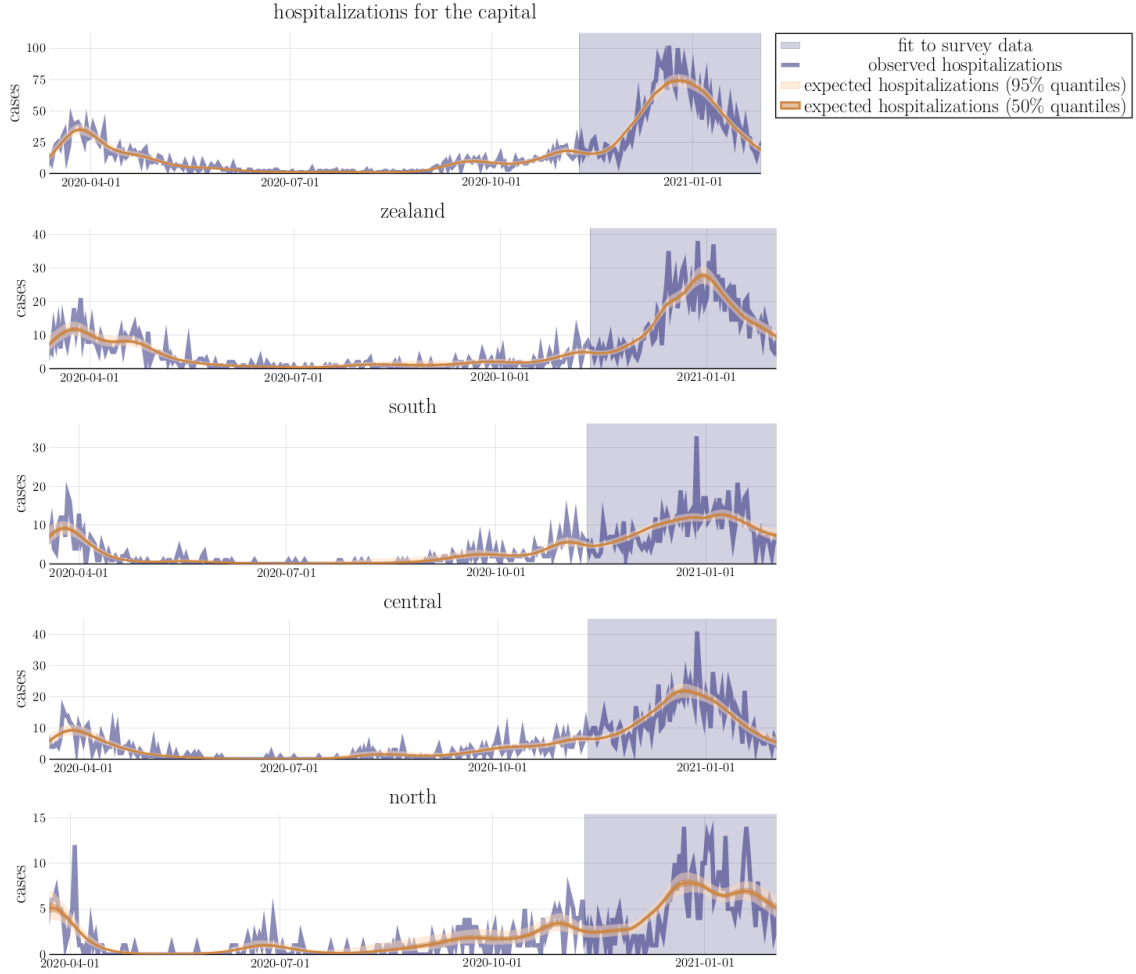
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Figure 1: Comparison between observed hospitalizations and the posterior average as blue and orange lines, respectively. The shaded area marks the second wave where the total number of contacts parametrizes R_t.

is the dominant factor across all regions (see Fig. 3). Hence, according to our model "contacts to strangers" drives the second wave if we assume no factors other than reported contacts.

3 Conclusion

In this study, we focused on two research question, namely (a) Can the number of contacts between individuals explain the epidemic trajectory during the second wave? and (b) Which type of contacts drives the pandemic?

We found that the total number of contacts, i.e. a single predictor, for each region of Denmark reproduces well the observed hospitalizations. This observation adds confidence to our hypothesis that reported contacts reflect the true number of contacts that drive the pandemic. Hence, behavioural changes as observed in the HOPE data plausibly explain parts of the epidemic dynamic.

A closer look at different contact types revealed that the reported number of contacts to strangers has the strongest effect on transmission. This observation is in line with a recent study that found random interactions to be the main transmission route as opposed to repeated interactions within families, friends or among colleagues [7]. A plausible explanation is that super-spreading events within small communities cannot develop to the same extend as in
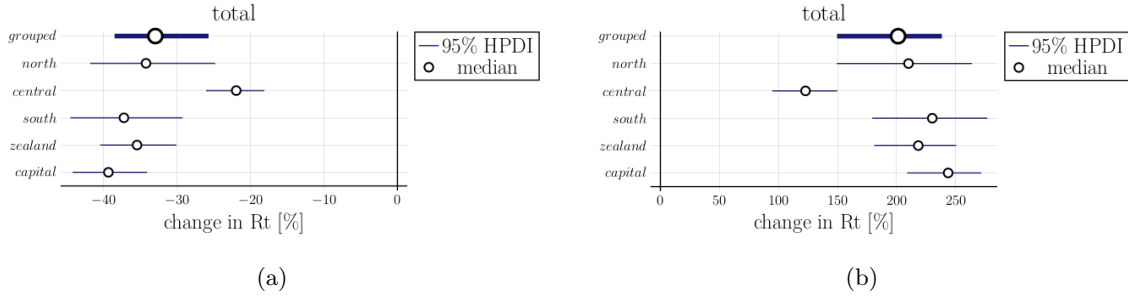
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Figure 2: Relative change in R_t after a change in the number of contacts by -50% and $+100\%$ in panel (a) and (b), respectively. We summarize the posterior effect size with a mean and the 95% highest posterior density interval (HPDI) for each region and the grouped effect size of all of Denmark.

crowded groups of strangers.

A potential intervention strategy focusing on contacts to strangers could, however, be misleading because different contact types are causally connected. For example, contacts to colleagues will increase when offices open up after a lockdown but, so does contacts to strangers as people use public transport to reach their work place.

Separating causal effects will be part of our future investigations. This will also include mediating factors such as awareness to social distancing and usage of masks as well as the role of seasonal effects and the interdependence with mobility.
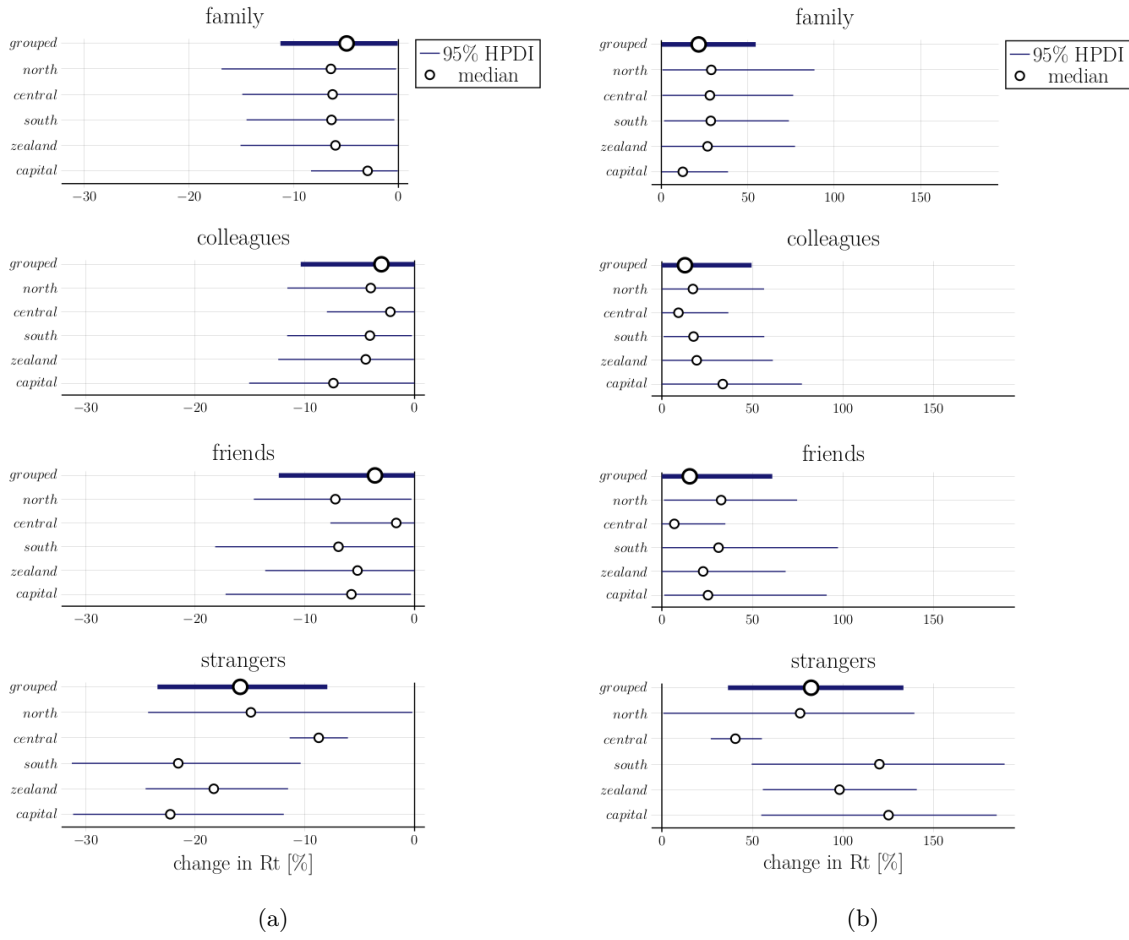
Figure 3: As in Fig. 2 but with contacts broken down by family, colleagues, friends and strangers.

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A   Appendix

A.1   Model specifics

The schematic overview in Fig. 4 gives a rough idea on how information flows through the different levels of our hierachical model: From the number of hospitalizations (level 1), we derive the unobserved number of past infections (level 2). These infections are them-self a consequence of earlier cases and the time-varying reproduction number R_t (level 3). At this level, we distinguish two time periods. (a) From the beginning of the pandemic up to 10 November 2020, i.e. just before the onset of the second wave, we track weekly changes in the reproduction number with a latent random walk model (level 4a). In order to improve the robustness of our model, we pool parameters including the basic reproduction number R_0 and the number of initially infected individuals across all regions (level 5a). (b) From the onset to the end of the second wave on 01 February 2021, we derive the daily reproduction number from a linear combination of contacts to family, colleagues, friends and strangers (level 4c). Here, we refer to effect size as parameters that translate a change in contacts to a corresponding change in R_t. Finally, we pool the estimates to obtain average effect sizes across all regions (level 5b).
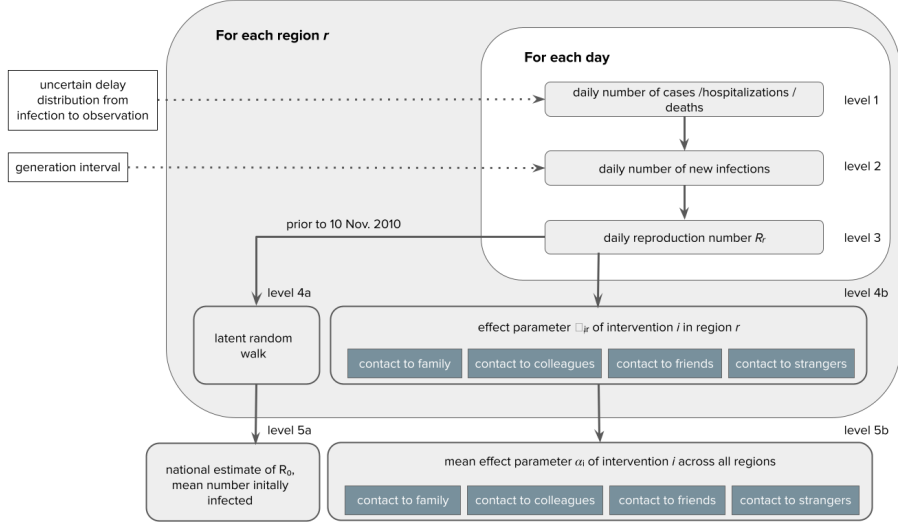
Figure 4: Schematic overview of the epidemic model.

A.2 Data

We are relying on a survey panel with approx. 500 participants every day. Respondents are asked to remember the number of people they have been physically close to past 24 hours. Physically close is here understood to be closer than 1 meters for at least 15 minutes. The question is further split into contacts with friends, family, colleagues and strangers.

As a basic pre-processing step, we remove outliers and take the daily average as predictors for the epidemic model.

A.3 Detailed inference results
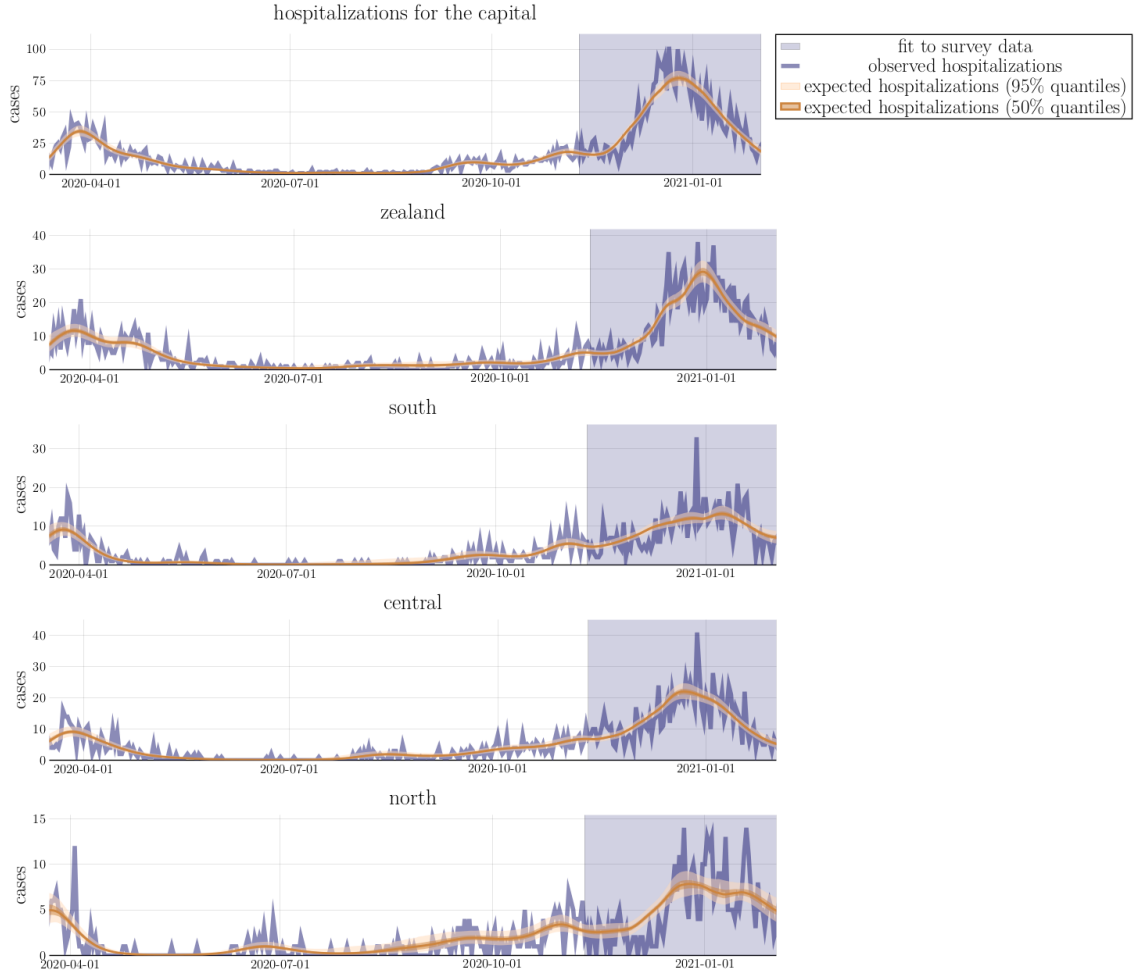
Figure 5: Comparison between observed hospitalizations and the posterior average as blue and orange lines, respectively. The shaded area marks the second wave where we parametrize R_t with a linear combination of contacts to friends, family, colleagues and strangers.
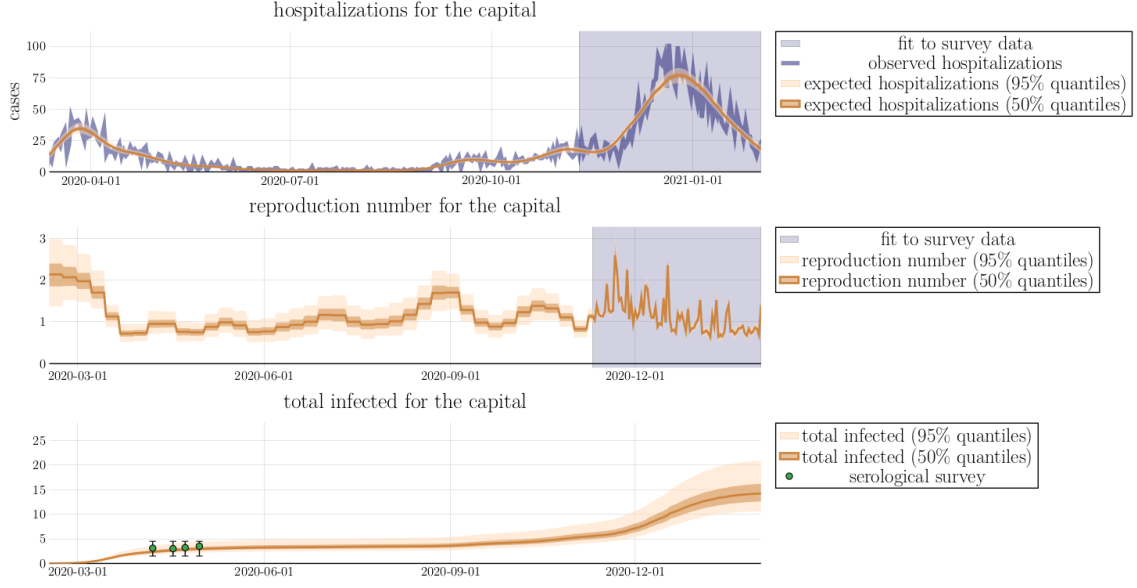
Figure 6: Inference summary for the capital region. Top panel: comparison between observed hospitalizations and the estimated mean value. Middle panel: inferred reproduction number. We use a random walk model to track changes up 10-November-2020. The shaded regions marks the period, where R_t is parametrized by a linear combination of contacts to friends, family, colleagues and strangers. Bottom panel: Posterior estimate of the total number of infected with observations from the serological study [2]
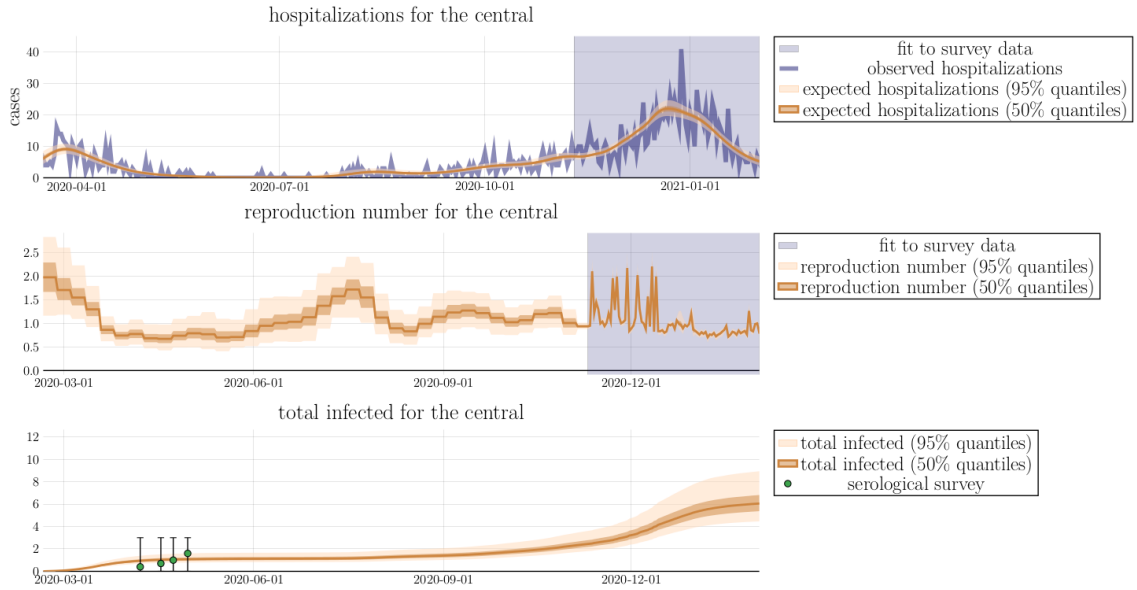

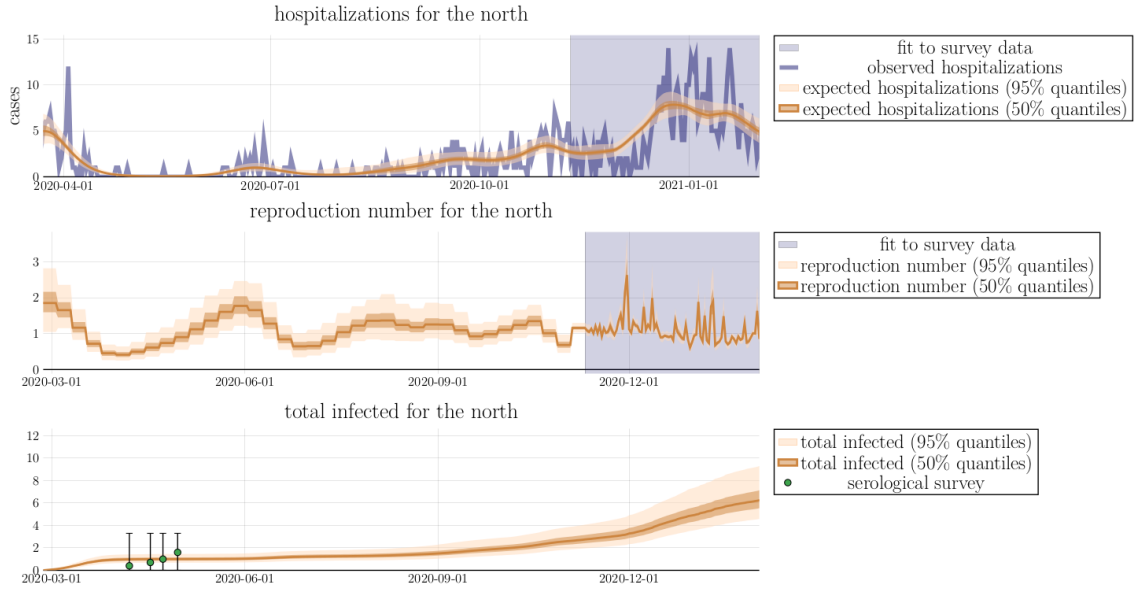Figure 7: As in Fig. 6, but for the central region.
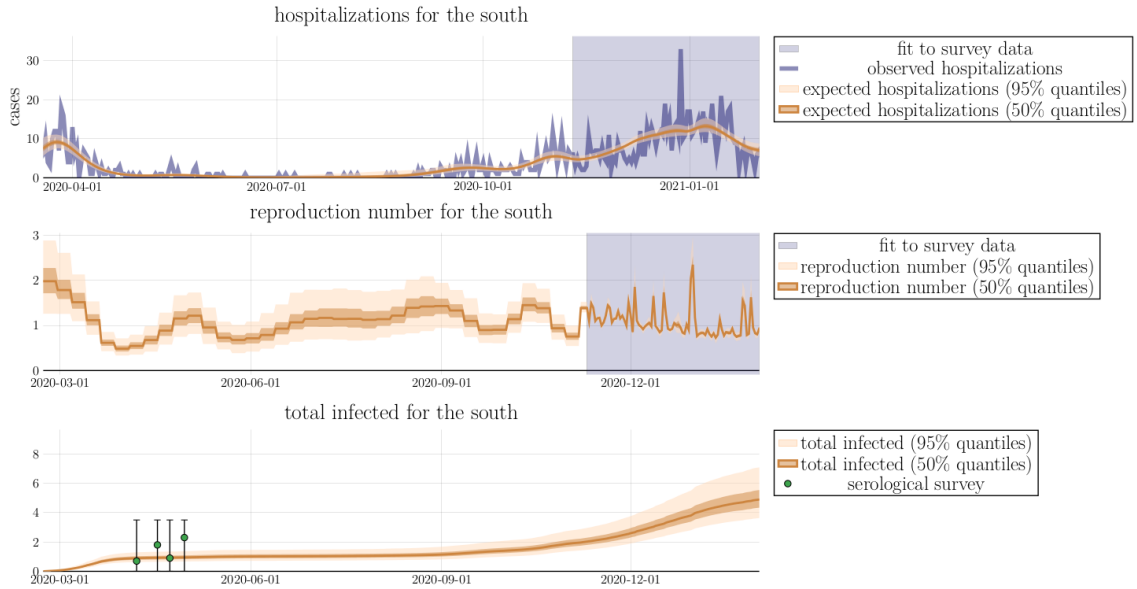
Figure 8: As in Fig. 6, for the northern region.
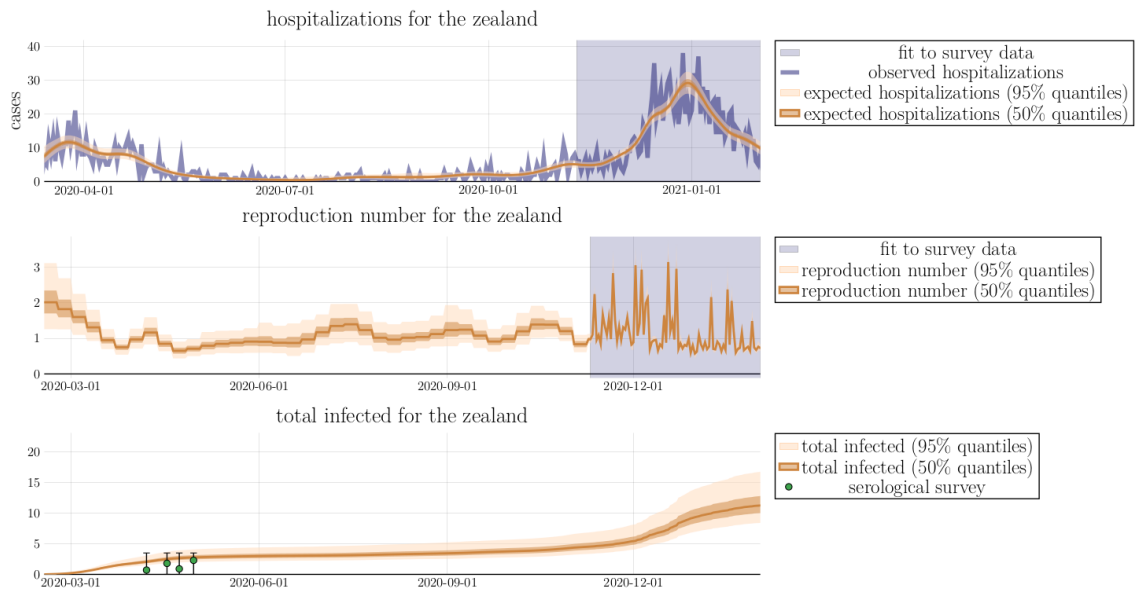

Figure 9: As in Fig. 6, for the southern region.

Figure 10: As in Fig. 6, for the region of Zealand.