

Characterizing super-spreading events and age-specific infectivity of COVID-19 transmission in Georgia, USA

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Abstract

As the current COVID-19 pandemic continues to impact countries around the globe, refining our understanding of its transmission dynamics and the effectiveness of interventions is imperative. In particular, it is essential to obtain a firmer grasp on the effect of social distancing, potential individual-level heterogeneities in transmission such as age-specific infectivity, and impact of super-spreading. To this end, it is important to exploit multiple data streams that are becoming abundantly available during the pandemic. In this paper, we formulate an individual-level spatiotemporal mechanistic framework to statistically integrate case data with geo-location data and aggregate mobility data, enabling a more granular understanding of the transmission dynamics of COVID-19. We analyze reported cases from surveillance data, between March and early May 2020, in five (urban and rural) counties in the State of Georgia USA. We estimate natural history parameters of COVID-19 and infer unobserved quantities including infection times and transmission paths using Bayesian data-augmentation techniques. First, our results show that the overall median reproductive number was 2.88 (with 95% C.I. [1.85, 4.9]) before the state-wide shelter-in-place order issued in early April, and the effective reproductive number was reduced to below 1 about two weeks by the order. Super-spreading appears to be widespread across space and time, and it may have a particularly important role in driving the outbreak in rural area and an increasing importance towards later stages of outbreaks in both urban and rural settings. Overall, about 2% of cases may have directly infected 20% of all infections. We estimate that the infected children and younger adults (<60 years old) may be 2.38 [1.30, 3.51] times more transmissible than infected elderly (≥ 60), and the former may be the main driver of super-spreading. Through the synthesis of multiple data streams using our transmission modelling framework, our results enforce and improve our understanding of the natural history and transmission dynamics of COVID-19. More importantly, we reveal the roles of age-specific infectivity and characterize systematic variations and associated risk factors of super-spreading. These have important implications for the planning of relaxing social distancing and, more generally, designing optimal control measures.

1 Introduction

The current COVID-19 pandemic continues to spread and impact countries across the globe. There is still much scope for mapping out the whole spectrum of the epidemiology and ecology of this novel virus. In particular, understanding of heterogeneities in transmission, which is essential for devising effective targeted control measures, is still limited. For instance, much is unknown about the variation of infectivity among different age groups [1, 2, 3]. Also, while super-spreading events have been documented, its impact and variation over space and time and associated risk factors have not yet been systematically characterized [1, 4, 5, 6].

For this reason, it is crucial to exploit the growing availability of multiple data streams during the pandemic, from which we may obtain a more comprehensive picture of the transmission dynamics of COVID-19. For example, shelter-in-place order could change the movement pattern (e.g. reduced

distance of travel) of a population. Such a change needs to be taken into account as movement is a key factor that shapes transmission [7]. Failing to capture this change would also bias the estimates of key model parameters including intervention efficacy and transmissibility parameters that are correlated with movement [8, 9, 10]. De-identified mobility data from mobile phone users have been made available to state governments and research institutes through partnerships with private companies such as Facebook. Integration of such mobility data with surveillance data would allow us to account for the change in movement, and therefore more accurately infer the transmission dynamics [7, 8, 10, 11]. Geo-spatial location data and detailed spatial distribution of population are also important for capturing heterogeneous mixing in space [8, 9, 10]. A key step is to enable individual-level model inference that can properly synthesize these datastreams, which would go beyond most efforts so far that have focused on aggregated level dynamics [2, 11, 12].

In this paper, building on a previous framework we developed for modelling Ebola outbreaks in Western Africa [8, 9], we formulate an individual-level space-time stochastic model that describes the transmission of COVID-19 and captures the impact of state-wide social distancing measure in the state of Georgia, USA. Our model mechanistically integrates detailed individual-level surveillance data, geo-spatial location data and highly-resolved population density (grid-)data, and aggregate mobility data (see *Study Data*). We estimate model parameters and unobserved model quantities including infection times and transmission paths using Bayesian data-augmentation techniques in the framework of Markov Chain Monte Carlo (MCMC) (see *Materials and Methods*). Our individual-level modelling framework also allows us to compute population-level epidemiological parameter such as the basic reproductive number R_0 and quantify the degree of super-spreading over space and time.

2 Study Data

We analyzed a rich set of COVID-19 surveillance data collected by the Georgia Department of Public Health, between March 1, 2020, and May 3, 2020, in five counties which had the largest numbers of cases. These counties include four counties Cobb, Dekalb, Fulton and Gwinnett in urban area, and one rural Dougherty county. This dataset contains demographic information of 9,559 symptomatic cases which include age, sex and race, and symptom onset times. It also contains geo-location of the residence of cases. Highly-resolved population-density data over 100×100 meter grids are obtained from <http://www.worldpop.org.uk>, and are used to modulate the spatial spread of the virus (see *Materials and Methods*). Aggregate mobility data are used to characterize change of movement before and after the implementation of state-wide social distancing measure. Specifically, we used high-volume mobility data accessed through Facebook’s Data for Good program [13]. These data represent Facebook users in Georgia who have location services enabled on their mobile device. These data provide information on the number of ‘trips’ (and trip distance) that occurred daily among users. A ‘trip’ is defined as a directional vector starting at the location where an individual spent most of their time during the previous 8-hour period and ending at the location where the same individual spent most of their time during the current 8-hour period.

3 Results

Natural History Parameters and Effectiveness of Social Distancing

We estimate that the median value of R_0 across five counties was overall between 2.88 with 95% C.I. [1.85, 4.9] before the intervention (i.e. shelter-in-place order). Dougherty county in the rural area had the largest prior-intervention R_0 (4.82 [4.31, 4.91]) and time-varying effective reproductive number R_{eff} at the earlier stage in March 2020 (Figure 1). Our results suggest the shelter-in-place order was effective, and in all the counties the R_{eff} declined below 1 in about two to three weeks since the intervention. It is also worth noting that R_{eff} appears to begin decline one to two weeks before shelter-in-place order in urban areas and earlier in Dougherty. We also estimate that the incubation period (i.e. waiting time from infection to symptoms onset) has a median value 6.34 days [5.17, 7.22]. These estimates are largely consistent with the literature [14, 15].

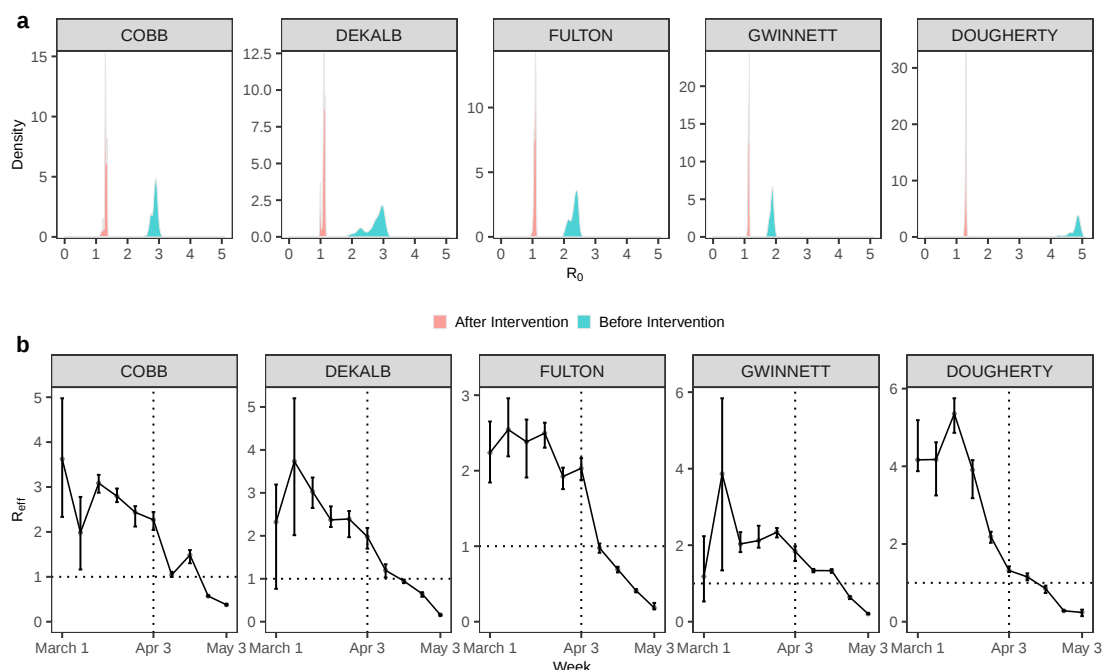


Figure 1: Posterior distribution of basic reproductive number R_0 and the effective reproductive number R_{eff} , before and after the implementation of state-wide shelter-in-place order on April 3, 2020. Errorbars represent 95% credible interval.

Systematic Characterization of Super-spreading

Super-spreading refers a phenomenon where certain individuals disproportionately infect a large number of secondary cases relative to an “average” infectious individual (whose infectivity may be well-represented by R_0). This phenomenon plays a key role in driving the spread of many pathogens including MERS and Ebola [8, 16]. A common measure of the degree of super-spreading is the dispersion parameter k , assuming that the distribution of the *offspring* (i.e. number of secondary cases generated) is negative binomial with variance $\sigma^2 = \mu(1 + \mu/k)$ where μ is the mean [16]. Generally speaking, a lower k corresponds to a higher degree of super-spreading; and k less than 1 implies substantial super-spreading. Our framework infers the transmission paths among all cases and therefore naturally generates the offspring distribution of each case (see *Materials and Methods*).

While super-spreading of COVID-19 has been observed [1, 4, 5, 6], systematic characterization of its impact and variation (e.g., over time and space) and associated risk factors is lacking. Our results (Figure 2a) suggest that super-spreading is a ubiquitous feature during different periods of the outbreak. Super-spreading may have a major impact for the rural area (Dougherty) during earlier periods – it has the lowest k in earlier periods among all counties (0.43 [0.39, 0.47] and 0.38 [0.34, 0.43]). Dougherty county has a disproportionately large outbreak compared to other more populated counties – having about only $\frac{1}{8}$ of the population of Cobb county (about 760,000), it has a comparable number of reported cases (1,628). Such an anomaly may be a consequence of the significant super-spreading and large (prior-intervention) R_0 in Dougherty (Figure 1a). This is also consistent with the evidence of super-spreading events due to a funeral in the area [17]. The increasing significance of super-spreading over time also highlights the importance of maintaining social distancing measures that may curtail close contacts (e.g. gatherings with densely packed crowds). Overall, top 2% of cases (that generate highest number of offsprings) are responsible directly for about 20% of the total infections. Our results also show that the younger infectees (children and younger adults who are <60) tends to the main driver of super-spreading (Figure 2b), which is also consistent with our estimates of higher infectivity in this age group (see *Age-specific Infectivity*).

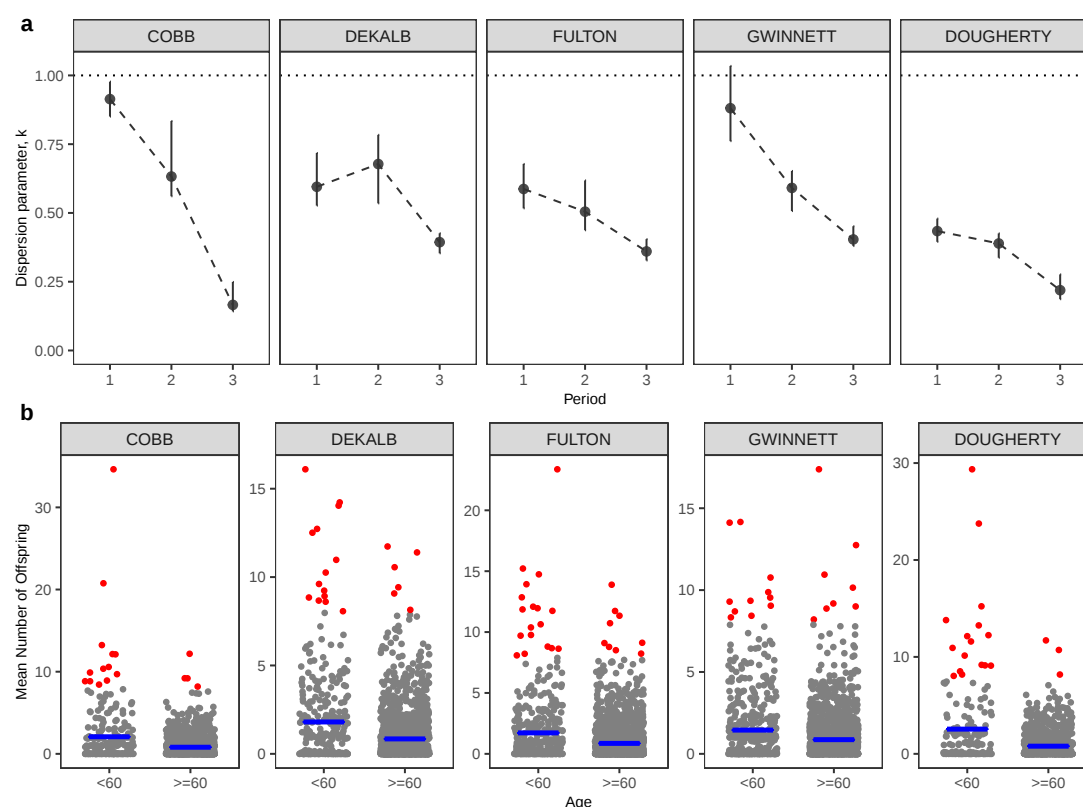


Figure 2: (a) Degree of super-spreading quantified by the dispersion parameter k (where $k < 1$ indicates significant super-spreading) during different periods of the outbreak. Let T be the day of announcing shelter-in-place order: period 1 is time $t < T$, period 2 is $[T, T + 14)$ and finally period 3 is $t > T + 14$. Overall, about top 2% of cases (that have highest mean number of offsprings) directly infected 20% of the total infections. (b) Mean number of offsprings generated by cases in each age group. Red dots represent those case have mean offspring ≥ 8 . The younger age group (<60) tends to have more cases that produce extreme number of offsprings, and also a larger average (blue lines) of the mean number of offsprings.

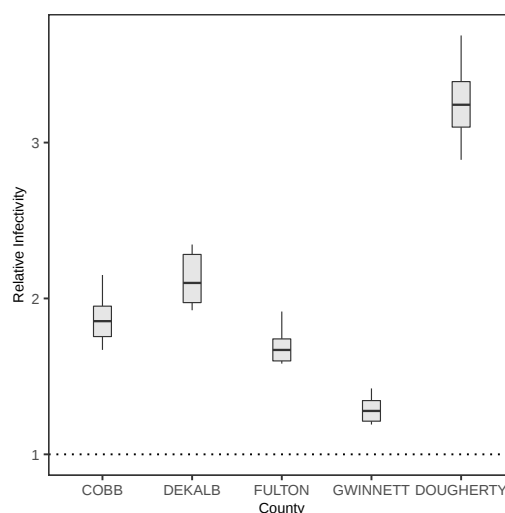


Figure 3: Infectivity of younger patients (<60) relative to the older patients (≥ 60).

3.1 Age-specific Infectivity

A markedly low proportion of cases among the younger children population is observed in the current COVID-19 pandemic, indicating heterogeneity of susceptibility among different age groups [3, 18, 19]. Much is unknown about the variation of infectivity among different age groups [1, 2, 3]. Our results suggest that the younger patients (children and adults who are <60) may be overall 2.38 [1.30, 3.51] times more transmissible than elderly patients (≥ 60). Due to the very small number of reported cases in children (e.g., <15), we do not consider a finer age stratification (see also *Discussion*). We also test the robustness of these results towards to under-reporting and take into account the discrepancy in the reporting rates of different age groups (see next section *Sensitivity Analysis*).

3.2 Sensitivity Analysis: Effect of Under-reported Cases

Under-reporting is ubiquitous feature of epidemiological data, and is particularly so for COVID-19 due to, in particular, a substantial number of asymptomatic cases and the lack of testings at the earlier stages of the pandemic. In particular, older people may tend to be more susceptible and develop severe symptoms, and hence have a higher probability of being reported [3, 18, 19]. Such a discrepancy in reporting rates may potentially affect our estimation of age-specific infectivity. We explore the effect of such under-reporting on our results under these probable scenarios: younger case (<60) has a probability 0.1 of being reported in March before the intervention, and this probability increases to 0.2 in April; the reporting probabilities for an elderly case are 0.3 and 0.6 in March and April respectively. Details of how to include under-reported cases are given in *Materials and Methods*. Figure 4 shows that the younger age group remains to be more infectious than the older age group. The estimated impact of super-spreading also appears to be robust: estimated overall dispersion parameter k is 0.38 for Cobb county, 0.49 for Dekalb, 0.47 for Fulton, 0.42 for Gwinnett, and 0.32 for Dougherty.

4 Discussion

Transmission dynamics of infectious diseases are often non-linear and heterogeneous over space and time. It is important to exploit available data that are relevant to describing and estimating such complex processes. A key step is to enable individual-level model inference that is able to statistically synthesize these datastreams, beyond aggregate-level dynamics [2, 11, 12]. In this paper, we incorporated multiple valuable datastreams including formal surveillance data into our individual-level spatio-temporal transmission modelling framework, achieving a more granular mechanistic understanding of the dynamics and heterogeneities in the transmission of COVID-19.

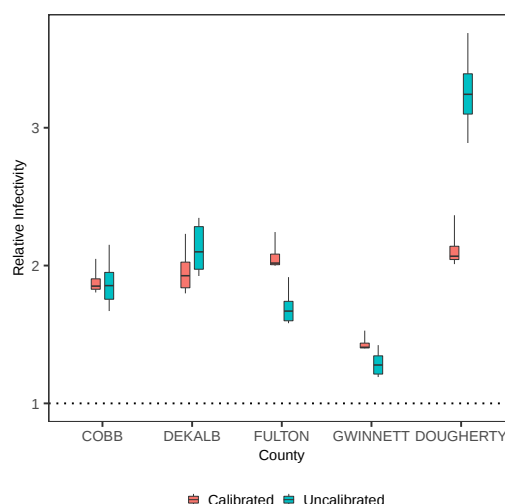


Figure 4: Infectivity of younger patients (<60) relative to the older patients (>=60), calibrated for under-reported cases.

Our results give similar estimates of important population-level epidemiological parameters such R_0 found in the literature, and reinforce the conclusion from most studies that social distancing measures are effective. This paper also advances our understanding of individual-level heterogeneities in the transmission of COVID-19, which is crucial for informing optimal interventions. We show that super-spreading is an important and ubiquitous feature throughout the pandemic, and it may have a pivotal role in driving the (large) outbreak in rural areas. The increasing significance of super-spreading over time also highlights the importance of maintaining social distancing measures that may curtail close contacts (e.g. gatherings with densely packed crowds). We also find that infected children and younger adults (<60) tend to be more transmissible and to promote super-spreading. Our results have important implications for designing more effective control measures – particularly, highlight the importance of more targeted interventions.

Our study has a number of limitations. First of all, due to the lack of widely available testings, the under-reporting rate was almost surely high during earlier phases of the pandemic. Also, severity of symptoms (and hence reporting rates) may vary among different age groups. We explore the robustness of our main results towards these possible under-reporting scenarios in the *Sensitivity Analysis*. Reassuringly, our main conclusions appears to be largely robust. Second, we only consider modelling age-specific infectivity in two age groups (<60 and >=60). The model would tend to be over-parameterized if we further break down the age groups that we have considered (e.g. by having a group for younger than 15), mainly due to imbalance of reported number of cases between age groups (particularly, markedly low reported numbers in very young population). Our current binning of age is still useful as the first group tends to be more socially active and is useful for informing the design of social distancing measures. Finally, although our analysis reveals the importance of age as a demographic risk factor of super-spreading, future work in linking them with biological factors (e.g., age-specific viral loads) may shed further light.

5 Materials and Methods

5.1 Spatio-temporal Transmission Process Model

We formulate an age-specific spatio-temporal transmission modelling framework that allows us to infer the unobserved infection times and transmission tree among cases, integrating detailed individual-level surveillance data, geo-spatial location data and highly-resolved population density (grid-)data, and aggregate mobility data. Our framework represents an extension of the models we developed *et al.* [8, 9], which were validated generally and applied successfully to dissect the transmission dynamics

of the Ebola outbreak in Western Africa between 2014-2016. This approach also allows us to infer explicitly the distribution of the *offspring* (i.e. number of secondary cases generated) of each case, hence informing the degree of super-spreading.

We estimate Θ (i.e. the parameter vector) in the Bayesian framework by sampling it from the posterior distribution $P(\Theta|\mathbf{z})$ where $\mathbf{z}$ are the data. Denoting the likelihood by $L(\Theta; \mathbf{z})$, the posterior distribution of Θ is $P(\Theta|\mathbf{z}) \propto L(\Theta; \mathbf{z})\pi(\Theta)$, where $\pi(\Theta)$ is prior distribution for Θ . Non-informative uniform priors for parameters in Θ are used. Markov chain Monte Carlo (MCMC) techniques are used to obtain the posterior distribution. The unobserved infection times and transmission network and missing symptom onset dates are also imputed in the MCMC procedure.

5.2 Sensitivity analysis: Effect of Under-reported Cases

The number of total under-reported cases m for a particular age group during a particular period is calculated as $m = n/p - n$, where n is the reported number of cases and p the probability of being reported. We consider these scenarios: a younger case (<60) has a probability 0.1 of being reported in March before the intervention, and this probability increases to 0.2 in April; the reporting probabilities for an elderly case are 0.3 and 0.6 in March and April respectively. The m cases are then assigned infection times and spatial locations according to the temporal and spatial distributions of observed cases in the time period, before merging with the observed data. The infection times and sources of infections of the m cases are also treated as unknown and are inferred in the data-augmentation procedure. Our main focus is to test how the potential discrepancy in reporting rate between age groups may impact our estimation of age-specific infectivity.

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