CRYPTIC TRANSMISSION OF SARS-CoV-2 AND THE FIRST WAVE OF THE COVID-19 PANDEMIC IN THE UNITED STATES

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INTRODUCTION

As an initial response to the emerging SARS-CoV-2 virus, many countries adopted a policy of only testing symptomatic individuals with a travel history linked to China. The narrowness of this criteria resulted in detecting only a small fraction of symptomatic cases, leaving many countries unaware of the local, domestic transmission.

We use a mechanistic modeling approach to provide a statistical analysis of the cryptic transmission phase and the ensuing first wave of the COVID-19 pandemic.

Specifically we analyze:
1. The onset of local transmission (i.e., when sustained transmission was achieved in each state)  
2. Possible sources of SARS-CoV-2 introductions to each US state and European country  
3. The burden of the first COVID-19 wave

We find that widespread transmission of SARS-CoV-2 was likely in several areas in the US by February 2020 and estimate that by early March only 1-4 cases were detected in 100 infections.

ONSET OF LOCAL TRANSMISSION

A majority of the states analyzed have a median date of onset of local transmission by early March, with many of them in February, 2020.

The posterior distribution of the onset of local transmission for the earliest 19 US states

The COVID-19 burden

Starting in March 2020, the COVID-19 epidemic trajectory in each state is driven by the establishment and timing of non-pharmaceutical interventions (NPIs) as well as by the epidemiological relevant features (i.e., population size and density, age-structure, etc.).

- The model incorporates a comprehensive set of policy interventions that modify the disease transmissibility and population mobility.
- We apply an ABC rejection analysis using as evidence the weekly reported deaths from March 22, 2020 through June 27, 2020 to analysis single state dynamics.

The estimated infection attack rates vary from 0.78%-15.2% by July 4, 2020.

CONCLUSIONS

- Reactive response strategies, such as issuing travel restrictions targeting countries only after local transmission is confirmed are highly inefficient.
- Anticipating the locations where the virus is most likely to spread to next could be instrumental in guiding enhanced testing and surveillance activities, and complement phylo-geographic inference approaches.
- The methods used in this analysis offer a blueprint to identify the most likely early spreading dynamics of emerging variants.

METHODS

GLEAM: The Global Epidemic and Mobility Model (GLEAM) is a stochastic, spatial, and age-structured metapopulation model, in the mode, that we have divided into over 3,500 geographic subpopulations constructed using a Voronoi tessellation of the Earth’s surface. Subpopulations, culminating around major transportation hubs (i.e., airports), consist of cells with a resolution of ±15 arc minutes. High resolution data are used to define the population of each cell. GLEAM integrates a human mobility layer, represented as a network, using both short-range (i.e., commuting) and long-range (i.e., inter-state) mobility data.

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Transmission Dynamics: The transmission dynamics takes place within each subpopulation and assume a classic SIR. The compartmental scheme for the disease progression, individual variation between compartments through stochastic chain binomial processes. Epidemiological parameters that govern these processes are chosen based on the most recent estimates (see table).

Calibration: We assume a start date of the epidemic in Wuhan, China; the date falls between Feb 13, 2020 and Dec 31, 2019. The model is initially calibrated using Approximate Bayesian computation rejection approach based on the observed national introductions from mainland China through Jan 21, 2020 taking into account different detection capacities among countries.

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