

Estimating short term trends in transmission and mortality rates during the Covid 19 Epidemic

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Introduction

The sudden advent of the COVID-19 pandemic provoked many political jurisdictions to advise people to “shelter in place” and to practice “social distancing”. If this advice has been effective, it should be possible to detect the effects of the advice by comparing changes in numbers of infected people and perhaps changes in transmission rates over time and between areas. The SIR models of epidemic spread divide the affected population into three compartments: Susceptible, Infected and Recovered. SIR models are usually

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expressed as coupled ordinary differential equations,

$$\frac{dS}{dt} = -\beta \frac{IS}{N} - \mu S \quad (1)$$

$$\frac{dI}{dt} = \beta \frac{IS}{N} - \mu I - \gamma I \quad (2)$$

$$\frac{dR}{dt} = -\mu R + \gamma I \quad (3)$$

$$N = S + I + R \quad (4)$$

where N is the population size, β is the instantaneous transmission rate ($[t^{-1}]$), μ is the instantaneous mortality rate ($[t^{-1}]$), and γ is the instantaneous recovery rate ($[t^{-1}]$).

Unfortunately, few data sets include data for each of these compartments. The New York Times’ “historical” data¹ is an easily accessible source of data. These data comprise daily totals of “cases” and “deaths” for each county in the United States. I assume that the data included as “cases” are a reasonable approximations of the Infected compartment (I) in a SIR model. There are simply no credible data of comparable scope on either the Susceptible or the Recovered compartments.

Model Structure

I make some simplifying assumptions in the face of incomplete data: (1) The entire population is susceptible so that $S/N = 1$. (2) Over the short term, the size of the Susceptible compartment does not change, $\frac{dS}{dt} = 0 = \frac{dN}{dt}$, eliminating the Susceptible compartment. (3) People who recover from a

¹<https://github.com/nytimes/covid-19-data/>

COVID-19 infection return to the Susceptible compartment, eliminating the Recovered compartment. With these assumptions, and with the addition of a “deaths” compartment, the simplified SIR model is

$$\frac{dI}{dt} = \beta I - \mu I - \gamma I \quad (5)$$

$$\frac{dD}{dt} = \mu I \quad (6)$$

and has state variables that might be matched to available observations.

The data available during the initial stages of the COVID-19 pandemic contain measurement errors of various types. Definitions and methods of detecting and reporting the numbers of infected persons vary between political jurisdictions (or “geographies” in the parlance of the New York Times) and may also change with time. Comparable uncertainties also occur in reporting of deaths caused by COVID-19 infection. There is additional variability in the biosocial processes that mediate disease transmission.

State-space models separate variability in the biosocial processes in the system (transition model) from errors in observing features of interest in the system (observation model). (See Harvey 1990).

The general form of a state-space process or transition model is

$$\alpha_t = T(\alpha_{t-1}) + \eta_t \quad (7)$$

where α_t is the state at time t and the function T embodies the dynamics mediating the development of the state at time t from the state at the previous time with random process error, η_t .

The transition model for the simplified SIR model is constructed from finite difference approximations of equation (5) with associated log-normal

random errors.

$$I_t = I_{t-\Delta t} (1 + \Delta t (\beta_{t-\Delta t} - \mu_{t-\Delta t} - \gamma_{t-\Delta t})) e^{\eta_t} \quad (8)$$

$$D_t = (D_{t-\Delta t} + \Delta t \mu_{t-\Delta t} I_{t-\Delta t}) e^{\eta_t} \quad (9)$$

where η is a normal random deviate, $\eta \sim N(0, \sigma_\eta)$, representing temporal variability in the biosocial factors that mediate the spread of the pandemic. The recovery rate, $\gamma_{t-\Delta t}$, in equation (8) is computed algebraically as

$$\gamma_{t-\Delta t} = \beta_{t-\Delta t} - \mu_{t-\Delta t} + (1 - \frac{I_t}{I_{t-\Delta t}}) \quad (10)$$

I have no particular justification, beyond the parsimony principle, for the assumption that the variance, σ_η , of the processes for I and D , should be the same.

One approach to modeling time-dependent rates of transmission and mortality, β and μ , is to treat them as random effects (Skaug and Fournier 2006). Random effects are appropriate if repeating a time series of observations would not yield the same outcome as the initial observations. Random effects are also appropriate when observing the same process in two different areas. I model the β and μ time series as log-normal random walks. I assume that

$$\log \beta_t = \log \beta_{t-\Delta t} + \varepsilon; \quad \varepsilon \sim N(0, \sigma_\beta) \quad (11)$$

$$\log \mu_t = \log \mu_{t-\Delta t} + \varrho; \quad \varrho \sim N(0, \sigma_\mu) \quad (12)$$

The general form of the state-space observation model is

$$x_t = O(\alpha_t) + \varphi_t \quad (13)$$

where the function O describes the measurement process with error ε in observing the state α .

I applied separate observation error models for cases and deaths. The observation model for cases is a simple log-normal error

$$\log \varphi_t = \left(\log \frac{1}{\sqrt{2\pi\sigma_I^2}} - \left(\frac{\log I_t - \log \hat{I}_t}{\sigma_I} \right)^2 \right) \quad (14)$$

where I is the observed number of cases and \hat{I} is the number of cases predicted by equation 8.

Not all those afflicted by COVID-19 have died; there are far fewer deaths than infections. In addition, the observed time series for both I and D begins at the first recorded case. The first recorded death occurs several days or weeks after the first recorded case. Therefor the deaths time-series inevitably contains a substantial number of recorded zeros. The observation model for deaths accommodates observed zeroes by assuming to be “zero-inflated” log normal likelihood given by

$$\log \varepsilon_t = \begin{cases} D_t > 0 : & (1 - p_0) \cdot \left(\log \frac{1}{\sqrt{2\pi\sigma_D^2}} - \left(\frac{\log D_t - \log \hat{D}_t}{\sigma_D} \right)^2 \right) \\ D_t = 0 : & p_0 \cdot \log \frac{1}{\sqrt{2\pi\sigma_D^2}} \end{cases} \quad (15)$$

where D is the observed number of deaths, \hat{D} is the number of deaths predicted by equation 9, and p_0 is the proportion of observed deaths equal to zero.

Model parameters are estimated by maximizing the joint likelihood of the process errors, observation errors, and random effects.

$$L(\theta, \alpha, x) = \prod_{t=2}^m [\phi(\alpha_t - T(\alpha_{t-1}), \Sigma_\eta)] \cdot \prod_{t=1}^m [\phi(x_t - O(\alpha_t), \Sigma_\varepsilon)] \quad (16)$$

Table 1: List of model variables for the simple SIR model. There are two state variables computed from the estimated parameters and random effects. There are two random effects and five estimated variance parameters.

Variable	Definition
<i>State variables:</i>	
I	Number of infected individuals or “cases”
D	Number of deaths
<i>Random effects:</i>	
β_t	Transmission rate
μ_t	Mortality rate
<i>Estimated parameters:</i>	
σ_I	Infectious compartment estimation standard deviation
σ_D	Deaths compartment estimation standard deviation
σ_η	Standard deviation of transmission and deaths process errors
σ_β	Standard deviation of transmission rate random walk
σ_μ	Standard deviation of mortality rate random walk

where m is the number of days elapsed since the first recorded case, x_t is the vector of daily observations of cases and deaths, α_t is the vector of the daily calculations of the state variables and random effects, and θ is a vector of model parameters (Table 1). The R package TMB (Kristensen et al. 2016 package was used to estimate the parameters of the model. The R and supporting C++ files are available on github.²

²simpleSIR4 at <https://github.com/johnrsibert/SIR-Models>

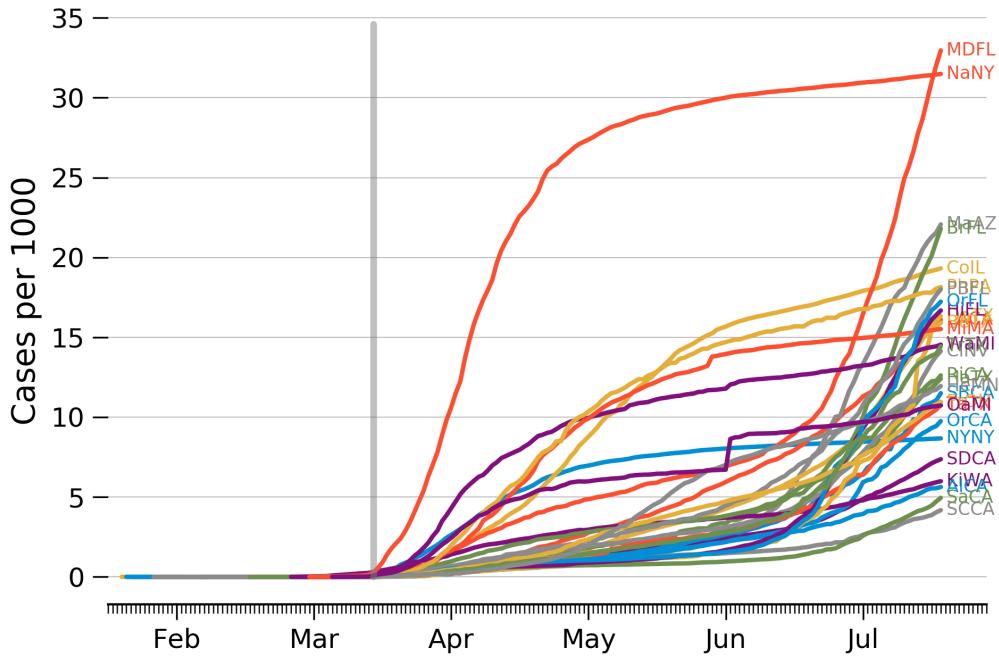


Figure 1: Trends in number of cases per 1000 people in the 30 most populous US counties. The vertical gray bar mark the date of the California shelter in place order.

Results

Trends in the per-capita number of cases in the thirty largest counties in the United States are shown in Figure (1). These trajectories fall into two more or less distinct groups: those that are concave downward, e.g. Nassau Co. NY (NaNY), and those that are concave upward, e.g. Miami-Dade Co. FL (MDFL).

Prevalence histories for six counties are shown in Figure 2 where the 11-day moving average of the daily increase in cases demonstrates clearly the

efficacy of control measures. All of these trends show extreme day to day variability in numbers of both cases and deaths. The variability is most notable in the deaths time series for smaller counties.

Model diagnostic plots are shown in figures 3 and 4 for convex downward and convex upward trajectories respectively. The model reproduces the observed numbers of cases and deaths almost exactly. The ‘+’ symbols in the Cases and Deaths graphs represent the observed cases (I) and deaths (D) from the data. The red lines overlaying the symbols are model predictions (\hat{I}) and (\hat{D}) of in cases and deaths. σ_I and σ_D are the estimated standard deviations for cases and deaths likelihood contributions, equations (14) and (15). The shaded areas bounded by red outlines are ± 2 estimated standard deviations around the estimated trends. These standard deviations are, in some cases, equivalent to an error of approximately one case or death.

The solid blue lines in the β and μ plots are the estimated transmission and death rate random effects. The shaded areas bounded by blue outlines are estimated random effects ± 2 standard deviations of the generating random walks. The red lines labeled $\tilde{\beta}$ and $\tilde{\mu}$ are the medians of the two random effects.

The estimated transmission rates are very high at the beginning of each time series, exceeding 1da^{-1} in Miami-Dade County, equivalent to a doubling time of less than one day.

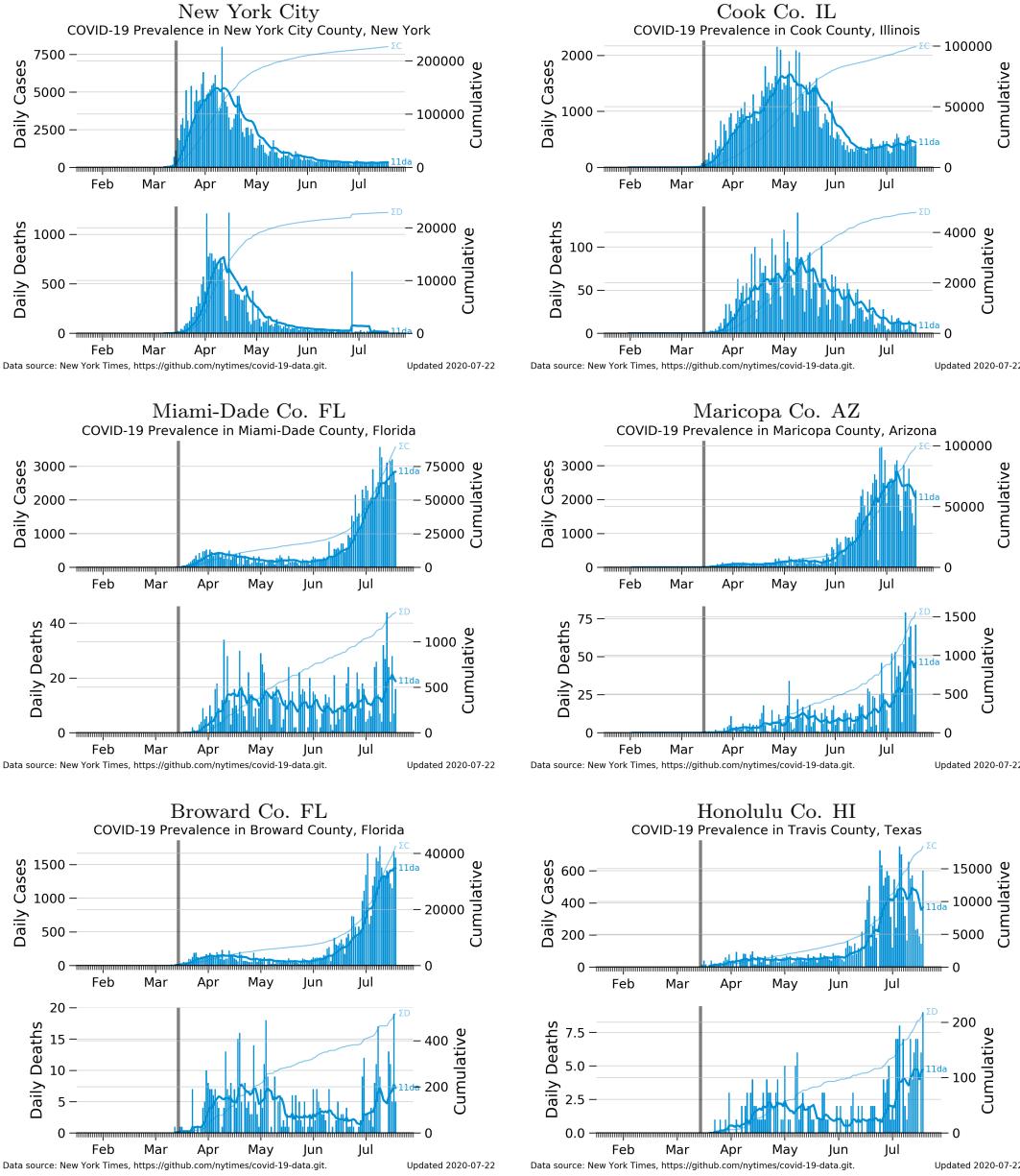


Figure 2: Prevalence trajectories for six US counties. Blue bars indicate daily increases in cases and deaths; dark blue lines indicate 11 day moving averages of daily increases (labeled “11da”; pale blue lines indicate cumulative numbers (labeled ΣC and ΣD); vertical gray bar marks the March 19, 2020 California shelter in place order. *remove annotations*.

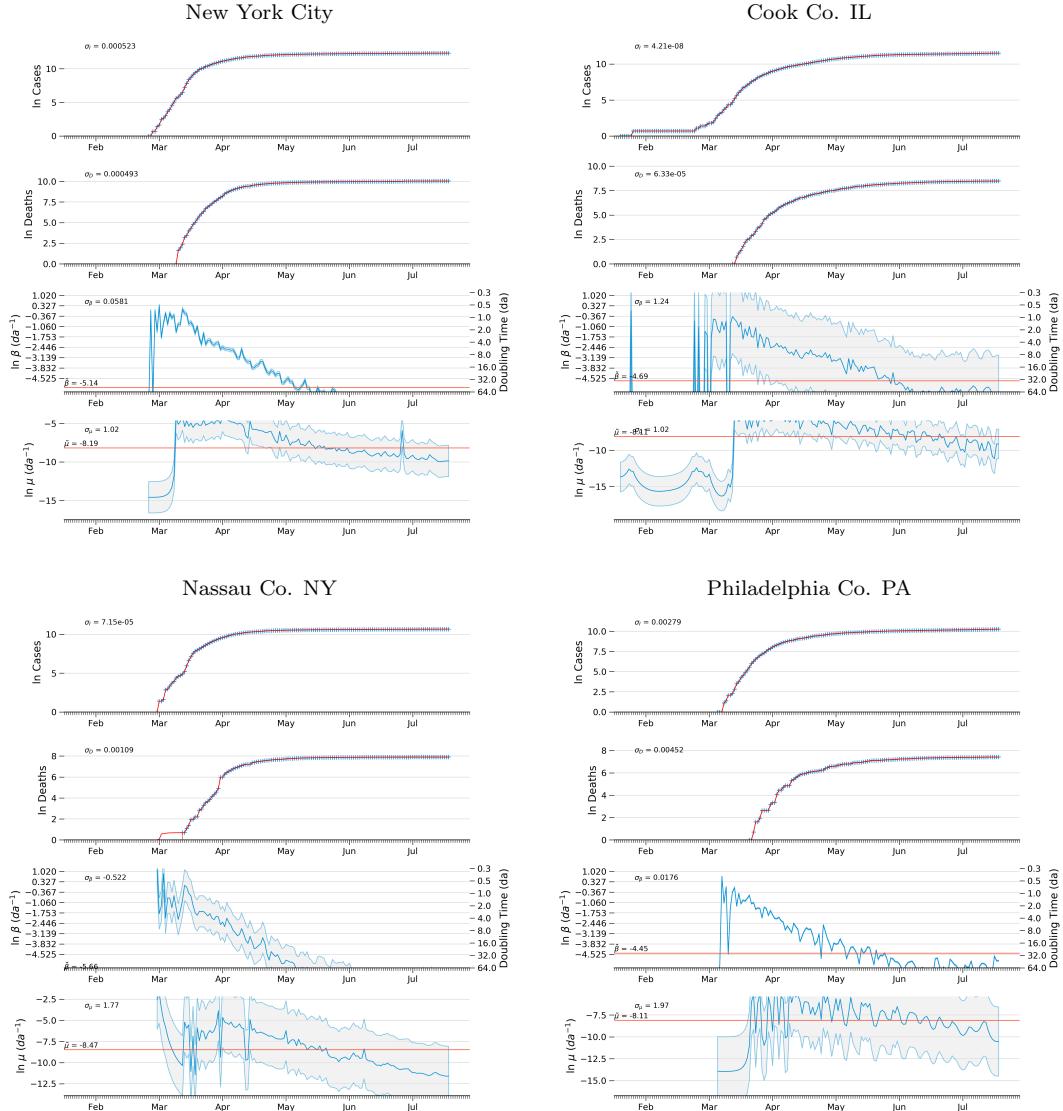


Figure 3: Model diagnostics for concave downward counties.

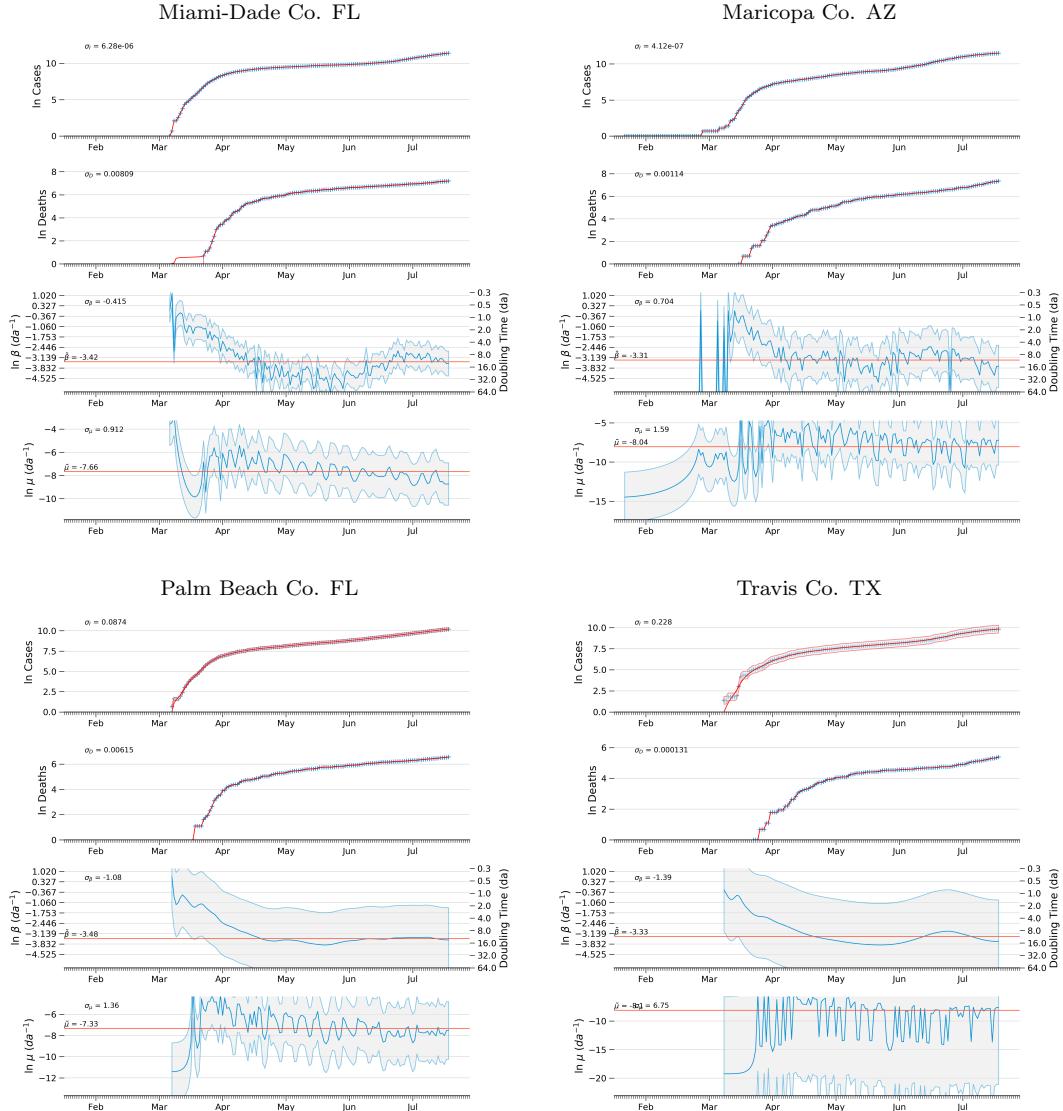


Figure 4: Model diagnostics for concave upward counties.

Table 2: Model results. Estimating β and μ trends as random effects with computed γ . Data updated 2020-07-22 from <https://github.com/nytimes/covid-19-data.git> 2020-07-22

County	n	p_0	f	C	σ_η	σ_β	σ_μ	σ_I	σ_D	$\tilde{\gamma}$	$\tilde{\beta}$	$\tilde{\mu}$
Nassau, NY	138	0.0863	-957	10	0.161	0.593	1.77	7.15e-05	0.00109	-9.45e-09	0.00349	0.000211
New York City, NY	142	0.0909	-834	0	0.196	1.06	1.02	0.000523	0.000493	-2.73e-08	0.00583	0.000278
Cook, IL	179	0.294	-990	10	0.118	3.46	1.02	4.21e-08	6.33e-05	-2.24e-07	0.00926	0.0003
Honolulu, HI	137	0.181	-1290	1	0.106	8.7	21.2	0.00372	3.41e-06	-5.51e-08	0.0109	4.39e-11
Philadelphia, PA	133	0.112	-608	0	0.167	1.02	1.97	0.00279	0.00452	-3.1e-08	0.0117	0.0003
Bexar, TX	160	0.242	-833	1	0.166	6.49	6.72	1.51e-08	9.81e-06	-7.18e-08	0.0283	2.73e-07
Tarrant, TX	133	0.0746	-570	0	0.146	1.25	1.37	0.0102	0.0034	-3.78e-08	0.0307	0.000285
Palm Beach, FL	131	0.0758	-428	0	0.143	0.34	1.36	0.0874	0.00615	-1.16e-08	0.0308	0.000658
Harris, TX	138	0.101	-380	0	0.117	0.265	0.895	0.167	0.0225	-2.15e-08	0.0308	0.000278
Miami-Dade, FL	132	0.112	-622	10	0.162	0.66	0.912	6.28e-06	0.00809	-9.54e-09	0.0327	0.00047
Hillsborough, FL	142	0.175	-595	1	0.145	1.65	48.2	7.61e-05	2.29e-07	-7.24e-08	0.0355	4.64e-05
Travis, TX	130	0.107	-361	10	0.11	0.25	6.75	0.228	0.000131	-1.68e-08	0.0358	0.000303
Maricopa, AZ	177	0.303	-878	1	0.118	2.02	1.59	4.12e-07	0.00114	-4.2e-07	0.0367	0.000321
Dallas, TX	133	0.0672	-452	1	0.136	0.305	1.19	0.0801	0.00954	-1.04e-08	0.0371	0.000405
Broward, FL	137	0.0797	-511	0	0.136	0.231	1.65	0.08	0.003	-2.03e-08	0.038	0.000277
Median	137	0.107	-608	1	0.143	1.02	1.59	0.00279	0.00114	-2.73e-08	0.0308	0.000285

Discussion

Whether the available data are sufficiently informative to enable estimation of the model parameters is a critical aspect of the evaluation of any statistical model. The speed at which the COVID-19 pandemic spread during the first quarter of 2020 means that the length of the time series doubled during the development of this model. The capability of the model improve conveniently during the model development period, but whether the improvement is attributable to changes in model structure or to the increase in the length of the time series is unclear. This ambiguity influenced the development of the model.

Sibert 2017; Nielsen and Berg 2014; Chen et al. 2020

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