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# Supplementary Materials for

## **Differential Effects of Intervention Timing on COVID-19 Spread in the United States**

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## **Materials and Methods**

### 1. Transmission model

The transmission dynamics are depicted by the following equations.

Daytime transmission:

$$
S_{ij}(t + dt_{1}) = S_{ij}(t) - \frac{\beta_{i}S_{ij}(t) \sum_{k} I_{ki}^{r}(t)}{N_{i}^{d}(t)} dt_{1} - \frac{\mu \beta_{i}S_{ij}(t) \sum_{k} I_{ik}^{u}(t)}{N_{i}^{d}(t)} dt_{1} + \theta dt_{1} \frac{N_{ij} - I_{ij}^{r}(t)}{N_{i}^{d}(t)} \sum_{k \neq i} \frac{\overline{N}_{ik} \sum_{l} S_{kl}(t)}{N_{ik}^{d}(t) - \sum_{l} I_{lk}^{r}(t)} - \theta dt_{1} \frac{S_{ij}(t)}{N_{i}^{d}(t) - \sum_{l} I_{li}^{r}(t)} \sum_{k \neq i} \overline{N}_{ki} (1) E_{ij}(t + dt_{1}) = E_{ij}(t) + \frac{\beta_{i}S_{ij}(t) \sum_{k} I_{ki}^{r}(t)}{N_{i}^{d}(t)} dt_{1} + \frac{\mu \beta_{i}S_{ij}(t) \sum_{k} I_{ik}^{u}(t)}{N_{i}^{d}(t)} dt_{1} - \frac{E_{ij}(t)}{Z} dt_{1} + \theta dt_{1} \frac{N_{ij} - I_{ij}^{r}(t)}{N_{i}^{d}(t)} \sum_{k \neq i} \frac{\overline{N}_{ik} \sum_{l} E_{kl}(t)}{N_{ik}^{d}(t) - \sum_{l} I_{lk}^{r}(t)} - \theta dt_{1} \frac{E_{ij}(t)}{N_{i}^{d}(t) - \sum_{l} I_{li}^{r}(t)} \sum_{k \neq i} \overline{N}_{ki} (2) I_{ij}^{r}(t + dt_{1}) = I_{ij}^{r}(t) + \alpha \frac{E_{ij}(t)}{Z} dt_{1} - \frac{I_{ij}^{r}(t)}{D} dt_{1}
$$
  
+  $\theta dt_{1} \frac{N_{ij} - I_{ij}^{r}(t)}{N_{i}^{d}(t)} \sum_{k \neq i} \frac{\overline{N}_{ik} \sum_{l} I_{kl}^{r}(t)}{N_{ik}^{d}(t) - \sum_{l} I_{lk}^{r}(t)} - \theta dt_{1} \frac{I_{ij}^{u}(t)}{N_{i}^{d}(t) - \sum_{l} I_{li}^{r}(t)} \sum_{k \neq i} \overline{N}_{ki} (4) N_{i$ 

Nighttime transmission:

$$
S_{ij}(t+1) = S_{ij}(t+dt_{1}) - \frac{\beta_{j}S_{ij}(t+dt_{1})\sum_{k}I_{kj}^{r}(t+dt_{1})}{N_{j}^{n}}dt_{2}
$$
\n
$$
- \frac{\mu\beta_{j}S_{ij}(t+dt_{1})\sum_{k}I_{kj}^{u}(t+dt_{1})}{N_{j}^{n}}dt_{2} + \theta dt_{2} \frac{N_{ij}}{N_{j}^{n}}\sum_{k\neq j} \frac{\overline{N}_{jk}\sum_{l}S_{lk}(t+dt_{1})}{N_{k}^{n}-\sum_{l}I_{lk}^{r}(t+dt_{1})}
$$
\n
$$
- \theta dt_{2} \frac{S_{ij}(t+dt_{1})}{N_{j}^{n}-\sum_{k}I_{kj}^{r}(t+dt_{1})}\sum_{k\neq j} \overline{N}_{kj} \quad (6)
$$
\n
$$
E_{ij}(t+1) = E_{ij}(t+dt_{1}) + \frac{\beta_{j}S_{ij}(t+dt_{1})\sum_{k}I_{kj}^{r}(t+dt_{1})}{N_{j}^{n}}dt_{2}
$$
\n
$$
+ \frac{\mu\beta_{j}S_{ij}(t+dt_{1})\sum_{k}I_{kj}^{u}(t+dt_{1})}{N_{j}^{n}}dt_{2} - \frac{E_{ij}(t+dt_{1})}{Z}dt_{2}
$$
\n
$$
+ \theta dt_{2} \frac{N_{ij}}{N_{j}^{n}}\sum_{k\neq j} \frac{\overline{N}_{jk}\sum_{l}E_{lk}(t+dt_{1})}{N_{k}^{n}-\sum_{l}I_{lk}^{r}(t+dt_{1})} - \theta dt_{2} \frac{E_{ij}(t+dt_{1})}{N_{j}^{n}-\sum_{k}I_{kj}^{r}(t+dt_{1})}\sum_{k\neq j} \overline{N}_{kj} \quad (7)
$$

$$
I_{ij}^{r}(t+1) = I_{ij}^{r}(t+dt_{1}) + \alpha \frac{E_{ij}(t+dt_{1})}{Z} dt_{2} - \frac{I_{ij}^{r}(t+dt_{1})}{D} dt_{2}
$$
 (8)  

$$
I_{ij}^{u}(t+1) = I_{ij}^{u}(t+dt_{1}) + (1-\alpha) \frac{E_{ij}(t+dt_{1})}{Z} dt_{2} - \frac{I_{ij}^{u}(t+dt_{1})}{D} dt_{2}
$$

$$
+ \theta dt_{2} \frac{N_{ij}}{N_{j}^{n}} \sum_{k \neq j} \frac{\bar{N}_{jk} \sum_{l} I_{lk}^{u}(t+dt_{1})}{N_{k}^{n} - \sum_{l} I_{lk}^{r}(t+dt_{1})} - \theta dt_{2} \frac{I_{ij}^{u}(t+dt_{1})}{N_{j}^{n} - \sum_{k} I_{kj}^{r}(t+dt_{1})} \sum_{k \neq j} \bar{N}_{kj}
$$
 (9)  

$$
N_{i}^{n} = \sum_{k} N_{ki}
$$
 (10)

Here,  $S_{ij}$ ,  $E_{ij}$ ,  $I_{ij}^r$ ,  $I_{ij}^u$  and  $N_{ij}$  are the susceptible, exposed, reported infected, unreported infected and total populations in the subpopulation commuting from county *j* to county  $i$  ( $i \leftarrow j$ );  $\beta_i$  is the transmission rate of reported infections in county  $i$ ;  $\mu$  is the relative transmissibility of unreported infections;  $Z$  is the average latency period (from infection to contagiousness);  $D$  is the average duration of contagiousness;  $\alpha$  is the fraction of documented infections;  $\theta$  is a multiplicative factor adjusting random movement;  $\overline{N}_{ij} = (N_{ij} + N_{ji})/2$  is the average number of commuters between counties *i* and *j*;  $dt_1$  and  $dt_2$  are the durations of daytime and nighttime transmission; and  $N_i^d$  and  $N_i^n$  are the daytime and nighttime populations of county *i*. We assume the  $I_{ij}^r$  population is immobile and does not participate in human movement. We integrate Eqs. S1-S10 using a Poisson process to represent the stochasticity of the transmission process.

In the transmission model, we consider two types of movement: daily work commuting and random movement. For daily work commuting, during the daytime,  $N_{ij}$  individuals living in location  $j$  commute to work place  $i$  and mix with the population present there. During the nighttime, those commuters return to their home and mix with other residents who live in location *j*. For random movement, individuals may travel among locations for reasons other than work. These random visitors circulate among subpopulations following a Markov process, causing a population exchange in all locations.

*Daily work commuting:* During the daytime, the population in location *i*,  $N_i^d(t) = N_{ii} +$  $\sum_{k\neq i} I_{ki}^r(t) + \sum_{k\neq i} (N_{ik} - I_{ik}^r(t))$ , is the sum of individuals who both live and work in location *i*, reported infected individuals who would otherwise commute to other locations  $k$  ( $k \neq i$ ), and individuals who work in location *i* from other locations  $k$  ( $k \neq i$ ) but are not reported infections. Within the subpopulation  $N_{ij}$ , new infections derive from two processes: contact with reported and unreported infections in location *i*. For each susceptible individual in  $S_{ij}(t)$ , the chance of contact with reported infections is  $\sum_k I_{ki}^r(t) / N_i^d(t)$ , where  $\sum_k I_{ki}^r(t)$  is the total number of reported infections who would commute to all locations  $k$  but have to stay in location  $i$ , and the chance of contact with unreported infections is  $\sum_k I_{ik}^u(t)/N_i^d(t)$ , where  $\sum_k I_{ik}^u(t)$  is the total number of unreported infections in location  $i$ . Those contacts lead to new infections

$$
\frac{\beta_i S_{ij}(t) \sum_k I^r_{ki}(t)}{N^d_i(t)} dt_1 + \frac{\mu \beta_i S_{ij}(t) \sum_k I^u_{ik}(t)}{N^d_i(t)} dt_1
$$

during a period of  $dt_1$  day. Note this term captures the mixing of populations from different locations due to work commuting, and represents intra-county transmission during the daytime in location  $i$ .

*Random movement:* Apart from work commuting, during the daytime,  $\theta dt_1 \overline{N}_{ik}$  persons, drawn uniformly from the population present in location  $k (k \neq i)$  (except for reported infections) move to location  $i$  and are randomly redistributed into the subpopulation there. Such population exchange exists for all pairs of locations. For example, for the susceptible population, we first compute the number of susceptible individuals entering into subpopulation  $S_{ij}(t)$ . In other locations  $k$  ( $k \neq i$ ), the probability of a random visitor is susceptible is  $\sum_l S_{kl}(t) / (N_k^d(t) \sum_l I_{lk}^r(t)$ ), where  $\sum_l S_{kl}(t)$  is the number of susceptible individuals present in location k from all locations l, and  $N_k^d(t) - \sum_l I_{lk}^r(t)$  is the total number of mobile population (i.e., total population minus reported infected population) in location  $k$ . Therefore, the total susceptible population entering location *i* is  $\theta dt_1 \overline{N}_{ik} \sum_{k \neq i} \sum_l S_{kl}(t) / (N_k^d(t) - \sum_l I_{lk}^r(t))$ . Those individuals are redistributed into subpopulations present in location  $i$ , where the fraction of people in subpopulation  $N_{ij}$  is  $(N_{ij} - I_{ij}^r(t))/N_i^d(t)$ . Finally, the number of susceptible individuals entering  $S_{ij}(t)$  is

$$
\theta dt_1 \frac{N_{ij} - I_{ij}^r(t)}{N_i^d(t)} \sum_{k \neq i} \frac{\overline{N}_{ik} \sum_l S_{kl}(t)}{N_k^d(t) - \sum_l I_{lk}^r(t)}.
$$

We then compute the number of susceptible individuals leaving  $S_{ii}(t)$ . The total number of individuals leaving location *i* is  $\theta dt_1 \sum_{k \neq i} \overline{N}_{ki}$ ; the fraction of susceptible people from  $N_{ij}$  is  $S_{ij}(t)/(N_i^d(t) - \sum_l I_{li}^r(t))$ . As a result, the number of susceptible persons leaving  $S_{ij}(t)$  is

$$
\theta dt_1 \frac{S_{ij}(t)}{N_i^d(t) - \sum_l I_{li}^r(t)} \sum_{k \neq i} \overline{N}_{ki}.
$$

Population exchange for other compartments can be computed similarly. Note there is no random movement in Eq. (3) as we assume reported infections,  $I_{ij}^r$ , are immobile. We can write Eqs. (6-10) for nighttime transmission similarly.

#### **2. The Ensemble Adjustment Kalman Filter**

Originally developed for use in weather prediction, the ensemble adjustment Kalman filter (EAKF) assumes a Gaussian distribution of both the prior and likelihood and adjusts the prior distribution to a posterior using Bayes' rule deterministically. To represent the state-space distribution, the EAKF maintains an ensemble of system state vectors acting as samples from the distribution. In particular, the EAKF assumes that both the prior distribution and likelihood are Gaussian, and thus can be fully characterized by their first two moments (mean and variance). The update scheme for ensemble members is computed using Bayes' rule (posterior  $\propto$  prior  $\times$ likelihood) via the convolution of the two Gaussian distributions. For observed state variables, the posterior of the *i*th ensemble member is updated through

$$
o_{t,post}^i = \frac{\sigma_{t,obs}^2}{\sigma_{t,obs}^2 + \sigma_{t,prior}^2} \bar{o}_{t,prior} + \frac{\sigma_{t,prior}^2}{\sigma_{t,obs}^2 + \sigma_{t,prior}^2} y_t + \sqrt{\frac{\sigma_{t,obs}^2}{\sigma_{t,obs}^2 + \sigma_{t,prior}^2}} (o_{t,prior}^i - \bar{o}_{t,prior}).
$$

Here  $o_{t,post}^{i}$  and  $o_{t,prior}^{i}$  are the posterior and prior of the observed variable (i.e., daily confirmed case or death in each county) for the *i*th ensemble member at time *t*;  $\bar{o}_{t, prior}$  is the mean of the prior observed variable;  $\sigma_{t,obs}^2$  and  $\sigma_{t,prior}^2$  are the variances of the observation and the prior observed variable; and  $y_t$  is the observation at time t. Unobserved variables and parameters are

updated through their covariability with the observed variable, which can be computed directly from the ensemble. In particular, the *i*th ensemble member of unobserved variable or parameter  $x^{i}$  is updated by

$$
x_{t,post}^i = x_{t,prior}^i + \frac{\sigma\left(\left\{x_{t,prior}\right\}_n, \left\{o_{t,prior}\right\}_n\right)}{\sigma_{t,prior}^2}\left(o_{t,post}^i - o_{t,prior}^i\right).
$$

Here  $x_{t,post}^{i}$  and  $x_{t,prior}^{i}$  are the posterior and prior of the unobserved variable or parameter for the *i*th ensemble member at time t; and  $\sigma(\{x_{t, prior}\}_n, \{o_{t,prior}\}_n)$  is the covariance between the prior of the unobserved variable or parameter  $\{x_{t, prior}\}_{n}$  and the prior of the observed variable  ${b_{t,prior}}_n$  at time t. In the EAKF, variables and parameters are updated deterministically such that the higher moments of the prior distribution are preserved in the posterior.

To account for the reporting delay of confirmed case and death, we modified the original EAKF implementation by adjusting model states using observations in the near future, when the effects of parameter change are manifested in observations. Specifically, for data assimilation at day  $t$ , we ran the transmission model forward to day  $t + 16$  using prior model state, and used the confirmed case at day  $t + 9$  and death at day  $t + 16$  to update model variables and parameters at day  $t$ . This look-ahead data assimilation considered an average delay of 9 days for infection confirmation and an average delay of 16 days for death reporting. For dates within 16 (9) days of May 3, we used reported death (case) numbers after May 3 to constrain the model.

In the EAKF, we assume a heuristic form of observation error variance (OEV)  $\sigma_{t,obs}^2$ . For confirmed cases, we used  $\sigma_{t,case}^2 = \max(25, y (case)_t^2/100)$ , where  $y (case)_t$  is the number of new confirmed cases averaged over day  $t - 6$  to day  $t$ ; for death, we used  $\sigma_{t,death}^2 =$ max (25, y(death) $_t^2$ /100), where y(death)<sub>t</sub> is the number of deaths averaged over day  $t - 6$ to day t. Similar forms of OEV have been successfully used for inference and forecasting for a range of infectious diseases (*38-40*). In this study, this OEV setting yields satisfactory fitting.



**Fig. S1. Intercounty commuting, selected counties, and daily confirmed cases and deaths in focus metropolitan areas.** (**A**) Visualization of inter-county commuting data from US census survey in 48 continental US states. Line thickness represents the intensity of human movement. (**B**) The 311 counties with cumulative cases >=400 as of May 3 2020. Color indicates cumulative cases on a log scale. Daily confirmed cases (**C**) and deaths (**D**) in six metropolitan areas as of May 3, 2020.



**Fig. S2. Posterior fitting at county level**. Posterior fitting to daily confirmed cases (**A**) and deaths (**B**) in 9 counties.



**Fig. S3. Inferred basic reproductive number for six metropolitan areas and the reduction of transmission rates in counties with increasing confirmed cases.** (**A**) We show the estimated  $R_t$  in the six metropolitan areas and the dates on which local social distancing orders were announced (vertical black dash lines). (**B**) We selected segments of increasing cases for counties with a maximum daily case level above 200 (right panel) and inspected the estimated transmission rates in those counties during the same period (left panel). The average weekly reduction of the transmission rate is 25% in those counties in response to increasing confirmed cases.



**Fig. S4. Sensitivity of model fitting to the duration of daytime and nighttime transmission.** Model fitting and parameter inference using a model with 12-hour daytime and nighttime transmission.



**Fig. S5. The estimated effective reproductive numbers in 3142 US counties.** The estimated effective reproductive numbers in 3142 US counties on March 15, March 29, April 12 and April 26.



**Fig. S6. The estimated fraction of susceptible population in the US and six metropolitan areas.** Blue line is the median estimate and grey dotted lines are 95% CIs.



**Fig. S7. Reporting delay and cumulative number of tests per 100,000.** (**A**) The reporting delay from symptom onset to confirmation follows a gamma distribution ( $a = 2.6$ ,  $b = 4.9$ , mean= 12.9 days). (**B**) National daily confirmed cases and deaths. The dotted red line is the death time series shifted 7 days backwards. A 7-day delay between the curves of confirmed cases and deaths is observed. (**C**) The cumulative number of viral tests per 100,000 persons in states available at the COVID tracking project (https://covidtracking.com/). RI has a higher per capita testing rate possibly due to its small population.



**Fig. S8. Effects of response time after control measures are relaxed in six counties**. We implement control relaxation (a weekly 5% increase of the transmission rate) starting on May 4 in all US counties. If local weekly case numbers in a county increases for 3 consecutive weeks, a weekly 25% reduction of the transmission rate is imposed for that county. Daily cases and transmission rates in the six counties are shown.



**Fig. S9. Effects of reopening in Florida on daily cases and deaths in Georgia and Alabama**. We compare the daily cases and deaths in GA and AL under two scenarios: with and without FL reopening on May 4, 2020. For the reopening scenario, we assume the transmission rates in FL counties increase by 20% after reopening and remain at this level until the end of the simulation. Projections were generated for 30 days beginning May 4, 2020.

county	case	PAE	PE	county	case	PAE	PE
Queens County NY	53640	0.19	0.04	Riverside County CA	4180	0.15	$-0.04$
Kings County NY	46839	0.24	0.16	Lake County IL	4161	0.13	$-0.11$
Cook County IL	42322	0.17	$-0.17$	Delaware County PA	4113	0.11	$-0.07$
<b>Bronx County NY</b>	38916	0.17	0.1	Hampden County MA	4067	0.15	$-0.03$
Nassau County NY	36780	0.2	$-0.19$	<b>Bristol County MA</b>	4019	0.24	$-0.14$
<b>Suffolk County NY</b>	34855	0.25	$-0.24$	Camden County NJ	3975	0.14	$-0.12$
Westchester County NY	29884	0.2	$-0.18$	San Diego County CA	3925	0.17	$-0.12$
Los Angeles County CA	25661	0.15	$-0.08$	Dallas County TX	3899	0.14	$-0.09$
New York County NY	22745	0.19	0.07	Erie County NY	3710	0.16	$-0.07$
Wayne County MI	17298	0.22	0.05	Somerset County NJ	3703	0.13	$-0.08$
Bergen County NJ	16185	0.14	$-0.07$	DuPage County IL	3611	0.12	$-0.08$
Hudson County NJ	15769	0.14	$-0.07$	Denver County CO	3345	0.38	$-0.29$
Middlesex County MA	15370	0.12	$-0.04$	St. Louis County MO	3325	0.16	$-0.13$
Essex County NJ	14521	0.15	$\boldsymbol{0}$	<b>Baltimore County MD</b>	3301	0.17	$-0.11$
<b>Suffolk County MA</b>	13777	0.14	$-0.06$	<b>Bucks County PA</b>	3286	0.1	$-0.05$
Passaic County NJ	13364	0.13	$-0.11$	Milwaukee County WI	3244	0.11	$-0.06$
Union County NJ	13225	0.18	$-0.09$	Palm Beach County FL	3130	0.12	$-0.05$
Philadelphia County PA	13179	0.18	$-0.15$	Dutchess County NY	3086	0.2	$-0.14$
Miami-Dade County FL	12775	0.19	$-0.18$	<b>Burlington County NJ</b>	3043	0.15	$-0.1$
Middlesex County NJ	12597	0.13	$-0.12$	Fulton County GA	2978	0.13	$-0.05$
<b>Richmond County NY</b>	12195	0.12	$-0.06$	Lehigh County PA	2924	0.27	$-0.21$
Rockland County NY	12025	0.23	$-0.18$	Franklin County OH	2905	0.19	$-0.13$
Fairfield County CT	11801	0.23	0.02	Davidson County TN	2904	0.14	$-0.07$
<b>Essex County MA</b>	9542	0.12	$-0.09$	<b>Berks County PA</b>	2886	0.2	$-0.07$
Orange County NY	8967	0.23	$-0.18$	Will County IL	2868	0.2	$-0.13$
New Haven County CT	8024	0.15	$-0.06$	Shelby County TN	2815	0.16	$-0.12$
Oakland County MI	7499	0.14	$-0.03$	Orange County CA	2742	0.12	$-0.09$
Prince George's County MD	7333	0.14	$-0.12$	Salt Lake County UT	2707	0.08	$-0.06$
Providence County RI	7028	0.17	$-0.15$	Arapahoe County CO	2706	0.12	$-0.02$
Ocean County NJ	6871	0.16	$-0.13$	Snohomish County WA	2510	0.18	$-0.1$
Harris County TX	6708	0.25	$-0.2$	<b>Tarrant County TX</b>	2503	0.16	$-0.09$
Orleans Parish LA	6538	0.33	0.04	<b>Sussex County DE</b>	2461	0.17	$-0.09$
King County WA	6448	0.12	$-0.04$	Cuyahoga County OH	2338	0.12	$-0.06$
Jefferson Parish LA	6388	0.28	$-0.09$	Marion County OH	2329	1.18	0.58
Monmouth County NJ	6290	0.16	$-0.1$	Baltimore city MD	2319	0.16	$-0.08$
Worcester County MA	6288	0.12	$-0.06$	Luzerne County PA	2240	0.35	$-0.24$
Norfolk County MA	6280	0.15	$-0.03$	Santa Clara County CA	2228	0.19	$-0.15$
Marion County IN	6176	0.15	$-0.1$	Northampton County PA	2214	0.21	$-0.15$
Hartford County CT	6112	0.15	0.06	San Bernardino County CA	2182	0.21	$\boldsymbol{0}$
Macomb County MI	5736	0.14	$-0.03$	DeKalb County GA	2181	0.15	$-0.06$
Morris County NJ	5517	0.14	$-0.08$	Hennepin County MN	2151	0.56	$-0.33$
Plymouth County MA	5507	$0.2\,$	$-0.09$	Minnehaha County SD	2142	0.28	$-0.06$
<b>Broward County FL</b>	5312	0.11	$-0.07$	East Baton Rouge Parish LA	2086	0.29	$-0.15$
Montgomery County MD	5150	0.13	$-0.09$	Lake County IN	2036	0.14	$-0.07$
District of Columbia DC	5016	0.14	$-0.09$	Prince William County VA	2027	0.1	$-0.08$
Maricopa County AZ	4584	0.12	$-0.09$	Gwinnett County GA	1974	0.12	$-0.04$
Montgomery County PA	4552	0.15	$-0.05$	Anne Arundel County MD	1960	0.12	$-0.08$
Mercer County NJ	4504	0.16	$-0.12$	Lancaster County PA	1936	0.14	$-0.08$
Fairfax County VA	4340	0.13	$-0.08$	Kane County IL	1935	0.11	$-0.05$
Clark County NV	4274	0.18	$-0.09$	New Castle County DE	1903	0.14	$-0.06$
county	death	<b>PAE</b>	PE	county	death	<b>PAE</b>	PE
Kings County NY	5508	0.28	$-0.25$	Clark County NV	218	0.4	0.11
Queens County NY	5279	0.31	$-0.31$	<b>Broward County FL</b>	207	0.34	0.02
<b>Bronx County NY</b>	3710	0.52	$-0.47$	<b>Bristol County MA</b>	198	0.33	0.32

**Table S1. Goodness of fit at county level.** Percentage absolute error (PAE) and percentage error (PE) for case (death) numbers in 100 counties with the most reported cases (deaths) through May 3. Numbers are proportions.

