Comparing and Integrating US COVID-19 Daily Data from Multiple Sources: A County-Level Dataset with Local Characteristics

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Abstract: Over the past several months, the outbreak of COVID-19 has been expanding over the world. A reliable and accurate dataset of the cases is vital for scientists to conduct related research and for policymakers to make better decisions. We collect the COVID-19 daily reported data from four open sources: the New York Times, the COVID-19 Data Repository by Johns Hopkins University, the COVID Tracking Project at the Atlantic, and the USAFacts, and compare the similarities and differences among them. In addition, we examine the following problems which occur frequently: (1) the order dependencies violation, (2) the delay-reported issue on weekends and/or holidays, and (3) abnormal data point or data period. We also integrate the COVID-19 reported cases with the county-level auxiliary information of the local features from official sources, such as health infrastructure, demographic, socioeconomic, and environment information, which are important for understanding the spread of the virus.

Key words and phrases: Anomaly detection; Coronavirus; Count time series; Data comparison; Data integration.

1 Background and Summary

Since the first infected case reported in December 2019, the outbreak of COVID-19 has unfolded across the globe. In the U.S., coronavirus has infected more than 1.8 million people and killed over 100,000 people, as of the time of writing. While essential public health, economic and social science research in measuring and modeling COVID-19 and its effects is underway, reliable and accurate datasets are vital for scientists to conduct related research and for governments to make better decisions (Killeen et al., 2020). Unfortunately, errors could occur in the data collection process, especially under such a pandemic. In this work, we focus on the data collection, comparison, data inconsistency detection, and the corresponding curating.

Living through unprecedented times, governments must rely on timely, reliable data to make decisions to mitigate harm and support their citizens. Every day, several volunteer groups and organizations work very hard on collecting data on COVID-19 from all the counties and states in the U.S. There are

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four major sources, including (1) the New York Times (NYT, 2020a), (2) the COVID Tracking Project at the Atlantic (Atlantic, 2020), (3) the data repository by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (JHU) (CSSE, 2020), and (4) USAFact (USAfacts, 2020). Although these sources usually obtain their confirmed infectious and death cases data from the government agencies, the counts still vary due to the time of their collection as well as several other issues. However, these differences can be critical for real-time analysis. In this work, we first collect and compare the COVID-19 daily reported data from the above four open resources.

The COVID-19 data poses unique data quality challenges due to its spatiotemporal nature, and the problem of delayed-reporting and under-reporting. After the detection of abnormal data, we explore various methods to detect and repair the problematic data. To be more specific, the entire data cleaning procedure has been divided into two categories: (1) manual cleaning, and (2) automatic cleaning. On the one hand, manual cleaning has very high accuracy; on the other hand, it is challenging to implement due to the high cost in time and effort.

Furthermore, it has been observed that the local characteristics, such as socioeconomic inequity, may also contribute to the spread of epidemic (Ahmed et al., 2020; Silver, 2020). For example, the intrinsic local community characteristics might influence and shape the spread of COVID-19, such as demographics, endemic infections, and environmental conditions. Census data availability thus leads us to model the infections, deaths, and recoveries accounting for all the epidemic data, control measures, and local information. To facilitate research in identifying the significant factors that affect the disease spread pattern and predict future infections, we also collect and combine local auxiliary information at the county level in the U.S. from reliable sources.

To help users better visualize the epidemic data, we developed multiple R shiny apps embedded into a COVID-19 dashboard launched on March 27, 2020. Currently, we provide both infectious and death maps and time series of the U.S. Moreover, we provide a short-term (7-day) forecast (Wang et al., 2020a) (updated daily) and a long-term (2-month) projection (Wang et al., 2020b) (updated weekly) of the COVID-19 infected and death count at both the county level and state level. For public usage, a Github repository (https://github.com/covid19-dashboard-us/cdcar) is established to provide daily updated and cleaned data. An R package cdcar is also created for abnormal data detection and repairing.

2 Methods

2.1 Raw Data

Thanks to the contribution of the data science communities across the world, multiple sources are providing different precision and focus of the COVID-19 data. In our article, we consider the reported cases from the following four sources: the NYT (NYT, 2020a), the Atlantic (Atlantic, 2020), the JHU
The NYT releases daily data at the country, state, and county levels at noon of the following day. The Atlantic releases daily state-level data along with testing, hospitalization, and recovered information, updated every afternoon. The COVID-19 Data Repository by the CSSE at JHU provides both state and county-level data daily, updated every night. USAFacts updates county-level data daily in early morning of the following day. Table 1 summarizes the differences among the four sources of data based on how the data are collected and compiled. For the cleaned data on the proposed repository, we first fetch data from the above four sources and compile them into the same format for further comparison and cross-validation. Then, we detect the anomalies in the data sources and choose the one with the least abnormalities to repair.

| Source          | NYT | Atlantic | JHU | USAFacts |
|-----------------|-----|----------|-----|----------|
| Infected & death* | 1,2,3 | 1,2 | 1,2,3 | 1,2,3 |
| Recovered       | 0   | 1,2      | 1   | 0        |
| Tested          | 0   | 1,2      | 2   | 0        |
| Hospitalized    | 0   | 1,2      | 0   | 0        |
| Islands**       | 2,3 | 2        | 2,3 | 0        |
| Unallocated***  | 3   | 0        | 3   | 3        |
| Place of infection*# | unknown | r,p | unknown | unknown |
| Place of fatality| r,p | r,p     | unknown | unknown |
| Probable infected## | y   | y       | y   | unknown |
| Probable death  | y   | y       | y   | y        |

Note. *: Country Level = 1, State Level = 2, County Level = 3. USAFacts only provides county level data for downloading. **: Whether the dataset includes Puerto Rico, American Samoa, Guam, Northern Mariana Islands, Virgin Islands. ***: Whether the dataset has unallocated/unassigned information, which is useful to match state-level and county-level data. #: How does the dataset assigns the cases to a place. p indicates the place of infection/fatality. r indicates the place of residence. r, p indicates both standards exist in the dataset, unknown indicates the information is not found. ##: Whether the dataset includes both confirmed and probable cases when probable data is available. y means yes. NYT releases daily live data for probable and confirmed cases separately, but historical data is unavailable.

In addition, there are two other issues, to which there is no perfect solution currently, but requires attention from the users when they try to draw conclusive statements using the COVID-19 related data.

1. **Probable versus Confirmed Cases.** Excluding the population with symptoms but not confirmed
by tests leads to the under-reporting issue of infectious counts. On April 5, 2020, the Council of State and Territorial Epidemiologists (CSTE) released an interim (Council of State and Territorial Epidemiologists, 2020) related to the COVID-19 reporting. It requires the local or state public health authority to submit a report of a condition to the Centers for Disease Control and Prevention (CDC) within 24 hours, and CDC should publish data for both “Confirmed” and “Probable” cases in the CDC Print Criteria. Before the interim was released, most of the states primarily reported confirmed cases. For the states and counties which started to report probable cases, thereafter, the count of the cases would incur an unavoidable jump after including the probable cases.

2. Antibody Test versus Virus Test. In general, there are two types of tests on infection, one is an antibody test, and the other is a virus test (also referred to as the PCR test). Unfortunately, in many datasets, the type of reported tests is not specified. The virus tested positive population is infected at the moment and suggested to be quarantined to avoid infecting others. Meanwhile, the antibody tested positive population must have been exposed to the virus, but there is no indication of whether they are still infectious or recovered (The U.S. Department of Health and Human Services, 2020). In addition, the antibody tests are known to be much less accurate. Mixing these two tests make positive cases uninterpretable. Some states and counties have started to separate antibody tests from virus tests (Madrigal and Meyer, 2020), while states such as Pennsylvania, Texas, Georgia, and Vermont did not specify the type of tests.

2.2 Comparison of the Time Series from Different Sources

In this subsection, we discuss a measure to assess the dissimilarity of the time series of the reported cases collected from different sources. Let $K$ be the number of all available sources in comparison, so for the county level comparison, $K = 3$ since the USAFacts does not have county level data, while for the state level, $K = 4$. Let $T$ be the number of days observed, or the length of each time series. Let $n$ be the number of counties or states. For source $k$, $k = 1, \ldots, K$, let $Y_{it}^{(k)}$ be the cumulative number of the reported cases of location $i$ on day $t$, where $i = 1, \ldots, n$, $t = 1, \ldots, T$. In the following, we define a dissimilarity measure to assess the difference between two time series: $Y_i^{(k)} = \{Y_{it}^{(k)}\}_{t=1}^T$ and $Y_i^{(k')} = \{Y_{it}^{(k')}\}_{t=1}^T$, for any $1 \leq k \neq k' \leq K$. Let $\overline{Y}_{it} = K^{-1} \sum_{k=1}^K Y_i^{(k)}$, then the difference between $Y_i^{(k)}$ and $Y_i^{(k')}$ is defined as:

$$d(k, k') \equiv d(Y_i^{(k)}, Y_i^{(k')}) := \begin{cases} \frac{1}{T} \| Y_i^{(k)} - Y_i^{(k')} \| / \overline{Y}_{IT}, & \overline{Y}_{IT} > 0 \\ 0, & \overline{Y}_{IT} = 0 \end{cases}$$

(1)

where $\overline{Y}_{IT}$ is used as the denominator to mitigate the variability of the current observed counts. By taking the L2-norm and dividing by the number of days observed, we obtain a measurement that effectively detects the counties and states with the most discrepancy between each pair of sources, and
also is meaningful in the comparison between different locations. In Fig. 1, we present the county map for infected and death counts collected from three different data sources. In Fig. 2 & 3, we present the state map for infected and death counts collected from four different data sources. Areas in dark blue in these three figures are detected to be different between the corresponding pair of two sources. Next, we look further into the underlying reasons for the dissimilarity at the county level and state level.

In Tables 2 and 3, for each pair of sources, we present the counties that are most dissimilar. For the state of New York, the difference between sources is caused by different geographical assignments. NYT and JHU combine Kings, Queens, Bronx, and Richmond counties with New York City while Atlantic does not perform the combination. For the state of Utah, JHU combines counties to jurisdictions to be consistent with the official state source, while NYT and Atlantic provides county level data. For the states of Michigan, Pennsylvania, and Wisconsin, the official county-level data is subject to frequent adjustments, which leads to discrepancies when one source corrects the errors while the other sources does not.

Table 2: Top 10 counties with the largest value of the dissimilarity measure of the infectious counts between pairs of sources.

| NYT vs JHU          | NYT vs Atlantic     | JHU vs Atlantic    |
|---------------------|---------------------|--------------------|
| Dukes, MA           | Valdez-Cordova, AK  | Nantucket, MA      |
| Nantucket, MA       | Wayne, IN           | Bronx, NY          |
| BoxElder, UT        | Ontonagon, MI       | Kings, NY          |
| Duchesne, UT        | Jackson, MO         | Queens, NY         |
| Garfield, UT        | Otero, NM           | Richmond, NY       |
| Kane, UT            | Bronx, NY           | Duchesne, UT       |
| Millard, UT         | Kings, NY           | Kane, UT           |
| Morgan, UT          | New York, NY        | Millard, UT        |
| Sevier, UT          | Queens, NY          | Morgan, UT         |
| Pepin, WI           | Richmond, NY        | Pepin, WI          |

Next, we look into the state level dissimilarity. According to our measure, states that show the dissimilarity from at least two pairs of sources include Georgia, Hawaii, Idaho, Indiana, Kentucky, Montana, New York, Washington, Wyoming, Nebraska, North Dakota, Pennsylvania, Texas, Vermont, and California. For state infected counts, Wyoming has the noisiest data, resulting from sources jumping significantly at different dates. This is due to the change of rule in including probable cases. Different sources make varied efforts in revising historical records. To our best knowledge, NYT traces back the longest history for the probable infected in Wyoming. In Michigan, Atlantic reports higher infectious counts in April, systematically higher than the other three sources and the state official website, which
Figure 1: County maps of the dissimilarity measure (left: infected, right: death). (a)-(b) NYT vs JHU. (c)-(d) NYT vs USAFacts. (e)-(f) JHU vs USAFacts.
Table 3: Top 10 counties with the largest value of dissimilarity measure of the death counts between pairs of sources.

| NYT vs JHU       | NYT vs Atlantic | JHU vs Atlantic |
|------------------|-----------------|-----------------|
| Crawford, IN     | Dukes, MA       | Nantucket, MA   |
| Clark, KS        | Nantucket, MA   | Antrim, MI      |
| Dukes, MA        | Allegany, NY    | Bronx, NY       |
| Allegany, NY     | Lewis, NY       | Cortland, NY    |
| Delaware, NY     | Queens, NY      | Lewis, NY       |
| Seneca, NY       | Lewis, NY       | Queens, NY      |
| Tompkins, NY     | Tompkins, NY    | Seneca, NY      |
| Davison, SD      | Davison, SD     | Dallam, TX      |
| Dallam, Texas    | Iron, UT        | Iron, UT        |
| Washington, UT   | Washington, UT  | Washington, UT  |

we think Atlantic did adjustment for a specific period. In Indiana, NYT started to report probably infected cases in late April. Therefore the infectious count of Indiana from NYT is higher than the other sources.

2.3 Abnormal Data Detection

Except for the issues mentioned above in the raw data collection, we observe three types of abnormalities in the data, including (1) order dependencies violation, (2) delayed-reported issue on weekend/holiday, and (3) abnormal data point or data period. Examples of these issues are illustrated in Fig. 4. One might need to clean and repair these issues before doing the analysis.

Order Dependencies Violation. Order dependency (OD) is widely used in the relational database. In this project, we incorporate this concept into the abnormal data detection and data repairing process of cumulative time series. To be more specific, OD for the cumulative time series can be defined as follows: for any two time points, \( t_1 \) and \( t_2 \), if \( t_1 < t_2 \), then \( Y_{t_1} \leq Y_{t_2} \), where \( Y \) represents the cumulative infectious/death count. Obviously, the time series in Fig. 4(a) violates the OD.

Weekend/Holiday Delay-Reported Issue. Weekend/holiday delay-reported issue refers to the situation significantly fewer daily new cases are reported on weekends, holidays and/or the days prior and post to those days. See Fig. 4(b) for an example. This effect is very prevalent at both the county level and state level. We use the R package seastests (function isSeasonal) \( \{\text{Ollech, 2019}\} \) to test the intra-week seasonality.

Abnormal Data Point or Data Period. A single abnormal point refers to the situation where there is one day of an abrupt increase in the cumulative time series, as shown in Fig. 4(c). This can
Figure 2: State maps of the dissimilarity measure (left: infected, right: death). (a)-(b) NYT vs JHU. (c)-(d) NYT vs USAFacts. (e)-(f) JHU vs USAFacts.

have multiple causes, including (1) the result of a large batch of tests was released; (2) the change of reporting standard, e.g., some states started to report probable cases from a specific date. Sometimes, we may experience a continuous abnormal period, referred to as the period where the increasing speed is significantly different from the previous and the subsequent period. Since this type of abnormal data could be a change of pattern in time series, we will only provide a warning message once detected. Note both the single abnormal point and the continuous abnormal period share are essentially the change point problem in time series. We apply the R package segmented (function segmented) (Muggeo, 2019) to detect the change points.

The data curation workflow is illustrated in Fig. 5. Once raw data is collected, we start with the OD violation detection and repairing. Next, we check for delay-reported issues on the weekend/holiday...
and let the user decide whether to repair it. Last, we check for the abnormal data point and data period. If an abnormal data point/period is detected, we suggest to check it manually first and then decide the method of repairing.

2.4 Abnormal Data Repairing

First of all, the infection and death count can be considered as count time series by nature. Therefore, when repairing for count time series, we need to take into account that the observations are nonnegative integers, and we should utilize the dependence structure among observations. Furthermore, in the study of the infectious disease, the population is usually assigned to compartments such as Susceptible (S), Infectious (I), or Recovered (R), and people may progress between compartments. Therefore,
Figure 4: Abnormal data characterizations. (a) Order dependency. (b) Weekend/holiday delay-reported issue. (c) Single abnormal point.

different compartments are usually considered as an entire system and studied together, for example, the SIR model (Brauer et al., 2008; Lawson et al., 2016; Pfeiffer et al., 2008). Third, the spread of the disease also has a spatial pattern. In this section, we propose data repairing methods to handle the issues mentioned in the above three categories. In this following, we summarize the background of these methods and give details on the implementation of the repairing procedure. All of these repairing procedures can be easily implemented in various areas whenever the variable is the number of events occurs observed over time, for instance, the daily number of hospital admissions, the number of stock market transactions, as well as the number of defected components from industrial engineering.

- **Time Series Model for Count Data.** One of the conventional methods to deal with these challenges is the generalized linear model (GLM), which models the observations conditionally on the past information. In this project, we consider both Poisson and Negative Binomial as the conditional distribution. The second important class for analyzing count time series is the integer autoregressive moving average (INARMA) models, and a comprehensive review is given by Weiβ (2008). State-space is another type of count time series models. Comparing with the GLM, it allows a more flexible data generating process. However, it requires a more complicated model specification. Due to the explicit formulation, the GLM-based models yield a more convenient way in predictions. Thus, in this project, we focus on the GLM-based method.

We denote $Y_t$ the infectious or death count at time $t$. To repair the dataset, we model the conditional mean $\mu_t = E(Y_t|Y_{t-1}, \mu_{t-1})$ in the following form

$$
\nu_t = \beta_0 + \sum_{k=1}^p \beta_k Y_{t-k} + \sum_{l=1}^q \alpha_l \nu_{t-l},
$$

where $\nu_t = \log(\mu_t)$. 
Figure 5: Data curation flowchart.

For this type of data repairing, we use the R package `tscount` (Liboshik et al., 2020), which conduct the model estimation by the quasi-conditional maximum likelihood method (function `tsglim`).

- **Combined Linear and Exponential Predictors (CLEP) (Altieri et al., 2020).** This method assembles the following three different models:

1. An individual county exponential predictor: model (2) uses a series of separate predictors for each county to capture the reported exponential growth of COVID-19 infectious and death counts, and we assume that

   \[ \log \{ E(Y_{i,t} | t) \} = \beta_{i0} + \beta_{i1} t, \]  

   where the parameters \( \beta_{i0} \) and \( \beta_{i1} \) are the coefficients for county \( i \) in the generalized linear model (GLM) using `glm` function in R with a Poisson link function.

2. An individual county linear predictor: model (3) fits a linear version of the separate county predictors, as shown in the following:

   \[ E(Y_{i,t} | t) = \beta_{i0} + \beta_{i1} t. \]  

3. An individual county exponential epidemic predictor: model (4) uses a series of disease related factor for each county to capture the reported exponential growth of COVID-19 infectious and death counts, and we assume that

   \[ \log \{ E(Y_{i,t} | Y_{i,t-1}) \} = \beta_{i0} + \beta_{i1} \log (Y_{i,t-1} + 1). \]
• **Spatio-Temporal Epidemic Model (STEM).** Based on the idea of the SIR models, [Wang et al. (2020c)](https://github.com/covid19-dashboard-us/cdcar) proposed the discrete-time spatial epidemic model which combines the susceptible state, infectious state, and removed state together. In the following, we denote $I_{it}$, $D_{it}$, and $R_{it}$ the count in infected, death and recovered states in location $i$ and time stamp $t$, respectively. We assume that the conditional mean value of daily new positive cases ($I_{it}$), fatal cases ($D_{it}$) and recovery ($R_{it}$) can be modeled via a link function $g$ as follows:

$$g(\mu_{I_{i,t}}) = \beta_{0I_{i,t}}(\text{lon}_i, \text{lat}_i) + \beta_{1I_{i,t}}(\text{lon}_i, \text{lat}_i) \log(I_{i,t-1}),$$

$$g(\mu_{D_{i,t}}) = \beta_{0D_{i,t}}(\text{lon}_i, \text{lat}_i) + \beta_{1D_{i,t}}(\text{lon}_i, \text{lat}_i) \log(I_{i,t-1}),$$

$$\mu_{R_{i,t}} = \beta_{0R} + \beta_{1R_{i,t}}I_{i,t-1}.$$

In practice, we use the bivariate spline over triangulation to approximate the spatially varying coefficient functions, $\beta_{0I_{i,t}}(\text{lon}_i, \text{lat}_i)$ and $\beta_{1I_{i,t}}(\text{lon}_i, \text{lat}_i)$. The triangulation can be obtained through various software packages; see for example, the Matlab code DistMesh, and the R package Triangulation ([Wang and Lai, 2019](https://github.com/covid19-dashboard-us/cdcar)). Based on a triangulation, the bivariate spline basis can be generated via the R package BPST ([Wang et al., 2019](https://github.com/covid19-dashboard-us/cdcar)). The entire estimation procedure is completed using a quasi-likelihood approach via the penalized spline approximation and an iteratively reweighted least-squares technique; see details in [Wang et al. (2020c)](https://github.com/covid19-dashboard-us/cdcar).

### 2.5 Code availability

For public usage, a Github repository at [https://github.com/covid19-dashboard-us/cdcar](https://github.com/covid19-dashboard-us/cdcar) has been established. A copy of the cleaned data set starting from January 22, 2020, has also been included in the R package cdcar. A live version of the data analysis will be continually updated on our dashboard at [https://covid19.stat.iastate.edu](https://covid19.stat.iastate.edu).

### 3 Data Records

We collect the epidemic data up to county level in the U.S. along with control measures and other local information, such as socioeconomic status, demographic characteristics, healthcare infrastructure, and other essential factors to analyze the spatiotemporal dynamic pattern of the spread of COVID-19. Our data covers about 3,200 county-equivalent areas from 50 U.S. states and the District of Columbia. The sources and introductions for these data are detailed in Table 3.

**I. Epidemic Data** The daily counts of cases and deaths of COVID-19 are crucial for understanding how this pandemic is spreading. Using the algorithm discussed in the section of methods, we aggregate the reported COVID-19 infected, death, and recovered cases from January 22, 2020 from (1) the NYT ([NYT, 2020a](https://github.com/covid19-dashboard-us/cdcar)), (2) the Atlantic ([Atlantic, 2020](https://github.com/covid19-dashboard-us/cdcar)), (3) the COVID-19 Data Repository from the JHU ([CSSE, 2020](https://github.com/covid19-dashboard-us/cdcar)), and (4) the USAFacts ([USAFacts, 2020](https://github.com/covid19-dashboard-us/cdcar)). These daily updated epidemic datasets are available on Github repository [https://github.com/covid19-dashboard-us/cdcar](https://github.com/covid19-dashboard-us/cdcar).
| Data Type                                      | Source                                                               |
|-----------------------------------------------|----------------------------------------------------------------------|
| COVID-19 Related Time-series                  |                                                                      |
| Infections Data                               | Atlantic (2020); CSSE (2020); NYT (2020a); USAFacts (2020)           |
| Fatality Data                                 |Atlantic (2020); CSSE (2020); NYT (2020a); USAFacts (2020)            |
| Recovery Data                                 | Atlantic (2020)                                                      |
| Dates of COVID-19 Related Policies            |                                                                      |
| Declarations of State Emergency               | iPoi3t3Acres (2020)                                                  |
| Shelter-in-place or Stay-at-home Order         | NYT (2020b)                                                          |
| American Community Survey (ACS) Data          |                                                                      |
| 2010-2018 Demographic and Housing Estimates   | U.S. Census Bureau (2018)                                            |
| 2005-2009 ACS 5-year Estimates                | U.S. Census Bureau (2010a)                                          |
| 2012 Economic Census                          | U.S. Census Bureau (2012)                                            |
| 2010 U.S. Decennial Census                    | U.S. Census Bureau (2010b)                                          |
| Homeland Infrastructure Foundation-level Data  | U.S. Department of Homeland Security (2020)                         |
| USA Counties Database                         | U.S. Census Bureau (2011)                                           |
| U.S. Census Bureau Gazetteer Files            | U.S. Census Bureau (2019)                                           |
In the state level epidemic data, we include the following variables. Among those variables, the variable **State** can be used as the key for data merge.

1. **State** – Name of state. There are the 48 mainland U.S. states and the District of Columbia.

2. **YYYY.MM.DD** – Cumulative infection or death cases related to the date of YYYY.MM.DD. YYYY, MM, and DD represent year, month and day, respectively. It starts from X2020.01.22. For example, the variable X2020.01.22 is either infection or death cases in a certain state (State) on 01/22/2020.

For county-level data, two more county-specific variables are included. As the key of this table, variable **ID** can be used for future data merge.

1. **ID** – County-level Federal Information Processing System (FIPS) code, which uniquely identifies the geographic area. The number has five digits, of which the first two are the FIPS code of the state to which the county belongs.

2. **County** – Name of county matched with ID. There are about 3,200 counties and county-equivalents (e.g. independent cities, parishes, boroughs) in the U.S.

3. **State** – Name of state matched with ID. There are 50 states and the District of Columbia in the U.S.

4. **YYYY.MM.DD** – Cumulative infection or death cases related to the date of YYYY.MM.DD. YYYY, MM, and DD represent year, month and day, respectively. It starts from X2020.01.22. For example, the variable X2020.01.22 is either infection or death cases in a certain (County) on 01/22/2020.

**II. Other Factors.** When analyzing the reported cases of COVID-19, many other factors may also be responsible for temporal or spatial patterns. For example, local features, like socioeconomic and demographic factors, can dramatically influence the course of the epidemic, and thus, the spread of the disease could vary dramatically across different geographical regions. Therefore, these data are also supplemented with the population information at the county level in our repository. We further classify these factors into six groups.

**II.1. State-level policy data.** To combat the coronavirus outbreak, the government introduced various control measures. Government declarations are used to identify the dates that different jurisdictions implemented various social distancing policies (emergency declarations, school closures, bans on large gatherings, limits on bars, restaurants and other public places, the deployment of severe travel restrictions, and “stay-at-home” or “shelter-in-place” orders). President Trump declared a state of emergency
on March 13, 2020, to enhance the federal government response to confront the COVID-19. By March 16, 2020, every state had made an emergency declaration. Since then, more severe social distancing actions have been taken by most of the states, especially those hardest hit by the pandemic.

Since the late April, all 50 states in the U.S. began to reopen successively, due to the immense pressures of the crippled economy and anxious public. A state is categorized as “reopening” once its stay-at-home order lifts, or once reopening is permitted in at least one primary sector (restaurants, retail stores, personal care businesses), or once reopening is permitted in a combination of smaller sectors. We compiled the dates of executive orders by checking national and state governmental websites, news articles, and press releases.

II.2. Demographic Characteristics. In the demographic characteristics category, we consider the factors describing racial, ethnic, sexual, and age structures. Specifically, we include the following six variables. Among these six variables, AA_PCT and HL_PCT are obtained from the 2010 Census (U.S. Census Bureau, 2010b). The other four variables are extracted from the 2010–2018 American Community Survey (ACS) Demographic and Housing Estimates (U.S. Census Bureau, 2018).

1. AA_PCT – The percent of the population who identify as African American;
2. HL_PCT – The percent of the population who identify as Hispanic or Latino;
3. Old_PCT – The percent of aged people (age $\geq 65$ years);
4. Sex_ratio – The ratio of male over female;
5. PD_log – The logarithm of the population density per square mile of land area;
   Pop_log – The logarithm of local population;
6. Mortality – The 5-year (1998-2002) average mortality rate, measured by the total counts of deaths per 100,000 population in a county.

II.3. Healthcare Infrastructure. We incorporated three features related to the healthcare infrastructure at the county level in the datasets. Among these variables, NHIC_PCT is available in the USA Counties Database (U.S. Census Bureau, 2011), EHPC is obtained from Economic Census 2012 (U.S. Census Bureau, 2012), and TBed is compiled from Homeland Infrastructure Foundation-level Data (U.S. Department of Homeland Security, 2020).

1. NHIC_PCT – The percent of persons under 65 years without health insurance;
2. EHPC – The local government expenditures for health per capita;
3. TBed – Total bed counts per 1,000 population.
II.4. Socioeconomic Status. We consider diverse socioeconomic factors in the county level datasets. All of these factors collected from 2005–2009 ACS 5-year estimates (U.S. Census Bureau, 2010a). We also calculate the Gini coefficient based on the household income data from the 2005–2009 ACS (U.S. Census Bureau, 2010a) to measure the income inequality.

1. Affluence – Social affluence generated by factor analysis from HighIncome, HighEducation, WCEmployment and MedHU;
2. HIncome_PCT – The percent of families with annual incomes higher than $75,000;
3. HEducation_PCT – The percent of the population aged 25 years or older with a bachelor’s degree or higher;
4. MedHU – The median value of owner-occupied housing units;
5. Disadvantage – Concentrated disadvantage obtained by factor analysis from HHD_PAIPCT, HHD_F_PCT and Unemployment_PCT;
6. HHD_PAIPCT – The percent of the households with public assistance income;
7. HHD_F_PCT – The percent of households with female householders and no husband present;
8. Unemployment_PCT – Civilian labor force unemployment rate;
9. Gini – The Gini coefficient, a measure for income inequality and wealth distribution in economics.

II.5. Environmental Factor. Another category of factors in the literature that affects the spread of epidemics significantly is the environmental factor, such as the urban rate and crime rate.

1. UrbanRate – Urban rate (U.S. Census Bureau, 2010b);
2. ViolentCrime – The total number of violent crimes per 1,000 population (U.S. Census Bureau, 2011);
3. PropertyCrime – The total number of property crimes per 1,000 population (U.S. Census Bureau, 2011);
4. ResidStability – The percent of the population residence in the same house for one year and over (U.S. Census Bureau, 2010b).

III. Geographic Information. The longitude and latitude of the geographic center for each county in the U.S. are available in Gazetteer Files from U.S. Census Bureau (2019).
Technical Validation

The entire detection and repairing procedure is illustrated in Figure 5. First of all, we obtained the data from all of the four data sources, and use the dissimilarity measure proposed in the above to compare them. We visualize and check the difference at the state level among different data sources based on the comparison results. For the county-level data, we calculate the measure and reported the top 10 counties, which are the most different pairwisely. Then, all the data are processed with all types of abnormal detection discussed in the section of abnormal data detection. Once an abnormality has been detected, a warning will be given automatically by R package cdcar. We handle the abnormal data differently depending on the type of problem. For example, if an order dependency violation is detected, we will repair that point using our data repairing algorithms. If a single abnormal point is detected, we first manually check possible legitimate reasons based on news and social media. If no such information can be found, we will repair the point using the proposed algorithm.

Usage Notes

The integrated data are publicly available to assist researchers to investigate the spread of COVID-19 in the U.S. We will continue to provide the cleaned data as the pandemic progresses. Both the R package and the datasets discussed in this article is hosted on our GitHub repository: https://github.com/covid19-dashboard-us/cdcar.

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Author contributions

L.G., X.L. and Z.G. collected the data. G.W., X.L., Y.S., M.K., Y.W., L.W. L.G. analyzed the data and explained the results. G.W., Y.S. and Z.G. prepared the R programming. All authors contributed to writing and editing the manuscript. L.W. supervised the project.
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